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OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:59:47 ; Search time 2944.03 Seconds

(Without alignments)
16933.650 Million cell updates/sec

Title: US-09-776-910-1

Perfect score: 1713

Sequence: 1 atgaattcaacgttagtt.....aacatagagatttatttg 1713

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3:  gb.in:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1713	100.0	1713	6	ARI53438
2	1711.4	99.9	1713	6	ARI53442
3	1709.8	99.8	1713	6	ARI53439
4	1706.6	99.6	1713	6	ARI53440
5	1701.8	99.3	1713	6	AR062837
6	1701.8	99.3	1713	6	ARI53441
7	1701.8	99.3	2240	3	LC063636
8	1676.6	97.9	1713	6	AR062838
9	987.2	57.6	2160	3	AF133341
10	959.4	56.0	2175	3	AF139082
11	956.6	55.8	1710	6	ARI53445
12	677.2	39.5	2017	3	AY051473
13	378.6	22.1	2660	3	AY121675
14	373.8	21.8	2820	3	DMU51050
15	369	21.5	57335	2	AC015272
16	369	21.5	188459	3	AC008312
17	369	21.5	197597	3	AC011253
18	369	21.5	309023	3	AE003671
19	365.4	21.3	1962	3	AY051497
20	323	18.9	2122	3	AY058637
21	303	17.7	1906	3	AY058345
22	300.4	17.5	13044	2	AC014297
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25	300.4	17.5	307363	3	AE003457
26	286.6	16.7	2050	3	AF216210
27	278.4	16.3	1205	3	AF216215
28	269.6	15.7	1809	6	AX260182
29	242	14.1	3946	3	DMU51044
30	241.4	14.1	1630	3	COESTRA2EA
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32	239.8	14.0	188459	3	AC008312
33	239.8	14.0	197597	3	AC011253
34	239.8	14.0	309023	3	AE003671
35	229.6	13.4	1724	3	AY069743
36	227.6	13.3	2401	3	DMU51054
37	224.2	13.1	933	3	AF216216
38	224.2	13.1	1836	3	COSERE51
39	224	13.1	3447	3	DMU51052
40	219.2	12.8	1630	3	COSERE52
41	214	12.5	84252	2	AC009207
42	212	12.4	1401	3	CPU43544
43	207.4	12.1	6028	3	AF177382
44	204.8	12.0	1401	3	CPU43546
45	199.8	11.7	1401	3	CPU43545

ALIGNMENTS

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RESULT 1
LOCUS      ARI53438
DEFINITION Sequence 1 from patent US 6235515.
ACCESSION  ARI53438
VERSION    ARI53438.1 GI:15120970
KEYWORDS
SOURCE
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 1713)
AUTHORS   Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
            Robin,G.Charlesde.,Quetteville.,Clandianos,C., Smyth,K.A.,
            Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
TITLE      Malathion carboxylesterase
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JOURNL	Patent: US 6252515-A 1 22-MAY-2001
FEATURES	Location/Qualifiers
SOURCE	1. 1713
	/organism="unknown"
BASE COUNT	515 a 304 c 370 g 524
ORIGIN	

Query Match	100.0%	Score 1713;	DB 6;	Length 1713;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1713;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

Oy	1	ATGAATTTCAACGGTAGTTGATGAGCAAAATTTAAATGCAAGATTTAAATGATTTGAAAT	60
Db	1	ATGAATTTCAACGGTAGTTGATGAGCAAAATTTAAATGCAAGATTTAAATGATTTGAAAT	60
Oy	61	AAATTTTAAACTATCGTTTAACATACCAATGAACGGTGGTAGCTGAACATGAATATGCG	120
Db	61	AAATTTTAAACTATCGTTTAACTACCAATGAACGGTGGTAGCTGAACATGAATATGCG	120
Oy	121	AAAGTGAAGAGCGCTTAAACGTTTAACGTGTACGATGATTCCTATACATACGATTTTGAGGG	180
Db	121	AAAGTGAAGAGCGCTTAAACGTTTAACGTGTACGATGATTCCTATACATACGATTTTGAGGG	180
Oy	181	ATACCGTACGGCCAAACCGCCACAGTGGTGAAGTGAATTTAAAGCACCCACGACCAACA	240
Db	181	ATACCGTACGGCCAAACCGCCACAGTGGTGAAGTGAATTTAAAGCACCCACGACCAACA	240
Oy	241	CCCTGGGATGGTGTGCGGTGATTTGGCAATCATATAAATATAGTCAGTCAGTGTGATTTT	300
Db	241	CCCTGGGATGGTGTGCGGTGATTTGGCAATCATATAAATATAGTCAGTCAGTGTGATTTT	300
Oy	301	ATTAACGGGCAAAAGTGTGGCTCAGAGAGATGTCTATACCTAAGTGTCTATACGAAATAT	360
Db	301	ATTAACGGGCAAAAGTGTGGCTCAGAGAGATGTCTATACCTAAGTGTCTATACGAAATAT	360
Oy	361	CTTAATCCCGAAACTAAACGTCGCCGTTTAACTATACATACATGCTGTGTTTATTATC	420
Db	361	CTTAATCCCGAAACTAAACGTCGCCGTTTAACTATACATACATGCTGTGTTTATTATC	420
Oy	421	GGTGAATAATCATCGTGATATGTATGTGCTCCATATTTCATTAATAAAGATGTGGCTTG	480
Db	421	GGTGAATAATCATCGTGATATGTATGTGCTCCATATTTCATTAATAAAGATGTGGCTTG	480
Oy	481	ATTAACATATCAATATCGTTTGGAGGCTTAGTGTTCATAGTTTAAATTCAGAAGACCTT	540
Db	481	ATTAACATATCAATATCGTTTGGAGGCTTAGTGTTCATAGTTTAAATTCAGAAGACCTT	540
Oy	541	AAATGTCGCCGGTAATGCGCGCTTAAAGATCAAGTCATGCGCTTGCGTTGGATTAAAT	600
Db	541	AAATGTCGCCGGTAATGCGCGCTTAAAGATCAAGTCATGCGCTTGCGTTGGATTAAAT	600
Oy	601	AAATGGGCAACATTTGTGTGGCAATCCGATATATTAACAGCTTTGGGAAAGTGGCGGT	660
Db	601	AAATGGGCAACATTTGTGTGGCAATCCGATATATTAACAGCTTTGGGAAAGTGGCGGT	660
Oy	661	GCTGCGCTACCCACATACATGATGTTTAAACGGAACAACTCGCGCTCTTTCATCGTGGT	720
Db	661	GCTGCGCTACCCACATACATGATGTTTAAACGGAACAACTCGCGCTCTTTCATCGTGGT	720
Oy	721	ATATCTAATGTGGGTAAATGCTATTTGTGCATTTGGCTATATACCCAATGTCAACATCGTGC	780
Db	721	ATATCTAATGTGGGTAAATGCTATTTGTGCATTTGGCTATATACCCAATGTCAACATCGTGC	780
Oy	781	TTTACCTTATGCAAAATTTGGCGCGCTATTAAGGGTGAAGTAATGATAGAGATGTTTGGAA	840
Db	781	TTTACCTTATGCAAAATTTGGCGCGCTATTAAGGGTGAAGTAATGATAGAGATGTTTGGAA	840
Oy	841	TTTTCTTATGAAGCCAAAGCCACAGATTTTAAATTAACCTTGAGGAAAAAGTTTAACTCTA	900
Db	841	TTTTCTTATGAAGCCAAAGCCACAGATTTTAAATTAACCTTGAGGAAAAAGTTTAACTCTA	900
Oy	901	GAAGACGTACAATTAAGTCAATGTTTCTTTGGTCCCACTGTGAGCATATCAAGACC	960
Db	901	GAAGACGTACAATTAAGTCAATGTTTCTTTGGTCCCACTGTGAGCATATCAAGACC	960

Dd	901	GAAGAGCGTACAAATTAAGTCATGTTTCCTTTTGGTCCACCTGTGAGGCATATACAGACC	960
Qy	961	GCTGATTTGTCTTAACCCAAACATCTCGGGAATTCGTTAAACTGCTTGGGGTAATTCG	1020
Dd	961	GCTGATTTGTCTTAACCCAAACATCTCGGGAATTCGTTAAACTGCTTGGGGTAATTCG	1020
Qy	1021	ATACCCACTATGATGGGTAAACATTTCAATAGAGGTCTATTTTCACCTCAATCTTAAG	1080
Dd	1021	ATACCCACTATGATGGGTAAACATTTCAATAGAGGTCTATTTTCACCTCAATCTTAAG	1080
Qy	1081	CAAAATGCGCTATGCTTTGTTAAGGAATTTGGAACCTGTGCAATTTTGTGCCAAGTAATG	1140
Dd	1081	CAAAATGCGCTATGCTTTGTTAAGGAATTTGGAACCTGTGCAATTTTGTGCCAAGTAATG	1140
Qy	1141	GCTGATGTTGAACGACGCCGCCACAGACCTTTGCAAAATGGTGCTAAATTTAAAAAGCT	1200
Dd	1141	GCTGATGTTGAACGACGCCGCCACAGACCTTTGCAAAATGGTGCTAAATTTAAAAAGCT	1200
Qy	1201	CATGTTACAGGAANACACACACCTGATTAATTTATGATACCTTGGCTGCACATCAT	1260
Dd	1201	CATGTTACAGGAANACACACACCTGATTAATTTATGATACCTTGGCTGCACATCAT	1260
Qy	1261	TTCTGTTGCCCATGCATCGTTTGTGTGAATTTACGTTTCAATCACACCTCCGGTACACC	1320
Dd	1261	TTCTGTTGCCCATGCATCGTTTGTGTGAATTTACGTTTCAATCACACCTCCGGTACACC	1320
Qy	1321	GTCTACTGTTATTCGCTTGACACTTGATTCGGGAAGATCTTATCAATCCCTATCGATTAATG	1380
Dd	1321	GTCTACTGTTATTCGCTTGACACTTGATTCGGGAAGATCTTATCAATCCCTATCGATTAATG	1380
Qy	1381	CGTAGTGAAGCGTGGTGTAAAGGTGTATAGTCATCGCTGAATTAACCTATTTTCTTCGG	1440
Dd	1381	CGTAGTGAAGCGTGGTGTAAAGGTGTATAGTCATCGCTGAATTAACCTATTTTCTTCGG	1440
Qy	1441	AATCAATTTGGCCAAACGTAATGCTTAAGAAGTGCGTGAATACAAAACAATTTGAACGTAATG	1500
Dd	1441	AATCAATTTGGCCAAACGTAATGCTTAAGAAGTGCGTGAATACAAAACAATTTGAACGTAATG	1500
Qy	1501	ACTGTATATATGATATACAAATTTGCCACACCTGTAATCCTTATAGCAATGAATTTGAAGST	1560
Dd	1501	ACTGTATATATGATATACAAATTTGCCACACCTGTAATCCTTATAGCAATGAATTTGAAGST	1560
Qy	1561	ATGGAATAATGTTTCCCTGGGATCCCAATTTAAGAAATCGATGAGGTATACAAAGCTTTGAAT	1620
Dd	1561	ATGGAATAATGTTTCCCTGGGATCCCAATTTAAGAAATCGATGAGGTATACAAAGCTTTGAAT	1620
Qy	1621	ATTAGTGAATGAATTTGAAAAATGATGATGCTTGAATGATTAACATTTGAATTTGGAG	1680
Dd	1621	ATTAGTGAATGAATTTGAAAAATGATGATGCTTGAATGATTAACATTTGAATTTGGAG	1680
Qy	1681	TGCATGTTTGAATAACATAGAGATTTATTTTGA 1713	
Dd	1681	TGCATGTTTGAATAACATAGAGATTTATTTTGA 1713	

RESULT 2	AR153442	1713 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR153442				
DEFINITION	Sequence 9 from patent US 6235515.				
ACCESSION	AR153442				
VERSION	AR153442.1	GI:15120974			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1713)				
	Russell, R., Joyce., Newcomb, R., David., Campbell, P., Malcolm.,				
	Robin, G., Charlede., Quetteville., Claudianos, C., Smyth, K., A.,				
	Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Collin.				
	Malachion carboxylesterase				
	Patent: US 6235515-A 9 22-MAY-2001.				
TITLE					
JOURNAL					
FEATURES	Location/Qualifiers				
source	1..1713				


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BASE COUNT      515 a      305 c      370 g      523 t
ORIGIN          /organism="unknown"

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Query Match	99.98;	Score 1711.4;	DB 6;	Length 1713;
Best Local Similarity	99.98;	Pred. No. 0;		
Matches 1712; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

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Db	1	ATGAAATTTCAACGCTTACTGTTGATGGAGAAATTTAAATGGAGAGTTTAAATGCATTTGAAAT	60
OY	61	AAATTTTAAACATATCGCTTTAACTACCAATGAAGAACCGGTGTAAGTGAACATGAATATGAC	120
Db	61	AAATTTTAAACATATCGCTTTAACTACCAATGAAGAACCGGTGTAAGTGAACATGAATATGAC	120
OY	121	AAAGTGAAGGCGCTTAAACGTTTAACTGTGTACGATGATCTCTACTACAGTTTGAAGGT	180
Db	121	AAAGTGAAGGCGCTTAAACGTTTAACTGTGTACGATGATCTCTACTACAGTTTGAAGGT	180
OY	181	ATACCGTAGCGCCCAACCGCCAGTGGGGAGCTGAGATTTAAAGCAACCCGACGACCAACA	240
Db	181	ATACCGTAGCGCCCAACCGCCAGTGGGGAGCTGAGATTTAAAGCAACCCGACGACCAACA	240
OY	241	CCCTGGGATGGTGTGCGCTGATTTGTCAATCATATAAGATTAAGTCAGTCGCAAGTTGATTT	300
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Db	601	AATGTGCCCAATTTGGTGGCAATCCCGATATATTACAGCTCTTGGTGAAAGTCCCGGT	660
OY	661	GCTGCTCTACCCACTCATGATGATTTAACGAAACAATCGGGGTCTTTTCCATGCTGCT	720
Db	661	GCTGCTCTCTACCCACTCATGATGATTTAACGAAACAATCGGGGTCTTTTCCATGCTGCT	720
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Db	781	TTACACCTTAGGCAAAATTTGGCGGCTATTAAGGGTGAGAGATTAATGATTAAGATGTTTGGAA	840
OY	841	TTTCTTATGAAGGCCACAGCATATTAATAAACTTGAGGAAAAAGTTTAACTCTA	900
Db	841	TTTCTTATGAAGGCCACAGCATATTAATAAACTTGAGGAAAAAGTTTAACTCTA	900
OY	901	GAAAGCGGTACAATTAAGTCATGTTTCCCTTTTGGTCCCACTGTGTGAGGCATATACAGAC	960
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Db	961	GCTATGTGTCTTACCCAAACATCCTCGGGAATGTTAAACAGCTTGGGTAATTCG	1020
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Db	1021	ATACCACACTATGATGGGTAAACACTTCATATGAGGGTCTATTTTTCACCTTCAATTCCTTAAG	1080
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Db	1081	CAATGCCATGCTGTGTTAAGAATTTGGAACCTGTGTCAATTTTGTGCCAAGTAATTG	1140
QY	1141	GCTATGTGTAAAGCAACCGCCGCCAGACCTTGGAAATGGGTCTAAATTTAAAGGCT	1200
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QY	1201	CATGTTACAGAGAAACACCAACAGCTGATATTTATGATGCTTGGCTCACATCAT	1260
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QY	1561	ATGGAATAATGTTCTCTCGGATCCCAATTTAAGAAATCCGATGAAGATATACAAGTGTATGAT	1620
Db	1561	ATGGAATAATGTTCTCTCGGATCCCAATTTAAGAAATCCGATGAAGATATACAAGTGTATGAT	1620
QY	1621	ATTAGTGATGATTTGAAATATGATTTGATGTGCTCGAAATGGATTAAGATTTAAACAATGGAG	1680
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QY	1681	TCGATGTTTGAANAACATAGAGATTAATTTTATG	1713
Db	1681	TCGATGTTTGAANAACATAGAGATTAATTTTATG	1713

RESULT 3						
ARI53439						
LOCUS	ARI53439	1713 bp	DNA	Linear	PAT 08-AUG-2001	
DEFINITION	Sequence 3 from patent US 6235515.					
ACCESSION	ARI53439					
VERSION	ARI53439.1	GI:15120971				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 1713)					
	Russell,R.Joyce, Newcomb,R.David, Campbell,P.Malcolm,Roblin,G.Charlesde.QUetteville, Cladianos,C., Smyth,K.A.,Boyce,T.Mark, Oakeshott,J.Graham, and Brownlie,J.Colin.					
TITLE	Malathion carboxylesterase					
JOURNAL	Patent: US 6235515-A 3 22-MAY-2001;					
FEATURES	Location/Qualifiers					
SOURCE	1..1713					
	/organism="unknown"					
BASE COUNT	515 a	306 c	370 g	522 t		
ORIGIN						

Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAAGAGATTAAATGATGAATGAAT 60
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Db 61 AAGTTTTTAACTATCGTTTAACTACCAATGAAACGGTGTAGCTGAAGTAATATGCG 120
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Db 121 AAAGTGAAGGCGTTTAAAGCTTTAACTGTACGATGATGCTTCTACTACAGTTTGAGGGT 180
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LOCUS AR062837
DEFINITION Sequence 1 from patent US 5843758.
ACCESSION AR062837
VERSION AR062837.1 GI:5990528
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.Joyce., Newcomb,R.David., Robin,G.Charlesde.Quetteville.,
Boyce,T.Mark., Campbell,P.Malcolm., Oakeshott,J.Graham. and Smyth,K.A.
TITLE Enzyme based bioremediation
JOURNAL Patent: US 5843758-A 1 01-DEC-1998;
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source location/Qualifiers
1..1713
BASE COUNT 516 a 305 c 370 g 522 t
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Query Match 99.3%; Score 1701.8; DB 6; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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RESULT 6
LOCUS AR153441 1713 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6235515.
ACCESSION AR153441
VERSION AR153441.1 GI:15120973
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Roblin, G. Charlesde-Quetleville., Claudiolos, C., Smyth, K. -A.,
Boyce, T. Mark., Oakesholt, J. Graham. and Brownlie, J. Colin.
TITLE Malathion carboxylesterase
JOURNAL Patent: US 6235515-A 7 22-MAY-2001;
FEATURES
source location/Qualifiers
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BASE COUNT 516 a 305 c 370 g 522 t
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Best Local Similarity Pred. No. 0;
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 ACCESSION
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 Oestroidea; Calliphoridae; Lucilia.
 1 (bases 1 to 2240)
 Newcomb,R.D., East,P.D., Russell,R.J. and Oakeshott,J.G.
 Isolation of alpha cluster esterase genes associated with
 organophosphate resistance in Lucilia cuprina
 Insect Mol. Biol. 5 (3), 211-216 (1996)
 JOURNAL
 MEDLINE
 PUBMED
 879740
 2 (bases 1 to 2240)
 Newcomb,R.D., Campbell,P.M., Russell,R.J. and Oakeshott,J.G.
 cDNA cloning, baculovirus-expression and kinetic properties of the
 esterase, E3, involved in organophosphorus resistance in Lucilia
 cuprina
 Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)
 JOURNAL
 MEDLINE
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 9061925
 3 (bases 1 to 2240)
 Newcomb,R.D., Campbell,P.M., Ollis,D.L., Cheah,E., Russell,R.J. and
 Oakeshott,J.G.
 A single amino acid substitution converts a carboxylesterase to an
 organophosphorus hydrolase and confers insecticide resistance on a

blowfly
Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997)
MEDLINE
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PUBMED
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AUTHORS
TITLE
4 (bases 1 to 2240)
Campbell, P.M., Newcomb, R.D., Russell, R.J. and Oakeshott, J.G.
Two different amino acid substitutions in the *alpha*-esterase, E3,
confer alternative types of organophosphorus insecticide resistance
in the sheep blowfly
Unpublished
5 (bases 1 to 2240)
Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
Direct Submission
Submitted (24-Apr-1996) Richard D. Newcomb, Molecular Genetics,
HortResearch, Private Bag 92 169, Auckland, New Zealand
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ACCESSION AR062838
VERSION AR062838.1 GI:5990529
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 1713)
Boyce, T. Mark, Campbell, P. Malcolm, Parker, A. Gerard, Oakeshott, J. Graham, and Smyth, K. A.
Enzyme based bioremediation
Patent: US 5843758-A 2 01-DEC-1998;
LOCATION/Qualifiers
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BASE COUNT 506 a 299 c 363 g 515 t 30 others
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 VERSION ARI53445.1 GI:15120977
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 ORGANISM Unknown.
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 AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
 Robin, G. Charlesde, Queteville., Claudiano, C., Smyth, K., A.,
 Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin.
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 JOURNAL Patent: US 6235515-A 14 22-MAY-2001;
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 AY051473
 DEFINITION
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 AY051473
 ACCESSION
 VERSION
 KEYWORDS
 FIL:CDNA.
 SOURCE
 ORGANISM
 Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 2017)
 AUTHORS
 Stapleton,M., Brokslein,P., Hong,L., Agbayani,A., Carlson,J.,
 Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R.,
 Gonzalez,M., Guarin,H., Li,P., Liao,G., Miranda,A., Mungall,C.J.,
 Nuno,J., Pacle,J., Paragas,V., Park,S., Phouanavong,S., Wan,K.,
 Yu,C., Lewis,S.E., Rubin,G.M. and Celisner,S.
 TITLE
 JOURNAL
 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA
 COMMENT
 Sequence submitted by:
 Lawrence Berkeley National Genome Project
 Berkeley Drosophila National Laboratory
 Berkeley, CA 94720
 This clone was sequenced as part of a high-throughput process to
 sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
 Science 2000). The sequence has been subjected to integrity checks
 for sequence accuracy, presence of a polyA tail and contiguity
 within 100 kb in the genome. Thus we believe the sequence to
 reflect accurately this particular cDNA clone. However, there are
 artifacts associated with the generation of cDNA clones that may
 have not been detected in our initial analyses such as internal
 priming, priming from contaminating genomic DNA, retained introns
 due to reverse transcription of unspliced precursor RNAs, and
 reverse transcriptase errors that result in single base changes.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our web site
 (<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.
 FEATURES
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BASE COUNT 522 a 487 c 519 g 489 t
ORIGIN

Query Match 39.5% Score 677.2; DB 3; Length 2017;
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Matches 1073; Conservative 0; Mismatches 638; Indels 3; Gaps 1;

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QY 1678 GAGTGTATGTTGAAACATGAGATTTATTTT 1711
DB 1771 GAGAGCTCTATGAGACAAACAAAGATTTATTTGT 1804

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DEFINITION	Drosophila melanogaster RE24825 full insert cDNA.			
ACCESSION	AY121675			
VERSION	AY121675.1	GI:21464397		
KEYWORDS	FIL CNA.			
SOURCE	fruit fly,			
ORGANISM	drosophila melanogaster			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
AUTHORS	Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 2660) Stratton,M., Brokstein,P., Hong,L., Abmayri,A., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Dresnek,D., Fafan,D., Frise,E., George,R., Gonzalez,M., Guarn,H., Krommiller,B., Li,P., Liao,G., Miranda,A., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas.V., Park,S., Patel,S., Phouenavong,S., Wan,K., Yu.C., Lewis,S.E., Rubin.G.M. and Celisler.S.			
TITLE	Direct Submission Submitted (13-JUN-2002) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA			
JOURNAL	Sequence submitted by: Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Berkeley, CA 94720			
COMMENT	This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection I (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and configity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fullyfly.berkeley.edu) or send email to: cna@fullyfly.berkeley.edu .			
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ORIGIN				


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Matches 1054:  Conservative 0:  Mismatches 612:  Indels 263:  Gaps

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DEFINITION	Drosophila melanogaster, ***	SEQUENCING IN PROGRESS	***	in ordered	

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VERSION	AC015272.1
KEYWORDS	HTG; HTGS_PHASE2.
SOURCE	Drosophila melanogaster

ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE	1 (bases 1 to 57335)
AUTHORS	Adams, M. and Venter, J.C.

TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive

Rockville, MD, USA
This sequence was identified as CDM:10213452 by the submitter.

For further information on this sequence e-mail to fly@celera.com
 * NOTE: This is a 'working draft' sequence.

- * This sequence will be replaced
- * by the finished sequence as soon as it is available and
- * the accession number will be preserved.

FEATURES	Location/Qualifiers
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QY 501 GGGAGCTCT----- 509
Db 35941 TGGGGCTTTGGGTATCTACTGTGTGCTATGCCAATATTTTGACTAATCATTTGTA 35882
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Db 35881 CCTACACAGGATTTATGATCTTAACTCCCGAGCTAAATGTACCGAGAAATCTGCGC 35822
QY 563 TTAAGATCAAGTCATGCGCTTGGCTTGAATTAATAATTTGCGCAACTTTGTGCA 622
Db 35821 TCAAGATCAAGTCGTGCGCTCAAGTGAATCAAGAACAAATTTGGCTAGTTTGGCGGAG 35762
QY 623 ATCCGATATATTTACAGTCTTTGTGAAGTCCGCTGCTGCTTACCCACTACATGA 682
Db 35761 ATCCCAATCCTACCTGTTTTTGGAGAGATGCTGGAGGCGCTCCACTACATCACTA 35702
QY 683 TGTAAACCGAACAACCTGCGGCTTTTCCATGCTGATATCTAATGTCGGGTAACTGA 742
Db 35701 TGTAAACCGAACAACCGGCTTTTCCATGCTGATATCTAATGTCGGGTAACTGA 742
QY 743 TTTGTCATTGGC---TAATACCAATGTCACATCGTGCCTTACCTTACCCAAATTTG 799
Db 35641 TTTGTCATTGGCCTTACCAAGGCGACATATACCAATGTCGGGTAACTGA 35582
QY 800 CCGGCTTAAGGGGATGATTAAGATGTTTGAATTTCTATTAAGAACCAAGC 859
Db 35581 TTTGCTCAAGGGGATGATTAAGATGTTTGAATTTCTATTAAGAACCAAGC 859
QY 860 CACAGATTTAATAAAGTTGAGGAAAGTTTAACTAGAGAGAGCTACAAATTAAG 919
Db 35521 CCAAGGATTTAATTCGCGTGAAGAAATGCTGACACTGAGAGAGAGATGAACAGA 35462
QY 920 TCAATGTTCTTTTGGCCCACTGTGAGCATATGACCGCTGATGTGCTTACCA 979
Db 35461 TCAATGTTCTTTTGGCCCACTGTGAGCATATGACCGCTGATGTGCTTACCA 979
QY 980 AACATCCTCGGAAATGTTAAACTGCTTGGGGTAAATGATACCAATGATGATG 1039
Db 35401 AGCCTCAAGAGATGATGAACGCGCTGAGTAACTCATCCCATGTTATAGGA 35342
QY 1040 ACACTTCATATGAGGCTCT----- 1058
Db 35341 ACACTTCATATGAGGCTCT----- 1058
QY 1059 -----ATTTTCACTCAATTTCTAAGCAATGCTATGCTGT 1097
Db 35281 TTTCTTCAATTAATTAATTTATTTTACAGAGATTAAGCTTATGCGCAGGCTGT 35222
QY 1098 TAAGAAATTTGAACCTTGTCTCAATTTTGTCCAAAGTGAATGCTGATTTGAACGAC 1157
Db 35221 GACGAGCTTGTATGTCGACACCTTTCAATTCACAAAGATTTGCTGCGCAGGACG 35162
QY 1158 CGGCCAGAGACTTGGAAATGGGCTCAATTAATAAGGCTCATGTTACAGAGAAAC 1217
Db 35161 TAAAGAAAGATGATGCTGAGATGACAGATTCAGATGTCATGCACTGCTCAGA 35102
QY 1218 ACCAAGAGCTGATATTTATGAT----- 1242
Db 35101 AACGACCCAGATTAATTAATGATGATTAAGTGTCTCAATTAAGTGTCTTACATTAATCAT 35042
QY 1243 -----CTTGTCTTCACATCTAATTTCTGTTTCCCATGATGCTT 1282

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Db 35041 AAGCTGTAATTTATTTACAGTCTGTTTCGATTTTCTACTTCTGTTTCCGCGCTGAGG 34982
QY 1283 TGTTCATTAATGCTTTCAATCACACCTCCGATACACCGGCTTACTGTATGCTTGCAT 1342
Db 34981 TGTTCATTTCCGACACGCGATGACGCGGTGAGCTCCAGTATTTCTATGATATGAT 34922
QY 1343 TCGATTTGGAAGATCTATCATATCCATATGATATATGCGTATGAGAGAGCTGTAAAG 1402
Db 34921 TCGATTTGGAAGATCTATTTTCTGATGATGATGATGATGATGATGATGATGATGATG 34862
QY 1403 GTGTTAGTATGCTGATGATTAATTAATTTCTTCTGAAATCAATTTGCCAAAGCTATG 1462
Db 34861 GGTTCAGCATGCGGAGATTTGAGTACCAATTTACAGACGCTGCTGCGCGGCTTGC 34802
QY 1463 CTAAAGATGCGGCTGATATACAAACAATTTAGCTATGATGATGATGATGATGATG 1522
Db 34801 CGAAGGAAGTCCGAGATACAGGAACATCGAACCAACCGTGGGCTATGAGCCAGTTG 34742
QY 1523 CCACCACTGATATCTTATAGCAATGAATTTGAAGTATGAGAAATGTTTCTGCGGATC 1582
Db 34741 CTGCGACGAGTAACTTCTACAGGAGAGATCAACGATATGACACTCTGACATTTGATC 34682
QY 1583 CAATTTAAGAAATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1642
Db 34681 CAGTTCCCAATCCGAGAGGTATCAAGTGTCTCAACATCAGTATGATGATGATGATGATG 34622
QY 1643 TTTGATGCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1702
Db 34621 TCGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 34562
QY 1703 ATTTATTT 1711
Db 34561 ATTTATTT 34553

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Search completed: April 11, 2003, 06:01:19
 Job time : 3017.03 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:58:21 ; Search time 246.905 Seconds

15624.094 Million cell updates/sec

Title: US-09-776-910-1

Sequence: 1 atgaattccaacgttagttt.....aacatagagatttatttag 1713

Scoring table: IDENTITY_NUC

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
1	1701.8	99.3	1713	16	AAO91561		OP-sensitive estere
2	1701.8	99.3	1713	18	AAI68596		Ic-alpha-E7 malath
3	1681	97.9	1713	16	AAO91566		OP-resistant estere
4	1677.8	97.9	1713	16	AAO91564		OP-resistant estere
5	1677.8	97.9	1713	16	AAO91563		OP-resistant estere
6	1676.2	97.9	1713	16	AAO91565		OP-resistant estere
7	1674.6	97.8	1713	16	AAO91562		OP-resistant estere
8	956.6	55.8	1710	18	AAI68597		Mk-alpha-E7 gene.
9	677.2	39.5	2001	23	AB102067		Drosophila melanog

10	381.8	22.3	1704	23	ABLO2081	Drosophila melanog
11	369	21.5	6175	23	ABLO2086	Drosophila melanog
12	368.2	21.5	1665	23	ABLO2099	Drosophila melanog
13	365.4	21.3	1792	23	ABLO4689	Drosophila melanog
14	323.2	18.9	1593	23	ABLO2103	Drosophila melanog
15	323	18.9	1861	23	ABLO1859	Drosophila melanog
16	311.4	18.2	1791	23	ABLO1033	Drosophila melanog
17	305.8	17.9	1719	23	ABLO2107	Drosophila melanog
18	303	17.7	1878	23	ABLO1947	Drosophila melanog
19	300.4	17.5	3856	23	ABLO1032	Drosophila melanog
20	300.4	17.5	67279	23	ABLO7668	Drosophila melanog
21	269.6	15.7	1809	24	ABAS9060	Drosophila melanog
22	239.8	14.0	4320	23	ABLO4688	Drosophila cell cy
23	229.6	13.4	1727	23	ABLO1943	Drosophila melanog
24	228.6	13.3	4242	23	ABLO2102	Drosophila melanog
25	224	13.1	5008	23	ABLO2080	Drosophila melanog
26	198.8	11.6	4294	23	ABLO2098	Drosophila melanog
27	198.8	11.6	4294	23	ABLO2100	Drosophila melanog
28	197.6	11.5	1987	19	AAV0762	C. fellis esterase
29	197.6	11.5	1987	19	AAV0763	C. fellis esterase
30	193.2	11.3	2613	23	ABLI9064	Drosophila melanog
31	192	11.2	1626	23	ABLO1945	Drosophila melanog
32	191.8	11.2	5132	23	ABLO1858	Drosophila melanog
33	187.4	10.9	1590	19	AAV0764	C. fellis esterase
34	187.4	10.9	1590	19	AAV0765	C. fellis esterase
35	179.6	10.5	1540	19	AAV0756	C. fellis esterase
36	179.6	10.5	1584	19	AAV0757	C. fellis esterase
37	179.6	10.5	2007	19	AAV0754	C. fellis esterase
38	179.6	10.5	2007	19	AAV0755	C. fellis esterase
39	179.6	10.5	2007	22	AAV0756	Ctenocephalides fel
40	167.6	9.8	4288	23	ABLO1942	Drosophila melanog
41	162.6	9.5	1783	23	ABLO2029	Drosophila melanog
42	148	8.6	4283	23	ABLO1946	Drosophila melanog
43	142.2	8.3	1488	19	AAV0767	C. fellis esterase
44	142.2	8.3	1590	23	AAV0743	C. fellis esterase
45	142.2	8.3	1590	22	AAV0743	Ctenocephalides fel

ALIGNMENTS

RESULT 1	
AA091561	
ID	AA091561 standard; CDNA; 1713 BP.
XX	
AC	AA091561;
XX	
DT	22-DEC-1995 (first entry)
XX	
DE	OP-sensitive esterase E3 Lc743 clone.
XX	
KW	Esterase; E3: bioremediation; organophosphate; carlinic
KW	insecticide; pesticide; water decontamination; meat
KW	ss.
XX	
OS	Lucilia cuprina.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
XX	1..1713
XX	/*tag= a
PN	W09519440-A1.
XX	
PD	20-JUL-1995.
XX	
PF	13-JAN-1995; 95WO-AU00016.
XX	
PR	13-JAN-1994; 94AU-000347.
XX	
PA	(CSTR) COMMONWEALTH SCI & IND RES ORG.
PI	Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG,
P1	Parker AG, Roblin GC, Russell RJ, Smyth K;

XX WI: 1995-263870/34.
 DR P-PSDB; AAR78142.
 XX
 PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organo-phosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 PS Claim 5; Page 12-17; 38pp; English.
 XX
 CC cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa. cDNA
 CC library was amplified using cluster-specific esterase primers.
 CC Isolated clone Lc743, a probable full-length cDNA, was expressed
 CC using a baculovirus vector in insect cells and shown to encode
 CC an OP-susceptible E3 esterase, useful in bioremediation.
 XX
 SQ Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;

Query Match 99.3%; Score 1701.8; DB 16; Length 1713;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAAATGATGCAATTAAT 60
 Db 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAAATGATGCAATTAAT 60
 QY 61 AAGTTTTTAACTATGCTTTAACTACCAATGAACGGTGTGAGCTGAATGATGCG 120
 Db 61 AAGTTTTTAACTATGCTTTAACTACCAATGAACGGTGTGAGCTGAATGATGCG 120
 QY 121 AAGTGAAGGCGTTAAAGCTTAAGCTGATGATGATGCTGATGATGATGATGATG 180
 Db 121 AAGTGAAGGCGTTAAAGCTTAAGCTGATGATGATGATGATGATGATGATGATG 180
 QY 181 ATACCGTACGCGCCAGCCAGTGGGTGAGCTGAGATTTAAAGCACCAGCCAGCACA 240
 Db 181 ATACCGTACGCGCCAGCCAGTGGGTGAGCTGAGATTTAAAGCACCAGCCAGCACA 240
 QY 241 CCTGGGATGATGCTGCTGATTTGTCATCATTAAGATTAAGTCAAGTGAATTT 300
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 QY 421 GGTGAATAATCATGATATGATGATGATGATGATGATGATGATGATGATGATG 480
 Db 421 GGTGAATAATCATGATATGATGATGATGATGATGATGATGATGATGATGATG 480
 QY 481 ATTAACATCAATATGCTTTGGAGCTAGCTTTCTAAGTTTAAATCAGAAAGCTT 540
 Db 481 ATTAACATCAATATGCTTTGGAGCTAGCTTTCTAAGTTTAAATCAGAAAGCTT 540
 QY 541 AATGTCGCCGATATCCGCGCTTAAAGATCAAGTATGATGATGATGATGATGAT 600
 Db 541 AATGTCGCCGATATCCGCGCTTAAAGATCAAGTATGATGATGATGATGATGAT 600
 QY 601 AATGTCGCCGATATCCGCGCTTAAAGATCAAGTATGATGATGATGATGATGAT 660
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 QY 661 GGTGCTTACCACTATCATGATGATGATGATGATGATGATGATGATGATGATG 720
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 QY 721 ATACTAATGTCGGGTAATGCTATTTGTCATTTGGCTAATACCAATGTCACATG 780
 Db 721 ATACTAATGTCGGGTAATGCTATTTGTCATTTGGCTAATACCAATGTCACATG 780

QY 781 TTACCTTAGCAAAATTTGGCGGCTATAGGGTGAAGATATGATAGATGTTTGGAA 840
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 QY 961 GGTGATGCTGCTTACCAAAATCTCGGGAATGTTAAACTGTTGGGTAATTCG 1020
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 QY 1141 GGTGATGCTGCTTACCAAAATCTCGGGAATGTTAAACTGTTGGGTAATTCG 1200
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 QY 1201 CATGTTACAGAGAAACACCAACGCTGATTAATTTATGATGATGATGATGATG 1260
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 QY 1261 TTTCTGTTCCCATATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
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 QY 1381 GGTGATGCTGCTTACCAAAATCTCGGGAATGTTAAACTGTTGGGTAATTCG 1440
 Db 1381 GGTGATGCTGCTTACCAAAATCTCGGGAATGTTAAACTGTTGGGTAATTCG 1440
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 QY 1501 ACTGATATATGATATGATATGATATGATATGATATGATATGATATGATATG 1560
 Db 1501 ACTGATATATGATATGATATGATATGATATGATATGATATGATATGATATG 1560
 QY 1561 ATGGAATAATGTTTCTGCGGATCAATTAAGAAATCCGAGAAAGTATACAAAGT 1620
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 QY 1621 ATTAGTATGATATGGAATGATGATGATGATGATGATGATGATGATGATGATG 1680
 Db 1621 ATTAGTATGATATGGAATGATGATGATGATGATGATGATGATGATGATGATG 1680
 QY 1681 TCGATGTTTGAAGAAACATGAGATTTATTTTAA 1713
 Db 1681 TCGATGTTTGAAGAAACATGAGATTTATTTTAA 1713

RESULT 2
 AAT68596
 ID AAT68596 standard; DNA; 1713 BP.
 XX
 AC AAT68596;
 XX
 DT 08-AUG-1997 (first entry)

XX LC-alpha-E7 malathion susceptible esterase clone Lc743.
 XX Malathion carboxylesterase; organophosphate; insecticide;
 KM pesticide; remediation; bioremediation; decontamination; esterase;
 KW ss.
 XX Lucilia cuprina.
 OS
 XX
 FH Key location/Qualifiers
 FT primer_bind complement (1..26)
 FT /*tag- a
 FT /note- "Lc743 5' primer"
 FT primer_bind 1686..1713
 FT /*tag- b
 FT /note- "Lc743 3' primer"
 FT 752
 FT /*tag- c
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 FT (Trp to Leu mutation)"
 FT 1344
 FT /*tag- d
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 FT 1362
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 FT 1599
 FT /*tag- f
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 FT 1629
 FT /*tag- g
 FT /note- "base 1629 is T in resistant clones
 FT (silent mutation)"
 FT MO9719176-A1.
 XX
 PD 29-MAY-1997.
 XX
 PF 22-NOV-1996; 96WO-AU00746.
 XX
 PR 23-NOV-1995; 95AU-0006751.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PI Boyce T, Brownlie JC, Campbell PM, Claudianos C;
 PI Newcomb RD, Oakshott JG, Robin GC, Russell RJ, Smyth K;
 XX
 DR WPI: 1997-298113/27.
 DR P-PSDB: AAM17765.
 XX
 PT DNA encoding enzyme that degrades organophosphate pesticides -
 PT useful for decontamination of soil, water, food etc
 XX
 PS Claim 4; Fig 1; 52pp; English.
 XX
 CC DNA molecule Lc743 (AAT68596) codes for an esterase (AAM17765) from
 CC a malathion susceptible strain of *Lucilia cuprina*. Comparison
 CC with a consensus sequence from derived from clones of the
 CC Lc-alpha-E7 resistant allele (see also AAM17768) indicated only one
 CC replacement site difference, a Trp to Leu substitution at amino
 CC acid position 251 (nucleotide position 752). This mutation is an
 CC excellent candidate for the malathion resistance mutation. The
 CC resistant enzyme acts as a malathion carboxylesterase and can be
 CC formulated for use in degrading environmental carboxylester or
 CC dimethyl general organophosphates.
 XX
 SQ Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;

Query Match 99.3%; Score 1701.8; DB 18; Length 1713;
 Best Local Similarity 99.6%; Pred. No. 0;

Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ATGAATTTCAACGTTACTTTGATGAGAAATTAATGAAGATTAATGATGAAT 60
 DB 1 ATGAATTTCAACGTTACTTTGATGAGAAATTAATGAAGATTAATGATGAAT 60
 QY 61 AAGTTTTAAACCTATCGTTTAACTACCAATGAACGGGTGAGTGAACGTAATGCG 120
 DB 61 AAGTTTTAAACCTATCGTTTAACTACCAATGAACGGGTGAGTGAACGTAATGCG 120
 QY 121 AAGTGAAGGCGTTAAACGTTTAACTGATGATGATGATGATGATGATGATG 180
 DB 121 AAGTGAAGGCGTTAAACGTTTAACTGATGATGATGATGATGATGATGATG 180
 QY 181 ATACCGTACGCGCCCAACCGCGCGGTGAGTGAATTAAGACACCCGACCAACA 240
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 QY 241 CCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
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 QY 301 ATACGGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 301 ATACGGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 361 CTAATCCCGCAACTAAACGTCCTTTTAACTATACATCAATCAATCAATCAAT 420
 DB 361 CTAATCCCGCAACTAAACGTCCTTTTAACTATACATCAATCAATCAATCAAT 420
 QY 421 GGTAAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 DB 421 GGTAAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 QY 481 ATTAACATACATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT 540
 DB 481 ATTAACATACATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT 540
 QY 541 AATGTCGGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
 DB 541 AATGTCGGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
 QY 601 AATGTCGGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
 DB 601 AATGTCGGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
 QY 661 GCTGCTTACCACTATGATGATGATGATGATGATGATGATGATGATGATGATG 720
 DB 661 GCTGCTTACCACTATGATGATGATGATGATGATGATGATGATGATGATGATG 720
 QY 721 ATACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 DB 721 ATACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 QY 781 TTACCTTACCACTATGATGATGATGATGATGATGATGATGATGATGATGATG 840
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OY 721 ATACTAATGTGGGTAATGCTATTTGTCATTGGCTTAATACCAATGCAACATGCTGCC 780
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OY 781 TTACCTTAGCCAAATTTGGCCGGCTATATAGGGTGAGGATTAAGATAGATGTTTGGAA 840
DB 781 TTACCTTAGCCAAATTTGGGCTATATAGGGTGAGGATTAAGATAGATGTTTGGAG 840
OY 841 TTTCTTGAAGAACCAAGCCACAGATTTAATAAACTTGAGAAAAAGTTTAACTGA 900
DB 841 TTTCTTGAAGAACCAAGCCACAGATTTAATAAACTTGAGAAAAAGTTTAACTGA 900
OY 901 GAAGAGCCGACAAATTAAGTCAATGTTCTTTGTCACAGCTGACGATATGACGAGAC 960
DB 901 GAAGAGCCGACAAATTAAGTCAATGTTCTTTGTCACAGCTGACGATATGACGAGAC 960
OY 961 GCTGATTTGCTCTTACCCCAACATCCTCGGAAATGGTTAAACCTGTTGGGGTAATTCG 1020
DB 961 GCTGATTTGCTCTTACCCCAACATCCTCGGAAATGGTTAAACATGCTTTGGGGTAATTCG 1020
OY 1021 ATACCCACTATATGAGGCTATATGAGGCTATATTTTCACTTCAATCTTANG 1080
DB 1021 ATACCCACTATATGAGGCTATATGAGGCTATATTTTCACTTCAATCTTANG 1080
OY 1081 CAAATGCCATGCTTGTAAAGAAATGGAACCTGTGCAATTTGTCGCAAGTGAATTG 1140
DB 1081 CAAATGCCATGCTTGTAAAGAAATGGAACCTGTGCAATTTGTCGCAAGTGAATTG 1140
OY 1141 GCTGATTTGAACGACGCCGCCAGAGACCTTGGAAATGGGCTTAAATTTAAAAAGGCT 1200
DB 1141 GCTGATTTGAACGACGCCGCCAGAGACCTTGGAAATGGGCTTAAATTTAAAAAGGCT 1200
OY 1201 CATGTTACGAGAAACACCAACAGCTGATATTTATGATCTTGGCTCAGATCTAT 1260
DB 1201 CATGTTACGAGAAACACCAACAGCTGATATTTATGATCTTGGCTCAGATCTAT 1260
OY 1261 TTCTGTTCCCATGATGTTTGTGCAATTAACGTTTCAATACACCTCCGGTACACCC 1320
DB 1261 TTCTGTTCCCATGATGTTTGTGCAATTAACGTTTCAATACACCTCCGGTACACCC 1320
OY 1321 GTCTACTTGTATGCTTGCCTGACCTTGATGGAAGATCTTATCAATCCCTATCTAT 1380
DB 1321 GTCTACTTGTATGCTTGCCTGACCTTGATGGAAGATCTTATCAATCCCTATCTAT 1380
OY 1381 CGTAGAGACGCTGCTTAAGGCTGTACTCATGCTGATGAATTAACCTATTTCTCTCG 1440
DB 1381 CGTAGAGACGCTGCTTAAGGCTGTACTCATGCTGATGAATTAACCTATTTCTCTCG 1440
OY 1441 AATCAATTTGGCCAAACGCTATGCTTAAGAAATGCGCTGATTAACAAACATTTGAACGTATG 1500
DB 1441 AATCAATTTGGCCAAACGCTATGCTTAAGAAATGCGCTGATTAACAAACATTTGAACGTATG 1500
OY 1501 ACTGCTATATGATATGATTTGGCCACTGCTATATCTTATAGCAATGAATTTGAAGGT 1560
DB 1501 ACTGCTATATGATATGATTTGGCCACTGCTATATCTTATAGCAATGAATTTGAAGGT 1560
OY 1561 ATGGAATAAGTTCCTGGGATCCAAATTAAGAAATCCGATGAAGTGAAGTGTGGAAT 1620
DB 1561 ATGGAATAAGTTCCTGGGATCCAAATTAAGAAATCCGATGAAGTGAAGTGTGGAAT 1620
OY 1621 ATTAGTATGATATGATTTGAATGATGCTGCAATGATTAAGATTAACATGGA 1680
DB 1621 ATTAGTATGATATGATTTGAATGATGCTGCAATGATTAAGATTAACATGGA 1680
OY 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713
DB 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713

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RESULT 4
AA091564
ID AA091564 standard; cDNA; 1713 BP.

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XX AC AA091564;
XX DT 22-DEC-1995 (first entry)
XX DE OP-resistant esterase Lc7L103C allele.
XX KW Esterase; E3; bioremediation; organophosphate; carbamate;
XX KW Insecticide; pesticide; water decontamination; meat decontamination;
XX OS Lucilia cuprina.
XX FH Key Location/Qualifiers
XX FT CDS 1..1713
XX FT /*tag= a
XX PN W09519440-A1.
XX PD 20-JUL-1995.
XX PE 13-JAN-1995; 95WO-AU00016.
XX PR 13-JAN-1994; 94AU-0003347.
XX PA (CSIR ) COMMONWEALTH SCI & IND. RES. ORG.
XX PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX DR WPI: 1995-263870/34.
XX PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX PT eliminate residues of organo:phosphate and carbamate pesticides from
XX PS water, meat etc.
XX PS Example 4; Page 12-17; 38pp; English.
XX CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
XX CC resistant strain, Llandillo 103. 4 isolated clones were
XX CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
XX CC esterases. The esterases, or cells expressing them, are used
XX CC in bioremediation.
XX SQ Sequence 1713 BP; 512 A; 308 C; 368 G; 525 T; 0 other;
XX
XX Query Match 97.9%; Score 1677.8; DB 16; Length 1713;
XX Best Local Similarity 98.7%; Pred. No. 0;
XX Matches 1691; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
OY 1 ATGAATTTACAGCTTACTGTTGATGAGAAATTTAAATGGAAGTAAATGCAATTTGAAAT 60
DB 1 ATGAATTTACAGCTTACTGTTGATGAGAAATTTAAATGGAAGTAAATGCAATTTGAAAT 60
OY 61 AAGTTTAAACATGATGTTTAACTACCAATGAACGGTGTACTGTAACATGATATGCG 120
DB 61 AAGTTTAAACATGATGTTTAACTACCAATGAACGGTGTACTGTAACATGATATGCG 120
OY 121 AAAGTAAAGCGCTTAAACGTTTAACTGTGTACGATGATTTCTATACAGTTTGAAGGT 180
DB 121 AAAGTAAAGCGCTTAAACGTTTAACTGTGTACGATGATTTCTATACAGTTTGAAGGT 180
OY 181 ATACCGTACGCCCAACCCGACAGGGGTGAGAGCTAGATTTAAACACCCGACGACACACA 240
DB 181 ATACCGTACGCCCAACCCGACAGGGGTGAGAGCTAGATTTAAACACCCGACGACACACA 240
OY 241 CCTGGAGATGCTGCTGATGTTTGTGCAATCATAAAGATAGTCAGTGAAGTGAATTT 300
DB 241 CCTGGAGATGCTGCTGATGTTTGTGCAATCATAAAGATAGTCAGTGAAGTGAATTT 300
OY 301 ATACGGGCAAGAGTGTGTGCTCAGAGGATGTTCTATACCTAAGTGTCTATACGAATAT 360
DB 301 ATACGGGCAAGAGTGTGTGCTCAGAGGATGTTCTATACCTAAGTGTCTATACGAATAT 360

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Db 301 ATTACGAGCAAAAGTGTGTGGCTACAGAGATGTCTATACCTAACCGCTATACGAATAT 360
QY 361 CTAATCCCGAACTAAACGTCGGTATTAGTATACATACATGCTGCTTTTATTATC 420
Db 361 CTAATCCCGAACTAAACGTCGGTATTAGTATACATACATGCTGCTTTTATTATC 420
QY 421 GGTGAATAATCATGCTGATGTATGTCTGATTTATTCATTTAAAGATGGTGGTTC 480
Db 421 GGTGAATAATCATGCTGATGTATGTCTGATTTATTCATTTAAAGATGGTGGTTC 480
QY 481 ATTACATACATATGCTTTGGAGCTCTAGTCTTCTAAGTTTAAATTCAGAACCTT 540
Db 481 ATTACATACATATGCTTTGGAGCTCTAGTCTTCTAAGTTTAAATTCAGAACCTT 540
QY 541 AATGCGCCGCGTAATGCGCGCTTAAAGATCAAGTCATGGCCCTTGGTGGATTAAT 600
Db 541 AATGCGCCGCGTAATGCGCGCTTAAAGATCAAGTCATGGCCCTTGGTGGATTAAT 600
QY 601 AATTGGCCCACTTTGGTGGCAATCCGATATATTATTAAGTCTTTGGTGAAGTCCGCT 660
Db 601 AATTGGCCCACTTTGGTGGCAATCCGATATATTATTAAGTCTTTGGTGAAGTCCGCT 660
QY 661 GCTGCTCTACCCATACATGATGTATACCGAAACACGCGGCTTTTCATGCTGCT 720
Db 661 GCTGCTCTACCCATACATGATGTATACCGAAACACGCGGCTTTTCATGCTGCT 720
QY 721 ATACTAATGTGGGTAATGCTATTTGTCCATTGGCTAATACCAATGTCACATGCTGC 780
Db 721 ATACTAATGTGGGTAATGCTATTTGTCCATTGGCTAATACCAATGTCACATGCTGC 780
QY 781 TTCACCTTACCAATTTGGCGGCTATTAAGGTGAGGATATGATTAAGATGTTTGA 840
Db 781 TTCACCTTACCAATTTGGCGGCTATTAAGGTGAGGATATGATTAAGATGTTTGA 840
QY 841 TTTCTTAAAGAACCAAGCACAGATTTAATAAACTTGAAGAAAGTTTAACTCTA 900
Db 841 TTTCTTAAAGAACCAAGCACAGATTTAATAAACTTGAAGAAAGTTTAACTCTA 900
QY 901 GAAGAGCGACAAATTAAGTATGCTTCTTTGCTCCACTGTTGAGCCATATCAGACC 960
Db 901 GAAGAGCGACAAATTAAGTATGCTTCTTTGCTCCACTGTTGAGCCATATCAGACC 960
QY 961 GCTGATGTGTCTTACCCAAACATCTCTGGGAAATGTTAAACGCTGGGGTAATTGC 1020
Db 961 GCTGATGTGTCTTACCCAAACATCTCTGGGAAATGTTAAACGCTGGGGTAATTGC 1020
QY 1021 ATACCACTATGATGGGTAACACTTCAATATGAGGCTATTTTCACTTCAATTTTAA 1080
Db 1021 ATACCACTATGATGGGTAACACTTCAATATGAGGCTATTTTCACTTCAATTTTAA 1080
QY 1081 CAATGCTATGCTTGTAAAGATTTGAAACTTGTCAATTTGTGCCAAGGATTCG 1140
Db 1081 CAATGCTATGCTTGTAAAGATTTGAAACTTGTCAATTTGTGCCAAGGATTCG 1140
QY 1141 GCTGATGTGTAAGCACCAGCCGCCAGAGACCTTGAAGATGGTGTCTAAATTAAGAGCT 1200
Db 1141 GCTGATGTGTAAGCACCAGCCGCCAGAGACCTTGAAGATGGTGTCTAAATTAAGAGCT 1200
QY 1201 CATGTTACAGAGAAACACCAACGCGGATTAATTTATGATCTTGTGCTCTCACTAT 1260
Db 1201 CATGTTACAGAGAAACACCAACGCGGATTAATTTATGATCTTGTGCTCTCACTAT 1260
QY 1261 TTTCTGTTCCCATGATGCTTTGTGCAATTAAGTTTCAATCAACCTCCGCTACACC 1320
Db 1261 TTTCTGTTCCCATGATGCTTTGTGCAATTAAGTTTCAATCAACCTCCGCTACACC 1320
QY 1321 GTCTACTTGTATGCTTGCATTCGATTTGGAAGATCTTATCAATCCCTATCTATTAG 1380
Db 1321 GTCTACTTGTATGCTTGCATTCGATTTGGAAGATCTTATCAATCCCTATCTATTAG 1380
QY 1381 CGTAGTGAAGCTGTGAAGGCTTAAAGCTGATGATGATTAACCTATTTCTCTG 1440
Db 1381 CGTAGTGAAGCTGTGTAAAGGCTTAAAGCTGATGATGATTAACCTATTTCTCTG 1440

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QY 1441 AATCAATGGCCAAACGATATGCTTAAAGATGCGGTAATCAAAACATTTGACGTATG 1500
Db 1441 AATCAATTTGGCCAAACGATATGCTTAAAGATGCGGTAATCAAAACATTTGACGTATG 1500
QY 1501 ACTGGTATATGATCAATTTTCCACACACTGTGTAATCTTTATGCAATGAATGAGCT 1560
Db 1501 ACTGGTATATGATCAATTTTCCACACACTGTGTAATCTTTATGCAATGAATGAGCT 1560
QY 1561 ATGGAATAATGTTCCGCGGATCCATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
Db 1561 ATGGAATAATGTTCCGCGGATCCATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
QY 1621 ATTAGTATGATTAATGAATGATGATGCTGTAATGATGATTAAGATTAACATGGAG 1680
Db 1621 ATTAGTATGATTAATGAATGATGATGCTGTAATGATGATTAAGATTAACATGGAG 1680
QY 1681 TCGATGTTGAAAAACATGAGATTTATTAG 1713
Db 1681 TCGATGTTGAAAAACATGAGATTTATTAG 1713

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RESULT 5
AA091565
ID AA091565 standard; cDNA: 1713 BP.
XX
AC AA091565;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103D allele.
XX
KW Esterase; E3; bioremediation; organophosphate; carbamate;
KW insecticide; pesticide; water decontamination; meat decontamination;
XX
OS Lucilia cuprina.
XX
FH Key 1.1713
FT CDS.
FT tag- a
XX
XX W09519440-A1.
XX
XX 20-JUL-1995.
XX
XX 13-JAN-1995; 95WO-AU00016.
XX
XX 13-JAN-1994; 94AU-0003347.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Boyce TM, Campbell PM, Newcomb RD, Oakshott JG;
XX Parker AG, Robin GC, Russell RJ, Smyth K;
XX
XX WPI: 1995-263870/34.
XX
XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX eliminate residues of organo:phosphate and carbamate pesticides from
XX water, meat etc.
XX
XX Example 4: Page 12-17; 38pp; English.
XX
XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX Op-susceptible esterase E3 of L. cuprina) from a diazinon
XX resistant strain, Llandillo 103. 4 Isolated clones were
XX sequenced (Lc7L103 A-D. AA091562-65) that encoded diazinon-resistant
XX CC esterases. The esterases, or cells expressing them, are used
XX in bioremediation.
XX
XX Sequence 1713 BP; 513 A; 307 C; 369 G; 524 T; 0 other;
XX
XX Query Match 97.9%; Score 1677.8; DB 16; Length 1713;

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Qy	1	ATGATTTTCAAGCTTGGTTGATGTGAGAAATTTAAATGGAAGATTAATATGCATTGAAT	60
Qy	1	ATGATTTTCAAGCTTGGTTGATGTGAGAAATTTAAATGGAAGATTAATATGCATTGAAT	60
Db	1	ATGATTTTCAAGCTTGGTTGATGTGAGAAATTTAAATGGAAGATTAATATGCATTGAAT	60
Qy	61	AAAGTTTAAACATGCTGTTAACTACCAATGAAACGGGTGATAGCTGAACATGATGGC	120
Db	61	AAAGTTTAAACATGCTGTTAACTACCAATGAAACGGGTGATAGCTGAACATGATGGC	120
Qy	121	AAAGTAAAGCGGTAAACGTTTAACTGTGTGCATGATTCCTACTACAGTTTGAAGGT	180
Db	121	AAAGTAAAGCGGTAAACGTTTAACTGTGTGCATGATTCCTACTACAGTTTGAAGGT	180
Qy	181	ATACCGTAGCCCAACCGCGACGAGGGGTGAGCTGAGATTTAAAGCAACCCACGACGAC	240
Db	181	ATACCGTAGCCCAACCGCGACGAGGGGTGAGCTGAGATTTAAAGCAACCCACGACGAC	240
Qy	241	CCCTGGATGCTGTGGCTGATTTGTTGCAATCAATTAAGATTAAGTCAGTCAAGTTGATTT	300
Db	241	CCCTGGATGCTGTGGCTGATTTGTTGCAATCAATTAAGATTAAGTCAGTCAAGTTGATTT	300
Qy	301	ATTAACGGCAAACTGTGTGCTCAGAGATTTGCTATACCTAATGCTCTAATACGAATAT	360
Db	301	ATTAACGGCAAACTGTGTGCTCAGAGATTTGCTATACCTAATGCTCTAATACGAATAT	360
Qy	361	CTAAATCCGAAACTAAAGCTCCCGTTTAAATATCATATCAATGAGGGGTTTATATAC	420
Db	361	CTAAATCCGAAACTAAAGCTCCCGTTTAAATATCATATCAATGAGGGGTTTATATAC	420
Qy	421	GGTGAATCATGCTGATATGATATGTGCTCGATTTTTCATTTAAAGAGATGTGGTGTG	480
Db	421	GGTGAATCATGCTGATATGATATGTGCTCGATTTTTCATTTAAAGAGATGTGGTGTG	480
Qy	481	ATTAACTAACAATATGCTTTGGAGCTCTAAGTTTCTAAGTTTAAATTCAGAGACTT	540
Db	481	ATTAACTAACAATATGCTTTGGAGCTCTAAGTTTCTAAGTTTAAATTCAGAGACTT	540
Qy	541	AATGTGCGCGTATGAGCGGCTTAAAGATCAAGCATGCGCTGCTGGATTTAAAT	600
Db	541	AATGTGCGCGTATGAGCGGCTTAAAGATCAAGCATGCGCTGCTGGATTTAAAT	600
Qy	601	AATGCGCCAACTTGTGTGGCAATCCCGATATATTACAGTCTTGTGTAAGTGGCCGT	660
Db	601	AATGCGCCAACTTGTGTGGCAATCCCGATATATTACAGTCTTGTGTAAGTGGCCGT	660
Qy	661	GTGTGCTCTACCACTACATGATGTTAAACGGAACAACCTCGCGTCTTTCCATGTGCT	720
Db	661	GTGTGCTCTACCACTACATGATGTTAAACGGAACAACCTCGCGTCTTTCCATGTGCT	720
Qy	721	ATTAATATGCGGGTATGCTATTTTCCATTGGCGTAATACCANTGCAACATGTGCC	780
Db	721	ATTAATATGCGGGTATGCTATTTTCCATTGGCGTAATACCANTGCAACATGTGCC	780
Qy	781	TTCACTTACCAAAATTTGGCGGCTTAAAGGGTGAAGATTAAGTAAAGATTTTGGAA	840
Db	781	TTCACTTACCAAAATTTGGCGGCTTAAAGGGTGAAGATTAAGTAAAGATTTTGGAA	840
Qy	841	TTTCTTATGAAGCCCAAGCACAAGATTTTAAATAACTTGAGGAAAAAGTTTAACTCTA	900
Db	841	TTTCTTATGAAGCCCAAGCACAAGATTTTAAATAACTTGAGGAAAAAGTTTAACTCTA	900
Qy	901	GAAAGGCTCAAAATTAAGTCAATGTTCTTTTGGGCCACGTGTGACACATACAGACC	960
Db	901	GAAAGGCTCAAAATTAAGTCAATGTTCTTTTGGGCCACGTGTGACACATACAGACC	960
Qy	961	GCTATTTGTCTTACCAACAATCCTCGGAAATGTTAAACATGCTTGGGATATTCG	1020
Db	961	GCTATTTGTCTTACCAACAATCCTCGGAAATGTTAAACATGCTTGGGATATTCG	1020
Qy	1021	ATACCACTATGATGGGTAAACCTTCATATAGAGGCTATTTTTCACCTTCAATTCCTAAG	1080

Dd	1021	ATACCCACTGATGGGTAAACCTTCATATAGAGGCCTATTTTTCTACTCGTTCTTAG	1080
Oy	1081	CAATAGCCTATGCTTGTTTAAGAAGATTGGAACAATGTGTCAATTTTTGTGCCAAGTGAATG	1140
Dd	1081	CAATAGCCTATGCTTGTTTAAGAAGATTGGAACAATGTGTCAATTTTTGTGCCAAGTGAATG	1140
Oy	1141	GCTGATGTGACGCCACC GCCCCAGAGACTTGGAAATGGGTGCTTAAATTAAAAAGCT	1200
Dd	1141	GCTGATGTGACGCCACC GCCCCAGAGACTTGGAAATGGGTGCTTAAATTAAAAAGCT	1200
Oy	1201	CATGTTACAGAGAAAACACCACAGCATGATTAATTTATGATCTTGTGCTCACATCTAT	1260
Dd	1201	CATGTTACAGAGAAAACACCACAGCATGATTAATTTATGATCTTGTGCTCACATCTAT	1260
Oy	1261	TTCGTGTTCCCCATGATCGTTTGTTGCAATTAACGTTTCAATCACACCTCCGGTACACC	1320
Dd	1261	TTCGTGTTCCCCATGATCGTTTGTTGCAATTAACGTTTCAATCACACCTCCGGTACACC	1320
Oy	1321	GTCNACTGTATGCGCTTCGACTTCGATTTGGGAAGATCTTATCAATCCCATGCTATTATG	1380
Dd	1321	GTCNACTGTATGCGCTTCGACTTCGATTTGGGAAGATCTTATTAATCCCATGCTATTATG	1380
Oy	1381	CGTAGTGACGCTGTGTTTAAGGGGTATGATGCTGATGAATTAACCAATTTCTTCGG	1440
Dd	1381	CGTAGTGACGCTGTGTTTAAGGGGTATGATGCTGATGAATTAACCAATTTCTTCGG	1440
Oy	1441	AATCAATTTGGCCAAACGATGCTATAAGAAATCGCGTGAATACAAAACAATTAACGATAG	1500
Dd	1441	AATCAATTTGGCCAAACGATGCTATAAGAAATCGCGTGAATACAAAACAATTAACGATAG	1500
Oy	1501	ACTGGTATATGATACAAATTTGCCACACGCTGTATACCTTATAGCAATGAATTTAAGT	1560
Dd	1501	ACTGGTATATGATACAAATTTGCCACACGCTGTATACCTTATAGCAATGAATTTAAGT	1560
Oy	1561	ATGCAAAATGTTTCTCGSGATCCCAATTAAGAATCCGATGAAGTATACAAGTGTGAAT	1620
Dd	1561	ATGCAAAATGTTTCTCGSGATCCCAATTAAGAATCCGATGAAGTATACAAGTGTGAAT	1620
Oy	1621	ATTAGTGATGAATTAAGAAATGATTGATGTGCTGAAATGGATPAAGATTAAACATGGAG	1680
Dd	1621	ATTAGTGATGAATTAAGAAATGATTGATGTGCTGAAATGGATPAAGATTAAACATGGAG	1680
Oy	1681	TCGATGTTGAAAAACATAGAGATTATTTTAG	1713
Dd	1681	TCGATGTTGAAAAACATAGAGATTATTTTAG	1713
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RESULT 6			
AAO91563			
XX	ID	AAO91563 standard; cDNA; 1713 BP.	
XX	AC	AAO91563;	
XX	DT	22-DEC-1995 (first entry)	
XX	DE	Op-resistant esterase Lc/L103B allele.	
XX	KM	Esterase; E3; bioremediation; organophosphate; carbamate;	
XX	KW	Insecticide; pesticide; water decontamination; meat decontamination;	
XX	KW	ss.	
OS		Lucilia cuprina.	
xx			
xx	FH	Key	Location/Qualifiers
FT	CDS	1..1713	
xx		/.*tag= a	
xx	PN	W09519440-AI.	
xx	PD	20-JUL-1995.	
PF		13-JAN-1995; 95WO-AU00016.	
xx			

AA091562
ID AA091562 standard; cDNA; 1713 BP.
XX
AC AA091562;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103a allele.
XX
KM Esterase; E3; bioremediation: organophosphate; carbamate;
KM insecticide; pesticide; water decontamination; meat decontamination;
KM ss.
XX
OS Lucilia cuprina.
XX
FH Key Location/Qualifiers
FT CDS 1..1713
FT /*tag- a
XX
PN MO9519440-A1.
XX
PD 20-JUL-1995.
XX
PF 13-JAN-1995; 95WO-AU00016.
XX
PR 13-JAN-1994; 94AU-0003347.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX
XX WPI; 1995-263870/34.
XX
PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
PT eliminate residues of organo:phosphate and carbamate pesticides from
PT water, meat etc.
XX
XX Example 4; Page 12-17; 38pp; English.
XX
XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
CC resistant strain, Llandillo 103. 4 isolated clones were
CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
CC esterases. The esterases, or cells expressing them, are used
CC in bioremediation.
XX
XX
SQ Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;
Query Match 97.88; Score 1674.6; DB 16; Length 1713;
Best Local Similarity 98.68; Pred. No. 0;
Matches 1689; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 301 ATAAAGGCAAAAGTGTGTGCTCAGAGATTCTATACCTAAGTGTCTATACGAATAT 360
Db 301 ATTAAGGCAAAAGTGTGTGCTCAGAGATTGTCTATACCTAAGTGTCTATACGAATAT 360
QY 361 CTAAATCCCGAACTAAACGTCCTGTTTACTATACATACATGCTGGTGTATATTC 420
Db 361 CTAAATCCCGAACTAAACGTCCTGTTTACTATACATACATGCTGGTGTATATTC 420
QY 421 GGTAAATATCTGATATATGATGTCCTGATATTTCATTAATAAGATGTGTGTTG 480
Db 421 GGTAAATATCTGATATATGATGTCCTGATATTTCATTAATAAGATGTGTGTTG 480
QY 481 ATTAACATACATATCTGTTGGAGCTCTAGCTTTCTAAGTTTAAATTCAGAACCTT 540
Db 481 ATTAACATACATATCTGTTGGAGCTCTAGCTTTCTAAGTTTAAATTCAGAACCTT 540
QY 541 AATGTGCGCGTAATGCCGCTTAAGATCATGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 AATGTGCGCGTAATGCCGCTTAAGATCATGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 AATGCGCGCACTTGGGCGCAATCCGATATATTAAGTCTTGTGGAAGTCCGCT 660
Db 601 AATGCGCGCACTTGGGCGCAATCCGATATATTAAGTCTTGTGGAAGTCCGCT 660
QY 661 GCTGCTCTACCCACTACATGATGTAAACGAAACAACTCCGCTCTTTCATCGTGT 720
Db 661 GCTGCTCTACCCACTACATGATGTAAACGAAACAACTCCGCTCTTTCATCGTGT 720
QY 721 ATACTAATGTGGGTAAATGCTATTTGTCATTTGCTAATACCAATGCAACATGCTGC 780
Db 721 ATACTAATGTGGGTAAATGCTATTTGTCATTTGCTAATACCAATGCAACATGCTGC 780
QY 781 TTCACCTAGCCAAATTTGCGCGCTATTAAGGTGATGATTAATGATTAAGATTTTGAA 840
Db 781 TTCACCTAGCCAAATTTGCGCGCTATTAAGGTGATGATTAATGATTAAGATTTTGAA 840
QY 841 TTCTCTTAAGAAAGCAAGCCACAGGATTTAATAAATCTGAGGAAAGTTTAACTGTA 900
Db 841 TTCTCTTAAGAAAGCAAGCCACAGGATTTAATAAATCTGAGGAAAGTTTAACTGTA 900
QY 901 GAAGAGCGTCAATTAAGTATGCTTTCTTTGCTCCACTGTTGAGCCATATCAGAC 960
Db 901 GAAGAGCGTCAATTAAGTATGCTTTCTTTGCTCCACTGTTGAGCCATATCAGAC 960
QY 961 GCTATGTCGCTTACCAACATCTGCGGAAATGTTAAACTGCTGGGGTATTCG 1020
Db 961 GCTATGTCGCTTACCAACATCTGCGGAAATGTTAAACTGCTGGGGTATTCG 1020
QY 1021 ATACCACTATGATGGGTAACTTCAATATGAGGCTATTTTCACTTCAATCTTAAG 1080
Db 1021 ATACCACTATGATGGGTAACTTCAATATGAGGCTATTTTCACTTCAATCTTAAG 1080
QY 1081 CAAATGCTATGCTTGTAAAGAAATTTGAAACTGTGTCAATTTTGTGCCAAGTGAATG 1140
Db 1081 CAAATGCTATGCTTGTAAAGAAATTTGAAACTGTGTCAATTTTGTGCCAAGTGAATG 1140
QY 1141 GCTGATGTGAAGCAGCCGCCAGACCTTGAATAGGCTGCTAAATTAAGAGCT 1200
Db 1141 GCTGATGTGAAGCAGCCGCCAGACCTTGAATAGGCTGCTAAATTAAGAGCT 1200
QY 1201 CATGTTACAGGAGAAACCAACAGCTGATTAATTTATGATCTTTGCTCACATCAT 1260
Db 1201 CATGTTACAGGAGAAACCAACAGCTGATTAATTTATGATCTTTGCTCACATCAT 1260
QY 1261 TTTGTTCCCATATGATGCTTTGTCATTAAGTTTCAATCACTCCGCTGATACACC 1320
Db 1261 TTTGTTCCCATATGATGCTTTGTCATTAAGTTTCAATCACTCCGCTGATACACC 1320
QY 1321 GTTACTTGTATGCTGCTTGAATGCTGATTTGCAAGATCTTATCAATCCCTATGAT 1380
Db 1321 GTTACTTGTATGCTGCTTGAATGCTGATTTGCAAGATCTTATCAATCCCTATGAT 1380
QY 1381 CGTAGTGAGCTGGGTAAAGGTTGATGTCATGCTGATGAATTAACCTATTTCTTCG 1440

QY 1004 CTGCTGGGGTAATTCGATACCACTATGATGGTAACACTTCATATGAGGCTATATTT 1063
 DB 1004 GCGCTGGGGAAATTCGATACCACTATGATGGTAACACTTCATATGAGGCTATATTT 1063
 QY 1064 TCACCTCAATTCCTTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1123
 DB 1064 CCAATCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1123
 QY 1124 TTGTCACAGTGAATTCGATATGCTTGTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1123
 DB 1124 ATGTCCTGGGGAGTGGCTACAGTGAATTCGATATGCTTGTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1123
 QY 1184 CTAAATTAAGGCTCATCTTACAGAGAGAACCAACGCTGATATATTTATGATC 1243
 DB 1184 CCATGTGTAAGGCTCATCTTACAGAGAGAACCAACGCTGATATATTTATGAGC 1243
 QY 1244 TTGCTCTACATCATATTCCTGCTTCCCATGATGCTTGTAAAGCAATTCGATATGCTTCAAT 1303
 DB 1244 TTGCTCTACATCATATTCCTGCTTCCCATGATGCTTGTAAAGCAATTCGATATGCTTCAAT 1303
 QY 1304 ACACCTCCGGTACACCGCTTACTGATGCTTGTAAAGCAATTCGATATGCTTCAAT 1363
 DB 1304 ACACAGCTGGGACCTCCATTTATGATGCTTGTAAAGCAATTCGATATGCTTCAAT 1363
 QY 1364 ATCCCTATCGTATATGCTTGTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1423
 DB 1364 ACCCTATCGTATATGCTTGTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1423
 QY 1424 TAACCTATTCCTGCTTCCCATGATGCTTGTAAAGCAATTCGATATGCTTCAAT 1483
 DB 1424 TAACCTATTCCTGCTTCCCATGATGCTTGTAAAGCAATTCGATATGCTTCAAT 1483
 QY 1484 AAACATTAAGGCTCATCTTACAGAGAGAACCAACGCTGATATATTTATGAGC 1543
 DB 1484 AAACATTAAGGCTCATCTTACAGAGAGAACCAACGCTGATATATTTATGAGC 1543
 QY 1544 GCAATGATATGCTTGTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1603
 DB 1544 GCAATGATATGCTTGTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1603
 QY 1604 TATACAGTGTGATATGCTTGTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1663
 DB 1604 TATACAGTGTGATATGCTTGTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1663
 QY 1664 AGATTAACATTCGATATGCTTGTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1710
 DB 1664 AGATTAACATTCGATATGCTTGTAAAGCAATTCGATATGCTTGTAAAGCAATTCGATATGCTTCAAT 1710

RESULT 9

ABL02067
 ID ABL02067 standard; cDNA; 2001 BP.
 AC ABL02067;
 DE 26-MAR-2002 (first entry)
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 683.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical; gene; ss.
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR P-PSDB; ABB57964.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Claim 1; SEQ ID NO 683; 21bp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB116175) and the encoded proteins
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (ABB57737-ABB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SO Sequence 2001 BP; 502 A; 488 C; 521 G; 490 T; 0 other;
 Query Match 39.5%; Score 677.2; DB 23; Length 2001;
 Best Local Similarity 62.6%; Pred. No. 7e-176;
 Matches 1073; Conservative 0; Mismatches 638; Indels 3; Gaps 1;
 QY 1 ATGATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAATGATGAAAT 60
 DB 95 ATGATTAAGAACCTGGCTTTGTGAGCGCTTGGCGGCCCTCAAAACCATGAGCAT 154
 QY 61 AAGTTTAAACATACGTTTAACTACCAATGAAGCGGTGAGTGAACATGATATGATG 120
 DB 155 AAAGTCCAGCATATGCGCACTGACCAATGAACAGTTTGTCCGACACGAGATGAGC 214
 QY 121 AAAGTGAAGCGCTTAAAGCTTAACTGTGATGATGATGATGATGATGATGATGATG 180
 DB 215 CAAAGGAGGAGTATCAACGCTATCTCTACGATGTCGCTTCACTTCACTGAGAGGT 274
 QY 181 ATACCGTACGCGCCACCGCCGAGTGGGTGATGATGATGATGATGATGATGATGATG 240
 DB 275 ATCCCGTACGCGCCACCGCCGAGTGGGTGATGATGATGATGATGATGATGATGATG 334
 QY 241 CCCTGGAGTGTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 335 CCCTGGAGTGTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 394
 QY 301 ATACGGGCAAGTGTGCTCAGAGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 395 GTCTTCATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 454
 QY 361 CTAAATCCGGAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 455 GTGAGCCCGCAACAGCTGCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 514
 QY 421 GGTGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 515 GGTGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 574
 QY 481 ATTAACATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 575 GTACAGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 634
 QY 541 AATGCGCGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 635 AATGCGCGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 694
 QY 601 AATGCGCGCACTTGTGTCGAATCCGATATATATATATATATATATATATATATATATAT 660


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Db 695 AATGGCCCTAGTTCCGGCGGAGATCCCACTGATCACTGTTTTTGGAGAGAGTGCGGA 754
Qy 661 GCTGCGCTACCCACTATGATGTTAAACCAAACTGCGGCTCTTTCATCGTGT 720
Db 755 GCGCCCTCCACTCCTACATGATGCTTAACGATCAGCCAAAGGCGCTTTCACCGGGC 814
Qy 721 ATACTAATGTCGGGTAATGCTATTTGTCATGTGC--TATAACCAATGCTCAACATCGT 777
Db 815 ATCTTCAGTCGGGCACTTGTCTTGGGCTACAAAGCGCATTTACCATTAAT 874
Qy 778 GCGTACCTTAGCAATTTGGCGGCTATTAAGGTAGATATGATTAAGATGTTTG 837
Db 875 CCGTACGATAGCAAGCTGTGGTGTACAAAGGCGAGACAAGCAAGGATGTGCTG 934
Qy 838 GAATTTCTTATGAAGCCACACAGATTTAATAAATTGAGAAAAAGTTTACT 897
Db 935 GAGTTCCTTGAGAAAGTAAGGCGCAAGATCTTATTCGCTGGAGAAAAATGCTTGACA 994
Qy 898 CTGAGAGAGCGTACAAATAAGTCATGTTTCTTTGGTCCACTGTTGAGCCATATCAG 957
Db 995 CTGAGAGAGCGATGAAGATATGTTTGCCTTGGCCATCCCTGGAACATCTCC 1054
Qy 958 ACGGCTGATGTGCTTACCCAAACATCCTCGGGAATGTTAAACTGCTTGGGGTAT 1017
Db 1055 ACGCCGAAATGTGATATCAAGCCCTCAAGAGAGATGATGAAGACCGCTGAGTAC 1114
Qy 1018 TCGATACCCATATGATGGGTAACTTCAATATGAGGGTATATTTTCACTTCAATCTT 1077
Db 1115 TCGATCCCATGTTTATAGAAACACTTCTGACAGAGGCTGCTGGGTTCCAGAGTA 1174
Qy 1078 AAGCAATGCTTATGCTTGTAAAGAAATGGAACCTTGTCATATTTGTGCCAAGTAA 1137
Db 1175 AAGCTTATGCGCAGAGTGCTGACAGCTGATGCTGACACCTTCAATCCCAAGAA 1234
Qy 1138 TTGGCTGATGTTGAGGCAACCGCCAGAGACCTTGGAAATGGCTGCTAAATTAAG 1197
Db 1235 TTGCTGGCCAGGAGCCAGTTAAAGAAACTGATTCGTGAGTCACAGATTCAGAT 1294
Qy 1198 GCTCATGTTACAGAGAAACACCAACAGCTGATATTTTATGATCTTGCCTCAGTC 1257
Db 1295 GTTCATGCGACGCTGCTCAGAAAGCACCAGATATTAATGATGATCTGTTGATTAAC 1354
Qy 1258 TATTTGCTGCTCCCATGATGCTTGTGTGCAATTAACGTTTCAATACACCTCCGTACA 1317
Db 1355 TACTTGTGTTCCGGCCCTGAGAGGTGTCATTCGCCACCGCTGAGGCTGAGGCT 1414
Qy 1318 CCCGCTACTTGTATGCTTGCATTCGATTCGAGATCTTATCAATCCCTATGCTATT 1377
Db 1415 CCGATATATTTCTATGATATGATCTGACTCGAGAGAGCTATTTTCCGTAACCCATT 1474
Qy 1378 ATGCGTAGTGAGACGTGTAAAGGTGTTAGTATGATGATGATTAACCTATTTCTTC 1437
Db 1475 ATGCGGTTGGGAGCGGCTGCAAGGGGTGACGATCGGAGATTTGAGCTACCAATTC 1534
Qy 1438 TGGAAATCAATTTGGCCAAAGCTATGCTAAAGAAATCCGGAATACAAACATTAAGCT 1497
Db 1535 AGAGGCTCTGCTGCTGCGGCTGCGAAGAAAGTCGAGAGTACGGAATCTGAAACA 1594
Qy 1498 ATGACTGATATATGATACAAATTTGGCACCACATGTAATCTTATGCAATGAATTTGA 1557
Db 1595 ACCGTGGGATCTGAGACCAAGTTTGTGCGACAGGGTATTCCTTACGCGAAGAGATCAAC 1654
Qy 1558 GGTATGGAATATGTTTCTGGAATCCAAATTAAGAAATCCGATGATATACAAGTTTGG 1617
Db 1655 GGTATGGAACACTGACATGATGATCAAGTTCGAAATTCGAGAGATCAATCAAGTCCCTC 1714
Qy 1618 AATATTAGATGATTAAGAAATGATGATGCTGGAATGATGATTAAGATTAACATG 1677
Db 1715 AATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1774
Qy 1678 GAGTCATGTTTGAAGAAACATAGATTTATTTT 1711

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Db 1775 GAGAGCCTTATGACGACAAACAAGATTTATGCT 1808
RESULT 10
ABL02081
ID ABL02081 standard; cDNA; 1704 BP.
XX
AC ABL02081;
XX
XX 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SBO ID NO 725.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX
XX pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX P-PSDB; ABB57978.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX
XX
XX Claim 1; SEQ ID NO 725; 21bp + Sequence Listing: English.
XX
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABB57737-ABB72072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
XX Sequence 1704 BP: 417 A; 445 C; 460 G; 382 T; 0 other.
XX
Query Match 22.3%; Score 381.8; DB 23; Length 1704;
Best Local Similarity 54.0%; Pred. NO. 1.2e-94;
Matches 879; Conservative 0; Mismatches 727; Indels 21; Gaps 4;
Qy 85 ACCAATGAAGCGGTGCTGACTGATGATGCAATGCAAGTGAAGGCGTTAAAGCTTTA 144
Db 64 ACCAATGACAAAGGTATGCGCCGACAGGCTTACGAAAGGTGAAGGGGTGAAGTGGCAG 123
Qy 145 ACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 204
Db 124 TCCATCTAGGCAACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 183
Qy 205 GGTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 264
Db 184 GCGAGCTCCGCTTCAAGCGCCCTGAGCCAGGACACTGATGATGATGATGATGATGATGATGAT 243
Qy 265 TGCATCAATGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 324
Db 244 ACACATGTTGCGCCCAAGCCCTGCGCAGGTCAACATGCTTCTGAAGCAGGTGCAAGGCGAC 303

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OY	325	GAGATGTCGTAATACCAACTGCTCTACAGAAATTAATCTAAATCCGGAACCTTAACGCTCC	384
Db	304	GAGACTGTCTGTAACCTCAATGTCTACACAGGGAATTCATCTCCACACAGACTTTGGCG	363
OY	385	GTTTTAACTATACATACATGCTGGTGGTTTTATTATGCGAATAATCATGTCATATGAT	444
Db	364	GTTCGTGGTGAATCTATGATGCGGGGTGATTCCAAAATGGAGAAAGCATCGGGGATCTGAC	423
OY	445	GCCTCCTATATTTCACTATAAAGATGTGCGTTGATTAAATATACATATCTGTTGGGA	504
Db	424	AGCCCGACATCAATTAATGATGAAACATGTCTGATCTGTATATTCATCTGGTTAGGA	483
OY	505	GCTCTAGGTTTTCTTAAGTTTAATTAATCAGAAGACCTTAATGATCCCGGTAATCGCGGCTT	564
Db	484	GCCTGGGATATCTCTTAATCTTTGACAGACAAAGAACTGGATGTTCTGGAAGACCGGACTA	543
OY	565	AAATATCAATGATAGGCTTCGCTTGATTTAAATAATTTGGGCCAATCTTTGGTGGCAAT	624
Db	544	AAGGATCAAGTTATAGGCTTGGCGGTGGGTCAAAACGGAAATTTGCCAGTCTTTTGTTGGCAT	603
OY	625	CCCATATATATTACAGCTCTTGGTGAAGAAGCGCGGTGCTCTCAACCATACATCATGATG	684
Db	604	CCGATATATATTAACCGTTTTTGGTGAAGAGTCTGGAGGTGCATCCACATATATATGATG	663
OY	685	TTAACCGAACAACTCGCGGTCTTTTCCATCGTGTATCTAATGTGGGGTAATGCTATT	744
Db	664	CTGACGATCAAGGCCCAAGGGCTATTTCACAAACATATATTATTTGCGGGATCCGCACTG	723
OY	745	TGTCCATTTGGCTATTAACCCAATGTCA--ACATCGTGCTTCACTTAACCCAATTTGGCC	801
Db	724	GCACCTCTGGGGGACACCCCAACCATTAATTTGGCCCTATGCGCTGGCACAGGCCACT	783
OY	802	GGCTATATAGGGTGAAGTAATGATAGAGATGTTTGGATTCTTATGAAGACCAAGCA	861
Db	784	GGCTACACAGAGATGCTAACGATCGGAGCATTTTTGCCCATCTCAAGAAATGTAAGGC	843
OY	862	CAGATTTAATTAACCTTGAGAGAAAAGTTTAACTCTGAAGAGCGTATCAATATAGT-	920
Db	844	AGTAGCATGCTGAAGGGTGGCGGAGGATATCATACCATGAGGAGAGACACAGCGGTG	903
OY	921	--CACTTTCCTTTTGGTCCCACTGTGTGAGCCATATCAACGCGTATGTCCTTACC	978
Db	904	ACCATGTTCACGCTTTGGACCCACCATGAGCCCTATTGATCTCTCATTTGTTGATTTCC	963
OY	979	AAACATCTCTGGGAAATGTTTAAACTGCTGGGGTAATTCGATACCCACTATGATGGGT	1038
Db	964	AAGTCGCCACATGAAATGATGCGGGAGCTGTGTGGGACAAAGCATTCCTATGCTACGGA	1023
OY	1039	AACACTTCATATGAGGGTCTATTTTTCACTTCATTTCTTAAGCAAAATGGCTATGCTGTT	1098
Db	1024	GGAAATCTCTTGAAAGTCTCTCTCATGTTTTCCGAAGTGAACAAGTGGCCGGAACCTGTT	1083
OY	1099	AAGGAATGAAACTTGTGTCAATTTTGTGCCAAGTGAATTTGGCTGATGTTGAAGCAACC	1158
Db	1084	TGCAGCTGGGTGACTCGAGAACTGCGCCCTCAAGATAGCCACAGTAGATAGCAGCA	1143
OY	1159	GCCCCAGAGACCTTGGAAATGAGGTGCTAAATTTAAAGAAGCTCATGTTACAGAGAAACA	1218
Db	1144	AGAAAGGCTTTGGAAAGAAAGTACGAGACATATATTTGGCGATAGGACTCTCGCAGG	1203
OY	1219	CCACAGCTGATATATTTATGATATCTTTTGGCTGCACATCTATTTTGGTTCGCCATGAT	1278
Db	1204	AAGACATATTTGGAGTACACGATCTCTCTGCTACAAATATTTTCTGGCATGGCATTCAT	1263
OY	1279	CGTTTGTGCAATTAAGTTTCAATCAACCTCCGGTACACCCGCTACTTATGATGCTTC	1338
Db	1264	AGGACTTGTGCTCGCTCGCTGCACACAGCCCACTTTGGCCCAAAATCTCTGACGCAATTC	1323
OY	1339	GACTTTCGATTTGGGAAGTCTTATCAATCCCTATACGATTAATGCGTAGAGAGTGTGTTT	1398
Db	1324	GATTTCCAGCTCG--AAGCACTTCAATATACGGAATTAATCACTGTGGCCGCAAGGTG	1380

RESULT 11

ABL02066
ID ABL02066 standard; cDNA; 6175 BP.

XX ABLO2066;
AC
XX
DT 26-MAR-2002 (first entry)
DE
XX
KW Drosophila melanogaster expressed polynucleotide SEQ ID NO 680.
KM Drosophila: developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ss.
OS Drosophila melanogaster.
PN WO200171042-A2.
PP
PD 27-SEP-2001.
PR 23-MAR-2001; 2001WO-US09231.
PX PF 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE) PE CORP NY.
PI Venter JC, Adams M, Li PMD, Myers EW;
PT WPI: 2001-656860/75.
DR P-PSTDB; ABB57963.
XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -
XX
PS Claim 1; SEQ ID NO 680; 21pp + Sequence Listing; English.
CC The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
(ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp://wipo.int/pub/published_pct_sequences.

DT 26-MAR-2002 (first entry)
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 779.
DE
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
PN WO200171042-A2.
XX
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
PR (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PMD, Myers EW.
PI WPI; 2001-656860/75.
DR P-PSDB; ABB57996.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 779; 21bp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in determining biological and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840-AB116175), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (AB101840-AB116175).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 1665 BP; 397 A; 446 C; 468 G; 354 T; 0 other;
SQ
Query Match 21.5%; Score 368.2; DB 23; Length 1665;
Best Local Similarity 52.4%; Pred. NO. 6.7e-91;
Matches 861; Conservative 0; Mismatches 773; Indels 9; Gaps 2;
QY 53 TTGAATAATAGTTTAACTATGTTTAACTACCAATGAAGCGTGTAGTGAAGTGG 112
DB 5 TCGACTTTAAAGTCCACACAGAGATACAGACAGGAAAGAACTCTCTCAGACCA 64
QY 113 AATATGCAAGTGAAGCGTTAAAGCTTAACTGTGTAGATGATTCCTACTACACT 172
DB 65 CCGTACGACCCATCAAGAGGTGTAAAGAGAGTCACTACGCGCAGTCTACTACT 124
QY 173 TTGAGGATATACCGTACCGCCAGCGGAGTGTAGTGAAGTGAAGTGAAGTGAAG 232
DB 125 TCGAGCGGATCCCTTCGCAACACGCGGTGGGAGCTACGCTACAAAGCTCCCGAGC 184
QY 233 GACCAACACCGTGGATGTTGCGTGTATGTCATCATTAAGATGAAGTGAAGTGAAG 292
DB 185 CCGCGGAGGTGTGAGAGAGTCAAGAGTCTCAGCTCCAGAGGTCCTCAAGCAGTCA 244
QY 293 TTGATTTTAAAGCGCAAGTGTGTGCTCAGAGATTTGTCTATACCTAAGTGTCTATA 352
DB 245 AGCACTTGCTGTGAGATGACCGATGCTCGAGAGTCTGCTCTACTCATGTCTACA 304
QY 353 CGAATATCTTAATCCGAACTAAGCTCCGTTTATGTTTACATCATGTGTGTGTT 412
DB 305 CAAGAATTTTATCCACCAACCAATGCGGTGATGCTGTGATGCTATGCGGTGCT 364

QY 413 TTATATCGTGAAATATCATGATATATGATGCTGATTTATTTTAAAGAGATG 472
DB 365 TCGAGTTGGGAGAGCCCTCAGAGGATGTATACAGTCGGATTTATTTGCTGAGATG 424
QY 473 TGTGTTGATTAACATATATATGCTTTGGAGCTCTAGTTTCTTAAGTTAAATTCAG 532
DB 425 TGTGTTGATTTATCACTAATCACTAGTGGAGCACTGGATTTCTGCTGAGCATG 484
QY 533 AAGACCTTAATGTCGCGGTATGCGGCTTAAAGATCAATGCTATGCGCTTGGTGA 592
DB 485 CCGAATCTGATGTGCGGCAATGCGGATCAAGATGATGTTGGCCCTGCGCTGG 544
QY 593 TTAATAATATGCGCCAACTTTGGTGGCAATCCGATATATTAATCACTTTGGTGAA 652
DB 545 TCAAGGCCAATGTTTGGGTTTGGAGGCAATTCGCGCAATTAATCAATTTTGGGACA 604
QY 653 GTGCGGTGTGCTCTTACCACTACATGATGTTAAACCAACAACTGCGGTCTTTTC 712
DB 605 GTGCGGGAAGTGCCTCGGTTCATCATATGATGATCAGACAGACGATGACTTTTC 664
QY 713 ATCGGTATATATGTCGGTATATGCTATTTGTCATTTGGCTATATCCCAATGTAAC 772
DB 665 ACAAGCCATCTGCAATGCGGTATATGCTTTCCCTCGGCACTGCTCTAGAGAA 724
QY 773 ATCGGTCTTACCTTACCAATTTGGCGGCTATAGGAGTATATATAGATG 832
DB 725 ACTGCGCATATGCGGTGCTGCTCCAGGCGGTTTACGAGGTGAACCAACCCCGATG 784
QY 833 TTTTGAATTTCTATGAAGCAAGCAAGATTTAATAAATCTGAGGAAAGTTT 892
DB 785 TCTGGAGTCTCTGAAAGCAAGCAAGGATCCGAATCATCAACCAATGAGAACTCT 844
QY 893 TAACCTGAAGAGGTCAATATAGTATGTTTCTTTTGGTGGCTGTTGAGCAT 952
DB 845 GCATTGACAGAGAGAGAGAGAGCGGATTTGATTTCTTTTGGCCCTATGCAACCT 904
QY 953 ATCAAGCCGCTGATGTTGCTTACCAACATCTCTGCGGAAATGTTAAACTGTTGG 1012
DB 905 ATGTACACGACGACTGTGTGGTGGAGGAAACCAATGAAATATGAAACCCGCTGA 964
QY 1013 GTAATTCATACCCCTATGATGTTGTAACACTTCAATATGAGGTTATTTTCACTTAA 1072
DB 965 GCAATTAATATCCCACTTATCATGCGAGGCTTTCCACAGGAGGCTCTCTTGTACTAG 1024
QY 1073 TTCTTAAGCAATGCTGCTGTTGTTAGGAATGGAATGTTGTTCAATTTTGGCAA 1132
DB 1025 AGACCAAGACGATCCGAGATGTCTAAAGAGTTGAGCACTGCGGTTTGTGCTGA 1084
QY 1133 GTGAATGGCTGATGTTGAAGCAACGC-----CCAGAGACTTGGAAATGGGTGCTA 1186
DB 1085 TCGAATTAATATGACAGGGAAGATGCTGTGCGGAGATGAGCGCATCAGTGAAGC 1144
QY 1187 AATTAATAAGCTCATGTATACAGAGAAACCAACAGCTGATATATTTATGATCTTT 1246
DB 1145 AGTGTACTAGCGGATTAAGAGCGCCAGTCTGAGACACCTGATATATCTTCAGATGG 1204
QY 1247 GCTTCACATATATTTTGTGTTCCCATGATGATGTTTGTGAATTTAGCTTTCAATCA 1306
DB 1205 TTTCCACAGAGTACTTGTGTTTCCCAATATACCGCAAGTATTTGCGCGCTGAGTACG 1264
QY 1307 CCTCGGATACACCGTGTACTTGTATGCTTCTGATGATGATGATGATGATGATGATG 1366
DB 1265 CTGCGAGTGGCGGAGATATTTGTACGCTTGTGACTTTGACTG---CAAGACTTCAAC 1321
QY 1367 CCTATGATTAATGCGTATGAGTGAAGTGTAAAGTGTATGATGATGATGATGATG 1426
DB 1322 ACTGTCGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1381
QY 1427 CCTATTTCTTGTGAATATATTTGGCAAACTGATGCTTAAAGATTTGCGGTGAATCAAA 1486
DB 1382 CCTACTGTTGTATACACTGCTGCGGAGAGAGCTCAACACACAGCGGAGATGAAGT 1441
QY 1487 CAATGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1546

QY	1190	TTTAAAGGCTCATGTTCACGAGAAACACCAACAGCTATATATTTATGATCTTTGCT	1249
Db	1281	TTCTACTTCAACACGAGATGACAGAAATGCATGAGATGTTGAGAGCCCTCGAATATATTTT	1340
QY	1250	CTCACATCTATTTTCTGGTTTCCCATCATCAGTTGTTGCAATTAGGTTTCATCACACT	1309
Db	1341	CGCATGCCAGATTTTGGCAGCATAGCCATTCGGTTATTTCTGCGCGTCAATCTTATGGCC	1400
QY	1310	CCGGTACACCCGTCCTACTTGTATTCGCTTGACTTGCATTGCGAAGATCTTATCAATCCCT	1366
Db	1401	CCAAACGGCCCACTATCTTTATTCGTTTGTACTTCACACAC---CCCGCACTTCATCATAT	1457
QY	1370	ATTCATATTATGCGTAGCGAGCAGCGTGGTAAAGGTTTGATGCTGTCGATGAATTAACCT	1429
Db	1458	TTGCGCGACATGCTGTGGCGGATTCGGATTCGCGGATACCCATGCGGATGACACTATAT	1517
QY	1430	ATTTCTTCTGGATCAATTTGGCCAAACGATGTCCTAAGAATCGCGTGAATACAAACAA	1489
Db	1518	ACCTGTTTCTACAAATCATATGCTGCCAAATCGATTAAGCATCGATGATCAAAACCA	1577
QY	1490	TTGACGATGACGTGATATGTGATACAAATTGCCACACGTGATATCCTTTACCATG	1549
Db	1578	TTTGAGAAATATGTTGGCATGTGACGTCGTTTGCTCCAGTGGGAATCCAAATTCGCCAG	1637
QY	1550	AAATTTGAGGTATGAAAATGTTTCTCGGAGATCCAAATTAAGAAATCCGATGAATATACA	1609
Db	1638	AACGTGATCTGCCAAATGTGGAAGCGGTCCAGC-----TTAAGAAATGCGCGTGAGA	1691
QY	1610	AGCTGTTGAATATTAGATGAGATTTGAAAATGATTTATGTGCGCTCGAATGAT	1662
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ID	ABLO2103 standard; cDNA; 1593 BP.
XX	
AC	ABL02103;
XX	
DT	26-MAR-2002 (first entry)
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KW	Drosophila; developmental biology; cell signalling; insecticide;
XX	
KW	pharmaceutical; gene; ss.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO200171042-A2.
XX	
PD	27-SEP-2001.
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PF	23-MAR-2001; 2001WO-US09231.
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PR	23-MAR-2000; 2000US-191637P.
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PR	11-JUL-2000; 2000US-0614150.
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PA	(PEKE) PE CORP NY.
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PI	Venter JC, Adams M, Li PMD, Myers EW;
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DR	MPI; 2001-656860/75.
XX	
DR	P-PsDB; ABB58000.
PT	New isolated nucleic acid detection reagent for detecting 1000 or more
XX	
PT	genes from Drosophila and for elucidating cell signalling and cell-cell
XX	
PS	interactions -
XX	
PS	Claim 1; SEQ ID NO 791; 21pp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent
XX	
CC	capable of detecting 1000 or more genes from Drosophila. The invention is

cell-cell interactions in higher eukaryotes for the development of
discloses genomic DNA sequences (AB161716-AB163511), expressed DNA
sequences (AB101840-AB161715) and the encoded proteins
(AB57737-AB97202).
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPAC
at ftp.wipo.int/pub/published_pat_sequences.

Sequence 1593 BP; 417 A; 394 C; 405 G; 377 T; 0 other;

Query Match	18.98;	Score 323.2;	DB 23;	Length 1593;
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Db 6 TGACTGCGGTCCTGTGCGGGGAGTGAAGAGAACAACAATCTGGGGAGGAAGCTACTTCAG 65

271 TTTGAGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCTCA 230

Db 66 TTTCGAGAAGATACCCCTTCGCAAAGCCTCCGGTGGAGATCTGGCTTCAAGGCCCGGA 125

231 GCGACCAACACCCCTGGGATGGTGTGCGTGATTGTTGCCAATCATAAGATAAGTCAGTGCA 290

Db 126 AGCAGTGGAGCCATGGATCAGGAATTGGATTGCACCTTCGCCGGCAGACAAGCCCTTCA 185

QY 291 AGTTGATTTTATAACGGGCAAGTGTGTGGCTCAGAGGATTGTTATACCTAAGTGTCTA 350

Db 186 GACACACATGTTTTCAGAAATACGGGCTCAGAGACTGCCCTCTACTTTAATGTGTA 245

351 TACGATAATCTAAATCCCGAACTAACCGTCCCGTTTCTAGTATACATACATGGTGTG 410

Db 246 TGTCAAGATCTGCAGCCGATAACTGCCGTCCCGTGATGCTTGGATCTACGGAGGAGG 305

411 TTTTATTATCGTGAAATCATCGTGATATGTATGGTCCGTGATTATTTCATTAATAAAGGA 470

Db 306 CTATCAAGTTGGCGAAGCTTCTCGGATATGTACAGTCCCGACTTTTTCATGTGAAGGA 365

QY 471 TGTGGTGTGATTACATACATAATCGTTTGGGAGCTCTAGGTTTCTAAGTTTAAATTC 530

Db 366 TGTGGTCATAGTCACCGTTGCTTATCGACTGGGTGCCCTGGGCTTCCTCAGCCTGGATGA 425

QY 531 AGAAGACCTTAATGTGCCCGTAATGCCGCTTAAGATCAAGTCATGCCCTTGCCTG 590

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 AC ABL01859:
 XX 26-MAR-2002 (first entry)
 XX DT
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 59.
 KW Drosophila: developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 XX 27-SEP-2001.
 PD 23-MAR-2001; 2001WO-US09231.
 XX

PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
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 PA (PEKE) PE CORP NY.
 PI Venter JC, Adams M, Li PWD, Myers EW:
 DR WPI: 2001-656860/75.
 XX P-PSDB: ABB57756.
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Claim 1: SEQ ID NO 59; 21pp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB57737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
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 SQ Sequence 1863 BP; 425 A; 493 C; 523 G; 422 T; 0 other:
 Query Match 18.9%; Score 323; DB 23; Length 1863;
 Best Local Similarity 52.4%; Pred. No. 1.9e-78;
 Matches 812; Conservative 0; Mismatches 725; Indels 14; Gaps 4;
 QY 1 ATGAATTTCAACGTTGATGATGAGAAATTAATGGAAGATTAATGATGAAAT 60
 DB 166 ATGAGATTCGAGATGGAGAGTGGCGATGCTGTAATGAGGACCAAGCTATTGGCCAC 225
 QY 61 AAGTTTAAATCAATGCTTTAACTACCAATGAACGCTGATGCTAACTAACTGATG 120
 DB 226 AAGATGCTCCAGTATGCTTGGCACAAGCAGAGAGTGTGCTGACCAAGGATG 285
 QY 121 AAGTGAAGGCGTTAAAGCTTAAGCTTAACTGCT---AGATGATTCCTACTACAGTTTGA 177
 DB 286 CAGGTGCGGAGATGCGGCAAGACACTCTACGAGAGAGATGATTCGCTTCCGAG 345
 QY 178 GGTATACCGTACGCCCAACCGCAGTGGTGAAGTTTAATGAACACCCAGCAGCA 237
 DB 346 GAATGCCCTTTGACAGCGCGGAGGAGAGTGGTCCGAGCCGCCAGCCAGCAGCA 405
 QY 238 ACACCCGAGATGCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 297
 DB 406 CATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 465
 QY 298 TTATTAACGGGCAAGTGTGTGCTGAGAGATGCTGATGCTGATGCTGATGCTGATGCTG 357
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 QY 478 TTGATTAACATACATATGCTTGGAGAGCTCTAGGTTTCTAAAGTTAAATTCAGAGAC 537
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GenCore version 5.1.4-p5_4578
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(without alignments)
16677.553 Million cell updates/sec

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Scoring table: IDENTITY_NIC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: gb_est3:*
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14: gb_est5:*
15: em_estfun:*
16: em_estom:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	282.4	16.5	649	9	AI388926 GH1977.5
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5	254.4	14.9	569	13	BI609541 RH14337.5
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10	246.8	14.4	672	13	BI614443 RH43812.5
11	246.4	14.4	670	13	BI233202 RE29491.5
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14	243.4	14.2	646	9	AI109901 GH09292.5
15	243.4	14.2	526	9	AI293416 LP06524.5
16	241	14.1	526	9	AI108080 GH06811.5
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18	239.2	14.0	658	13	BI654586 RH61888.5
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ALIGNMENTS

RESULT 1
LOCUS AI062034 778 bp mRNA
DEFINITION GH01076.5prime GH Drosophila melanogaster head p0T2 Drosophila melanogaster cDNA clone GH01076 5prime similar to U51050:
Drosophila melanogaster alpha esterase (aet) gene, partial cds,
mRNA sequence.

ACCESSION AI062034
VERSION AI062034.1 GI:3337873
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 778)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.

BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798

Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
Plate: 10 row: G column: 4

High quality sequence stop: 363.
Location/Qualifiers

FEATURES

QY	908	GACAAATAAGGTCATCTTCCCTTTGGGCGCCAGCTTGAGCCATATCAGACCGCGTGAAT	967
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QY	968	GTGTCTTACCCAAACATCTCGGGGAAATGTTTAAACCTGTTGGGGTAAATTGATACCCA	1027
DB	544	GTGTGATATCCACAGCGCTCCAAAGAGATGATGAAACACCGCGCTGGAGTAACTCATCCCA	603
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DB	604	TGTTTATAGAAACACTTCTGTCAGAGCGCGCTGCTGT	639
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VERSION	Al103569.1	GI:4246656	
KEYWORDS	EST.		
SOURCE	fruit fly.		
ORGANISM	Drosophila melanogaster		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
AUTHORS	Harvey,D., Brokslein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.		
TITLE	BDGP/HHMI Drosophila EST Project		
JOURNAL	unpublished (2001)		
COMMENT	Contact: Stapleton, M.		
	BDGP		
	Lawrence Berkeley National Lab		
	One Cyclotron Rd. Berkeley, CA 94720, USA		
	Fax: 510 486 6798		
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu		
	Plate: 230 row: C column: 12		
	High quality sequence stop: 648.		
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	/lab_host="DHS - alpha"		
	/note="Organ: head; Vector: por2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into por2. Plasmid cDNA library."		
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Best Local Similarity	65.2%; Pred. No. 3.5e-61;		
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DEFINITION	GH28740.5,prlme GH Drosophila melanogaster head, pot2 Drosophila melanogaster cDNA clone GH28740 5prime similar to U51050:			
LOCATION	Drosophila melanogaster alpha esterase (aet) gene, partial cds, mRNA sequence.			
ACCESSION	A1517692			
VERSION	A1517692.1	GI:4420792		
KEYWORDS	EST.			
SOURCE	fruit fly.			
ORGANISM	Drosophila melanogaster			
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidae; Drosophilidae; Drosophila.			
REFERENCE	1 (bases 1 to 671)			
AUTHORS	Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.			
TITLE	BDGP/HHMI Drosophila EST Project			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Stapleton, M.			
	BDGP			
	Lawrence Berkeley National Lab			
	One Cyclotron Rd, Berkeley, CA 94720, USA			
	Fax: 510 486 6798			
	Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu			
	Plate: 287 row: D column: 4			
	High quality sequence stop: 538.			
	Location/Qualifiers			
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BASE COUNT
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ORIGIN
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    Matches 372; Conservative 0; Mismatches 196; Indels 0; Gaps 0.

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QY	17	GTGTTATGAGCAAAATTAATAAATGGAAGATTAAATGCTTGAAGAAATTAAGTTTAAATATC	76			
Db	1	GCTTTGTGAGAGCGCTGGGGGTGGGCCCTCAAAACCATGAGACATTAAGTCCAGCAGATATC	60			
QY	77	GTTTAACTAACCATGAACAAACGGTGTAGCTGAACACTGAAATATGCGAAATGGAAGCCGTTA	136			
Db	61	GCCAGTGCAGCAATTAACAAACAGTTGTGGCGACACGAGATAGCGCCAAAGTGAAGGGGTATCA	120			
QY	137	AACGTTTAAGTCTGTAGCAATGATGATCTCTACTACAGTTTGTAGGGGTATACCGTACGCCAAC	196			
Db	121	ACCGTCTATCTCTTACCAATGTGGCCCTACTTTCAGTCTGAGAGGTATCCCGTACGCCAGC	180			
QY	197	CGCCAGTGGGTGAGCTGAGATTTAAAGCACCCACGACCAACACCCCTGGGATGTTGC	256			
Db	181	CTCCGGTGGGGAGTTGCGGTTTAAGGCCCCCTCAGAGGCCCAATCCCTGGGAGCGAGTTCC	240			
QY	257	GTGATTTGTTCACAAATATAAGATTAAGTACAGTCCAGTCAAGTTGATTTTAACGGGCAAGTGT	316			
Db	241	GGCACTGCAGCCACGCCGGAAGGATTAAGGCCCTCAGAGTCAAGTTGCTTTCATTAAGGTAG	300			
QY	317	GTGGCTCAGAGGATTTGCTCTATCTAAGTGTCTATACGAATATCTAAATCCCAACTA	376			
Db	301	AGGGCTCCGAGGACCTGCTCTATCTCAATGTGTACACCAACATGTGAAGGCCCAAGG	360			
QY	377	AACGTCCCGTTTATGATACATACATAGGTGGTGTATTTATTCGGTGAATTCATCGG	436			
Db	361	CTCGCCCGGTTATGTTTGGATTACAGGAGAGGGCTCATATCGGCGAAGCCCAATCCGG	420			
QY	437	ATATGATGTGCTCGATTTATTTTCATTAACAAAGATGTGCTGTGATTAACATACAAATTC	496			
Db	421	AATGATATGCCCCGATTTACTTTATGAAGAAGATGTTGTCTCGACAGATACAGTACC	480			
QY	497	GTTTGGAGCTTCTAGGTTTCTTAAGTTTAAATTCAGAAACCTTAATATGCGCCGGTAATG	556			
Db	481	GACTTGGGGCTTTGGGATTTATGAGTCTTAAGTCCCGCAGATTAATGTATCCAGGAATG	540			
QY	557	CGGGCTTAAGAGATCAAGTCATGGCCTT	584			
Db	541	CTGGCCTCAAGATCAAGTGTCTGGCCT	568			
RESULT 6						
BI628316						
LOCUS	BI628316	674 bp	mRNA			
DEFINITION	RH56682.5:prime RH Drosophila melanogaster, normalized head plc-1					
Drosophila melanogaster cDNA clone RH56682.5 similar to alpha-Est7:						
F8ano001112 GO: [carboxylesterase (GO:0004091); carboxylesterase						
(GO:0004091)] located on: 3R 84D5-84D5;: 08/22/2001, mRNA sequence.						
ACCESSION BI628316						
VERSION BI628316.1 GI:15530524						

KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota:
Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
REFERENCE
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
, J., Champagne, M., Chavez, C., Dorsett, Y., Farfan, D., Frise, E., George
, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,
Mungall, C.J., Nuno, J., Pacleb, J., Paragas, V., Park, S.,
Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celisner, S. and Rubin
, G.M.
TITLE BDGP/HHMI RH Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: RH.566 Row: G Column: 10
High quality sequence stop: 558.
Location/Qualifiers
1. 674
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pR1c-1"
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/dev_stage="Adult"
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/note="Organ: head; Vector: pR1c1; Site:1: XhoI; Site:2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
BASE COUNT 153 a 170 c 195 g 155 t 1 others
ORIGIN
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Best Local Similarity 65.2% Pred. No. 4.9e-57;
Matches 367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
OY 1 ATGATTTCAACGTTAGTTGATGAGAAATTAAGAGATTAATGATGATGAAT 60
DB 111 ATGATTAAGAACTGCGCTTTGAGCGCTTGGCGCTTAAACATCGACAT 170
OY 61 AAGTTTAACTATCGTTTAACTACCAATGAACGTTGAGTGAACATGATATGCG 120
DB 171 AAGTCCAGCAAGTATCGCGACGACCAATGAACAGTTTGCACGACGAGTACGCG 230
OY 121 AAGTGAAGCGTTAAAGCTTTAACTGTAGATGATTCCTACTACAGTTTGGGGT 180
DB 221 CAAGTGAAGGCTATCAACGCTCTATCTCTACGATGTGCTTACTTACGTTGAGG 290
OY 181 ATACCGTACGCCAACCCGACGCTGAGTGAATTAAGCAACCCGACGACCAACA 240
DB 291 ATCCCGTACGCCACGCTGCGGTGGGAGTGGCGTTAAGGCCCTCAGAGGCCCAT 350
OY 241 CCTGCGATGCTGCTGATGTTGCAATCATAAAGATTAAGTCAAGTCAAGTATTT 300
DB 351 CCTGCGAGCAAGTTCGCGACTGACGACGACCAAGATTAAGGCCCTCAGAGTTC 410
OY 301 ATAAAGGCAAGTGTGCTCAGAGATGTCTAATCAATGATGTTATACGAATAT 360
DB 411 GTCTTCGATAGTAGAGGCTCCGAGACTGCCCTATCAATGTGTACACCAAT 470
OY 361 CTAATCCGCAACATCAACGTCGCTTTATATACATACATACATACATACATAT 420
DB 471 GTGAAGCCGCAAGAGCTGCGCGGTATAGTTTCAAGGAGGAGGCTTCAATATC 530
OY 421 GGTGAATATCATCTGATATGTATGTCTGATTAATTTCAATTAAGATGATGTG 480

DB 531 GGCGAGCCCAATCGGAGATGATGCGCCGATTAATTAAGAGATGTGTCTC 590
OY 481 ATTAACATACATATATCTTTGGAGCTCTAGTTTTCATAGTTTAATTCAGAACCTT 540
DB 591 GTACAGATACAGTATACCGACTTGTGAGCTTATGATTAAGTCCCTCCAGTAC 650
OY 541 AATGCGCCGGAATGCGCGCT 563
DB 651 AATGACCAAGGAATGCTGGCT 673
RESULT 7
B1635372
LOCUS
DEFINITION B1635372 676 bp mRNA linear EST 10-SEP-2001
SD16705.5prime SD Drosophila melanogaster Schneider L2 cell culture
PORT Drosophila melanogaster cDNA clone SD16705 5 similar to
alpha-Est7: Fban0001112 GO: [carboxylesterase (GO:0004091);
carboxylesterase (GO:0004091)] located on: 3R 84D5-84D5:: 05/18/2001
, mRNA sequence.
ACCESSION B1635372
VERSION B1635372.1 GI:15537582
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota:
Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
REFERENCE
AUTHORS 1 (bases 1 to 676)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
TITLE BDGP/HHMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: SD.167 Row: A Column: 5
High quality sequence stop: 641.
Location/Qualifiers
1. 676
/organism="Drosophila melanogaster"
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/clone="SD16705"
/clone_lib="SD Drosophila melanogaster Schneider L2 cell
culture PORT2"
/lab_host="DH5-alpha"
/note="Vector: PORT2; Site:1: EcoRI; Site:2: XhoI; Sized
fractionated cDNAs were directly ligated into PORT2.
Plasmid cDNA library."
BASE COUNT 155 a 173 c 194 g 154 t
ORIGIN
Query Match 14.6% Score 249.4; DB 13; Length 676;
Best Local Similarity 65.2% Pred. No. 7.1e-57;
Matches 367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
OY 1 ATGATTTCAACGTTAGTTGATGAGAAATTAAGAGATTAATGATGATGAAT 60
DB 114 ATGATTAAGAACTGCGCTTTGAGCGCTTGGCGCTTAAACATCGACAT 173
OY 61 AAGTTTAACTATCGTTTAACTACCAATGAACGTTGAGTGAACATGATATGCG 120
DB 174 AAGTCCAGCAAGTATCGCGACGACCAATGAACAGTTTGCACGACGAGTACGCG 233
OY 121 AAGTGAAGCGTTAAAGCTTTAACTGTAGATGATTCCTACTACAGTTTGGGGT 180
DB 234 CAAGTGAAGGCTATCAACGCTCTATCTCTACGATGTGCTTACTTACGTTGAGG 293
OY 181 ATACCGTACGCCAACCCGACGCTGAGTGAATTAAGCAACCCGACGACCAACA 240

Db	294	ATCCCGTAGCGCCAGCCTCCGGTGGGGAGTGGGTTTAAGGCCCTCCAGAGGCCATT	353
Qy	241	CCCTGGGATGGTGTGCGTGATTTGGCAATCATTAAGATTAAGTCAGTGCAGTTGATTTT	300
Db	354	CCCTGAGGACGACGTTCCCGACTGCAGCCAGCCGGAAGATGAGGCCGTCAGGTCAGCTTC	413
Qy	301	ATAACGGGCAAGTGTCGGCTCAGAGGATTTGTCATACCTAAGTGTCTATACGATTAAT	360
Db	414	GTCCTCGATTAAGTAGAGAGGCTCCGAGGACTGCTTATCTCAATGTGTACACCAACAT	473
Qy	361	CTAATCCCGGAACCTAAACGTCGCCGTTTATGATATACATACATGCTGTGGTTTATATAC	420
Db	474	GTCGAAGCCCGCAAGGCTCGCCCGGTATGGTTTGATTCAGGAGGAGGCTCATATAC	533
Qy	421	GGTGAATAATCATGCTGATATGTATGTGCTCGATTTATTTCAATTAAGAAAGATGTGCTTG	480
Db	534	GCGCAGGCCATCGGAATGTATAGGCCCGGATTACTTAATGAAGAAGAAATGTTGTTCTC	593
Qy	481	ATTAACTACCAATATCGTTTGGGAGCTTACGTTTCTAAGTTAAATTCAGAGACCTT	540
Db	594	GTCAGAGATACAGTACCGCACTTGGGGCTTTGGGATTTATGAGCTTTAAGTCCCCCGAGCTA	655
Qy	541	AATGTGCCGGTAATGCCGCGCT	563
Db	654	AATGTACCAAGAAATGCTGGCT	676

RESULT 8	LOCUS	DEFINITION	FEATURES	ORIGIN
B1639486	B1639486	SD22067.7, Spine SD <i>Drosophila melanogaster</i> Schneider L2 cell culture	660 bp mRNA linear EST 10-SEP-2001	
		PM22 <i>Drosophila melanogaster</i> cDNA clone SD22057.5 similar to alpha-Est1; Fban0001112 GO: [carboxylesterase (GO:0004991); carboxylesterase (GO:0004991)] located on: 3R 84D5-84D5:: 05/19/2001		
		carboxylesterase. mRNA sequence.		

ACCESSION	BI639486	
VERSION	BI639486.1	GI:15541696
KEYWORDS	EST.	
SOURCE	fruit fly,	
ORGANISM	Drosophila	melanogaster

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 660)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.	Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha, Ephydroidea: Drosophilidae: Drosophila.	Bdcp/Hhmi Drosophila EST Project	Unpublished (2001)
	Unpublished (2001)	Contact: Stapleton, M.		

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, esefruitfly@berkeley.edu
Plate: SD 220 row: F column: 7
High quality sequence stop: 546.

FEATURES
source

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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="SD2067"
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culture pot2"
/lab_host="DH5-alpha"
/notes="Vector: pot2; Site_1: EcoRI; Site_2: XhoI. Sized
fractionated cDNAs were directly ligated into pot2.
Plasmid cDNA library."
BASE COUNT      169 a      170 c      176 g      145 t
ORIGIN

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Query Match	14.5%	Score 248.6;	DB 13;	Length 660;
Best Local Similarity	64.3%	Pred. No. 1.2e-56;		
Matches 390; Conservative	0;	Mismatches 214;	Indels 3;	Gaps 1;

QY	535	GACCTTAATGCGCCGGTAATGCGGCCCTTAAAGTCATCAAGTCATGCGCTTCGTTGATT	594
Db	9	GAGCTAAATGTACCAAGCAAGAAATCTGGCCTCAAGATATCAGTGTCTGGCCCTAAATGGATC	68
QY	595	AAAAATAATATGCGCCCAACTTTGGTGGCAATCCCGATATATTACAGTCTTTGGTGAAGT	654
Db	69	AAGAAACAAATTCGCGTAGTTTCGGGGAGATCTCCAACTGCATCAGCTGTTTGGAGAGAT	128
QY	655	GCCGGTGTGGCTCTACCCACTACATGATGTAAACCGAACAACTCGCGGCTCTTCCAT	714
Db	129	GCTGAGGCGGCTCCACATCACTACATGATGCTAACCCGATCAGACCAGGCGCTCTTCAT	188
QY	715	CGTGTAATACATAATGTGGGGTAATGCTATTGTGTCATTGGC--TAATACCAATGTGCA	771
Db	189	GCGGCGATCTTGCACTGCGGAGTGCATTTGTCTTGCGCCTACAGCGCGACCTTACC	248
QY	772	CATCGTGCCTTCACCTTAGGCCAAATTTGGCCGGCTTAAAGGTTGAGGATTAATGATAAGAT	831
Db	249	CATATTCCTTAAGAGATTAGCCAGCTGGTGGCTTCAAGGCGAGACAGACAAAGAT	308
QY	832	GTTTGGAAATTTCTTATTAAGACCGACAGCCAGTTAATAAATCTGGAGAAAATTT	891
Db	309	GGTGGGAGTTCTTCAGACAGCTTAAAGGCCAAGATCTTATTCGGGTGAGGAAAAATGTC	368
QY	892	TTAATCTAGAAGACGATPACAAATAAGTCAATGTTCTCTTCTTTGGTCCACTGTTAGCCA	951
Db	369	CTGACACTGAGAAGACGATGAACAAAGATTAATGTTGGCTTGGCCCATTCCTGSAADCA	428
QY	952	TATCAGACCGCGATGTGTCTTACCACAAACATCCTCGGAAATGTTAAAACTGCTTGG	1011
Db	429	TTCTCCACCGCCGATGTGTGATATTCAAAGCCTCCAAAGGAGATGATGAGACCCGCTGG	488
QY	1012	GGTAATTTGATPACCCACTATGATGGGTAACTACTCATATAGAGGGCTATTTTTCACCTCA	1071
Db	489	AGTAATCTCATCCCATGTTTATPAGGAACACTTGTGAGAGGGCTGTGTGGTTCCA	548
QY	1072	ATTCTTAAGCAATGCTTATGCTGTTTAAAGAAATGGAAATTTGTCAATTTTGTGCCA	1131
Db	549	GAGGTAAAGACTTATGCGCGCAGGTGCTGACGACGTGATGATGTGGGCAACACTTTCATCTCC	608
QY	1132	ACTGAAT 1138	
Db	609	AAAGATT 615	

LOCUS	673 bp	mRNA	linear	EST 07-SEP-2001
B614181				
DEFINITION	B614181	673 bp	mRNA	linear
				EST 07-SEP-2001
				Head pfc1-1
				similar to alpha-Est7
				Drosophila melanogaster cDNA clone RH43493.5
				similar to alpha-Est7
				FBAR0001112 GO:carboxylesterase (GO:0004091); carboxylesterase
				(GO:0004091) located on: 3R 84D5-84D5; 08/18/2001, mRNA sequence

ACCESSION	BI14181	GI:15509706
VERSION	BI14181.1	
KEYWORDS	EST.	
SOURCE	fruit fly.	
ORGANISM	<i>Drosophila</i>	<i>melanogaster</i>

REFERENCE
AUTHORS

Stapleton, M., Brooks, P., Hong, L., Tyler, D., Berman, B., Carlson
J., Champ, M., Chavez, C., Dorsett, V., Parton, D., Frise, E., George
R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Luo, G., Mista, S.,
Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, E., Park, S.,
Phonaneaovong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin
E. (bases 1 to 673)

Ephydriidae: Drosophilidae: Drosophila.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Euryptera,
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydriidae: Drosophilidae: Drosophila.

TITLE BDGP/HHMI RH Drosophila EST project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab

QY	Db	471	GTGAAAGCCGCAAGAGCGTGGCCCGGTTATGGTTTGATTCACGAGGAGGCGTTCATTATC	530
QY	421	GGTGAATAATCATCGTGAATATGATGCTCTGATTAATTTCAATTAAGAGATGCTGTG	480	
Db	531	GGCGGAGCCCATCGGGAATGGTATGGCCCGGATTAAGTAAAGAAAGATGGTCTC	590	
QY	481	ATTACATACATATATCGTTTGAGACCTCTAGGTTTTCATAGTTTAATTCAGAGACCTT	540	
Db	591	GTACAGATACAGATACCGACTTGGGCTTTGGGATTATGAGCTTAAGTCCCGCAGCTA	650	
QY	541	AATGTGCCCCGTTATGCGGCC	562	
Db	651	AATGTACCAAGAAATGTGCGC	672	
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DEFINITION	BT233202	670 bp	mRNA	linear EST 11-JUL-2001
ACCESSION	BT233202			
VERSION	BT233202.1	GI:14700784		
KEYWORDS	EST			
SOURCE	fruit fly.			
ORGANISM	Drosophila melanogaster			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
AUTHORS	1 (bases 1 to 670) Stapleton,M., Brockslein,P., Hong,L., Tyler,D., Berman,B., Carlson J., Champagne,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George ,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S., Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin ,G.M.			
TITLE	BDGP/BHMT RE Drosophila EST Project			
JOURNAL	Unpublished (2001)			
COMMENT	BDGP Contact: Stapleton, M. Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST , estfruitfly.berkeley.edu Plate: RE.294 row: H column: 7 High quality sequence stop: 534. Location/Qualifiers 1. 670 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="RE29491" /clone_1lib="RE Drosophila melanogaster normalized Embryo pPic-1" /sex="male and female" /dev_stage="0-24 hours mixed stage embryonic" /lab_host="DHS-alpha Tona" /note="Organ: embryo; Vector: pPic1; Site:1; Site:2 BamHI. Library was kindly generated by Piero Carrinuci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library." BASE COUNT 152 a 168 c 194 g 155 t 1 others ORIGIN			
Query Match	14.4%	Score 246.4	DB 13	Length 670
Best Local Similarity	64.9%	Pred. NO. 4.6e-56		
Matches 364	Conservative 0	Mismatches 197	Indels 0	Gaps 0
QY	1	ATGAATTTACAGCTAGCTTGATGAGCAATTAATAATGACAGATTAATGCACTTGAAT	60	
Db	110	ATGAAATAGAACTCGGCTTTGTGTGAGCGCTTGCCTGCGGCTCAAAACATCAGAGCAT	169	
QY	61	AAGTTTAACTATCTGTTAACTCAACATGAAGCGTGTAGCTGAATCAATATGCT	120	

DB	170	AAAGCCGACGATATCGCCAGCCACCAATGAAGACAGTGTCTGCCGACACGAGATACGGC	229
QY	121	AAAGGAAAGCGCTTAACGCTTTAACTGTACAGATATTCCTACTACAGTTTGGAGGT	180
Db	230	CAAGGAGGGGATCAACGCTCTATCTCTACAGATGTCCTTACTTCACTTCAAGGCT	289
QY	181	ATACCGTACGGCCCAACCCCACTGGGTAGCTGATTTAAAGCACCCAGCGACCAACA	240
Db	290	ATCCGCTACGCCACACCTCCGGTGGGGAGTGTGCGTTTAAAGCCCTCAGAGGCCCAT	349
QY	241	CCCTGGGATGTGTGTCGCTGATTTGTTCATATCAATAAGATAAGTCAAGTGAATTT	300
Db	350	CCCTGGGAGCGAGTTTGGGACTGACGACGACCGAAGGATTAAGCCGTCACGGTGCATTC	409
QY	301	ATAAAGGACCAAGTGTGTGGCTCAAGAGATTTGTCTATACCTAAGTCTATACGAATAT	360
Db	410	GCTCTTCGATTAAGTAGTAGAGGCTCGAGAGACGTGCCCTATCTCAATGTGTACCAACAAT	469
QY	361	CTAAATVCCCGAAATCAAAAGCTCCCGTTTACTATATACATACATAGTGTGTGTTATATC	420
Db	470	GTAAGAGCCCGACAAAGCGTCCCGGCTTATGTTTGATTTACGAGGAGGCGCTCATATTC	529
QY	421	GGTGAATATCATGCGATATGATGTGTCTGTATTTATTTATTAATAAAGATGTGTGTG	480
Db	530	GCGGAGGCCAAATCGGGAATGTATGGCCCGGATTACTTATGANAAGATTTGTCTTC	589
QY	481	ATTATACATACATATATCGTTTGGGACTGTAGTCTTAAAGTTTAATTCAGAGACCTT	540
Db	590	GTCACAGATACAGATACCGACTTGGGCTTGGGATTTATGAGCTTAAGTCCCGACGTA	649
QY	541	AATGTGCCCGGATATATGCCGC	561
Db	650	AATGTACCAAGAAATGTCTGC	670

RESULT 12

LOCUS	A113763	A113763	648 bp	mRNA	linear	EST 19-APR-2001
DEFINITION	GH10213.5pr1me GH Drosophila melanogaster head pot2 Drosophila melanogaster cDNA clone GH10213 5pr1me similar to U51050; Drosophila melanogaster alpha esterase (aE7) gene, partial cds, mRNA sequence.					
ACCESSION	A113763					
VERSION	A113763.1 GI:3514566					
KEYWORDS	EST.					
ORGANISM	fruit fly.					
REFERENCE	Drosophila melanogaster					
AUTHORS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.					
TITLE	1 (bases 1 to 648)					
JOURNAL	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.					
COMMENT	BDGP/HMT Drosophila EST Project					
	Unpublished (2001)					
	Contact: Stapleton, M.					
	BDGP					
	Lawrence Berkeley National Lab					
	One Cyclotron Rd Berkeley, CA 94720, USA					
	Fax: 510 486 6798					
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu					
	Plate: 102 row: B column: 1					
	High quality sequence stop: 435.					
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Query Match 14.3%; Score 245; DB 9; Length 648;
Best Local Similarity 65.0%; Pred. No. 1.1e-55;
Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: 224 row: F column: 4
High quality sequence stop: 533.
Location/Qualifiers
1. 648
/organism="Drosophila melanogaster"
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XhoI; Sized fractionated cDNAs were directly ligated into
pot2. Plasmid cDNA library."

BASE COUNT 150 a 165 c 184 g 149 t
ORIGIN
Query Match 14.3%; Score 245; DB 9; Length 648;
Best Local Similarity 65.0%; Pred. No. 1.1e-55;
Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

FEATURES
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1. 648
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH22464"
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/sex="male and female"
/dev_stage="adult"
/lab_host="DHS - alpha"
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XhoI; Sized fractionated cDNAs were directly ligated into
pot2. Plasmid cDNA library."

Query Match 14.3%; Score 245; DB 9; Length 648;
Best Local Similarity 65.0%; Pred. No. 1.1e-55;
Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

Query Match 14.3%; Score 245; DB 9; Length 648;
Best Local Similarity 65.0%; Pred. No. 1.1e-55;
Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

Query Match 14.3%; Score 245; DB 9; Length 648;
Best Local Similarity 65.0%; Pred. No. 1.1e-55;
Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

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Best Local Similarity 65.0%; Pred. No. 1.1e-55;
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              Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 646)
AUTHORS      Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
              Lewis, S. and Rubin, G.M.
TITLE        BDGP/HMI Drosophila EST Project
JOURNAL      Unpublished (2001)
COMMENT      Contact: Stapleton, M.
              BDGP
              Lawrence Berkeley National Lab
              One Cyclotron Rd, Berkeley, CA 94720, USA
              Fax: 510 486 6798
              Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
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OY 61 AAGTTTAAACTATGCTTAACTACCAATGAACGCTGAGTGAACCTGAATATGCG 120
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ACCESSION  A1293416
VERSION    A1293416.1  GI:3942823
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            Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
            Lewis, S. and Rubin, G.M.
            BDGP/HMI Drosophila EST Project
            Unpublished (2001)
            Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
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            High quality sequence stop: 493.
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              /lab_host="DHS-alpha"
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BASE COUNT   151 a 163 c 184 g 148 t
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Query Match      14.2%; Score 243.4; DB 9; Length 646;
Best Local Similarity 64.8%; Pred. No. 3e-55;
Matches 361; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

OY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATAATGAAGATTAAATGCAATGAAAT 60
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1706.6	99.6	1713	4	US-09-068-960-5
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C	38	138	8.1	1515	4	US-09-005-051-17	Sequence 17, Appl
C	39	138	8.1	1982	3	US-08-747-221B-13	Sequence 13, Appl
C	40	138	8.1	1982	3	US-08-747-221B-15	Sequence 15, Appl
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ALIGNMENTS

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; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
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; LENGTH: 1713
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; ORGANISM: Lucilia cuprina
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DB 481 ATTAACATATCATATGCTTGGAGCTTAGGTTTCTAAGTTTAAATTCAGAGACCTT 540
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DB 1501 ACTGCTATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 ATGGAATAATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 ATGGAATAATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 ATTAGTATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 ATTAGTATGATGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 TCGATGTTGAAAACATAGATGATTTATTTAG 1713
DB 1681 TCGATGTTGAAAACATAGATGATTTATTTAG 1713

RESULT 2

US-09-068-960-9
; Sequence 9, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; NUMBER OF SEQ ID NOS: 1995-11-23
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilla cuprina
US-09-068-960-9

Query Match 99.9%; Score 1711.4; DB 4; Length 1713;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATTTCAAGCTTGTGATGAGAAATTAATGAGATTAATGCAATTTGAAT 60
DB 1 ATGAATTTCAAGCTTGTGATGAGAAATTAATGAGATTAATGCAATTTGAAT 60
QY 61 AAGTTTAACTAATGCTTAACTACCAATGAACCGTGTAGCTGAACATGATGCT 120
DB 61 AAGTTTAACTAATGCTTAACTACCAATGAACCGTGTAGCTGAACATGATGCT 120
QY 121 AAAGTAAAGCGCTTAAAGCTTAACTGCTGATGATGATTTCTTCTTCTTCTT 180
DB 121 AAAGTAAAGCGCTTAAAGCTTAACTGCTGATGATGATTTCTTCTTCTTCTT 180
QY 181 ATACGCTAGGCCAACCGCAGTGGTGAAGTGAATTAAGACCAACCGACGACCA 240
DB 181 ATACGCTAGGCCAACCGCAGTGGTGAAGTGAATTAAGACCAACCGACGACCA 240
QY 241 CCTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 CCTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 ATACGCGCAAAAGTGTGTGCTGAGAGATGCTATTAACCTAAGTCTTAACGAAT 360
DB 301 ATACGCGCAAAAGTGTGTGCTGAGAGATGCTATTAACCTAAGTCTTAACGAAT 360
QY 361 CTAAATCCGGAACATAAGCTCCCGTTTATATATACATACATGCTGGTGTATATC 420
DB 361 CTAAATCCGGAACATAAGCTCCCGTTTATATATACATACATGCTGGTGTATATC 420

OY 421 GGTGAAATCATCGTATATGATGCTGATTTATTTCAATTAAGAGATGGTGTG 480
|||||
Db 421 GGTGAAATCATCGTATATGATGCTGATTTATTTCAATTAAGAGATGGTGTG 480
OY 481 ATTAACATACATATCGTTTGGAGCTCTAGGTTTTCTAGTTTAAATTCAGAGACCTT 540
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Db 481 ATTAACATACATATCGTTTGGAGCTCTAGGTTTTCTAGTTTAAATTCAGAGACCTT 540
OY 541 AATGTCGGGGTAAATGCCGGCTTAAGATCAAGTCAGGCTTGGCGTTGAATTAAT 600
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Db 541 AATGTCGGGGTAAATGCCGGCTTAAGATCAAGTCAGGCTTGGCGTTGAATTAAT 600
OY 601 AATGCGGCACTTGGTGGCAATCCGATATATTACAGCTTTGGTGAAGTCCGGT 660
|||||
Db 601 AATGCGGCACTTGGTGGCAATCCGATATATTACAGCTTTGGTGAAGTCCGGT 660
OY 661 GCTGCTCTACCACTACATGATGTTAACGACAACTCGCGTCTTTCCATCGTGT 720
|||||
Db 661 GCTGCTCTACCACTACATGATGTTAACGACAACTCGCGTCTTTCCATCGTGT 720
OY 721 ATACTAATGTGGGTAATGCTATTTGTCATTTGGCTAATACCAATGTCACATCGTCC 780
|||||
Db 721 ATACTAATGTGGGTAATGCTATTTGTCATTTGGCTAATACCAATGTCACATCGTCC 780
OY 781 TTCACCTTAGCCAAATTTGGCGGCTATAAGGTGAGATTAATGATAGATGTTTGA 840
|||||
Db 781 TTCACCTTAGCCAAATTTGGCGGCTATAAGGTGAGATTAATGATAGATGTTTGA 840
OY 841 TTTCTTATGAAGCCAAAGCCACAGAGATTTAATAAACTTGAGAAAAAGTTTAACTCTA 900
|||||
Db 841 TTTCTTATGAAGCCAAAGCCACAGAGATTTAATAAACTTGAGAAAAAGTTTAACTCTA 900
OY 901 GAAGAGCTTAATAATAGTATGTTCTTTTGTCCCATGTTGACCATATACAGCC 960
|||||
Db 901 GAAGAGCTTAATAATAGTATGTTCTTTTGTCCCATGTTGACCATATACAGCC 960
OY 961 GCTGATTTGCTTTAACCCAAATCCTCGGAAATGTTAAACGCTGGGGTAAATTCG 1020
|||||
Db 961 GCTGATTTGCTTTAACCCAAATCCTCGGAAATGTTAAACGCTGGGGTAAATTCG 1020
OY 1021 ATACCCTATGATGGGTAAACACTTCAATGAGGGTCTATTTTTCACCTCAATTTTAA 1080
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Db 1021 ATACCCTATGATGGGTAAACACTTCAATGAGGGTCTATTTTTCACCTCAATTTTAA 1080
OY 1081 CAATGCTATGCTTTGTTAAGGAATGGAATCTGTCAATTTTGTGCCAAGTAAATG 1140
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Db 1081 CAATGCTATGCTTTGTTAAGGAATGGAATCTGTCAATTTTGTGCCAAGTAAATG 1140
OY 1141 GCTGATTTGTTAAGCCAGCCGCCAGAGACCTTGAATGGGCTAAATTAAGAAAGGCT 1200
|||||
Db 1141 GCTGATTTGTTAAGCCAGCCGCCAGAGACCTTGAATGGGCTAAATTAAGAAAGGCT 1200
OY 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTTGCTCCACATCTAT 1260
|||||
Db 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTTGCTCCACATCTAT 1260
OY 1261 TTTGCTGTTCCCATGCAATGCTTTGTCGAATTAAGCTTTCAATCACACCTCCGGTACACC 1320
|||||
Db 1261 TTTGCTGTTCCCATGCAATGCTTTGTCGAATTAAGCTTTCAATCACACCTCCGGTACACC 1320
OY 1321 GTTACTGTTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1380
|||||
Db 1321 GTTACTGTTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1380
OY 1381 CGTAGTGCAGCTGTGTAAAGGTTTATGCTATGCTGATGATTAACCTATTTCTTCTGG 1440
|||||
Db 1381 CGTAGTGCAGCTGTGTAAAGGTTTATGCTATGCTGATGATTAACCTATTTCTTCTGG 1440
OY 1441 AATCAATTTGCCAAACGATATGCTTAAGAAATGCGGTGAATACAAACAAATGAACGTATG 1500
|||||
Db 1441 AATCAATTTGCCAAACGATATGCTTAAGAAATGCGGTGAATACAAACAAATGAACGTATG 1500

OY 1501 ACTGATATGATGATCAATTTTCCACACCTGCTAATCTTTATGACATGAATGAAGT 1560
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Db 1501 ACTGATATGATGATCAATTTTCCACACCTGCTAATCTTTATGACATGAATGAAGT 1560
OY 1561 ATGAAAAATGTTTCTGGATCCAAATTAAGAAATCCGATGAAGTATTAAGTGTGTAAT 1620
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Db 1561 ATGAAAAATGTTTCTGGATCCAAATTAAGAAATCCGATGAAGTATTAAGTGTGTAAT 1620
OY 1621 ATTAGTATGATTAATTAATGATGATGCTGCTGAATGATGATTAACATTAAGTGA 1680
|||||
Db 1621 ATTAGTATGATTAATTAATGATGATGCTGCTGAATGATGATTAACATTAAGTGA 1680
OY 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
|||||
Db 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTTAG 1713

RESULT 3

US-09-068-960-3

: Sequence 3, Application US/09068960A

: Patent No. 6235515

: GENERAL INFORMATION:

: APPLICANT: Commonwealth Scientific and Industrial Rarch. Org.

: TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE

: FILE REFERENCE: Attorney Docket No. 6235515 50179-051

: CURRENT APPLICATION NUMBER: US/09/068,960A

: EARLIER FILING DATE: 1998-05-20

: EARLIER APPLICATION NUMBER: PCT/AU96/00746

: EARLIER FILING DATE: 1996-11-22

: EARLIER APPLICATION NUMBER: AU 6751

: NUMBER OF SEQ ID NOS: 43

: SOFTWARE: PatentIn Ver. 2.0

: SEQ ID NO 3

: LENGTH: 1713

: TYPE: DNA

: ORGANISM: Lucilia cuprina

US-09-068-960-3

Query Match 99.8%; Score 1709.8; DB 4; Length 1713;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAAGAAATGAATGAATGAAT 60
|||||
Db 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAAGAAATGAATGAATGAAT 60
OY 61 AAGTTTAACTATCGTTTAACTACCAATGAAGCGTGTAGTGAATGATGATG 120
|||||
Db 61 AAGTTTAACTATCGTTTAACTACCAATGAAGCGTGTAGTGAATGATGATG 120
OY 121 AAAGTGAAGCGTTAAAGCTTTAACTGTACGATGATGCTTCTACTACAGTTTGA 180
|||||
Db 121 AAAGTGAAGCGTTAAAGCTTTAACTGTACGATGATGCTTCTACTACAGTTTGA 180
OY 181 ATACCGTACGCCAACCCGACAGTGGTGAAGTATTAAGCAACCCAGGACACACA 240
|||||
Db 181 ATACCGTACGCCAACCCGACAGTGGTGAAGTATTAAGCAACCCAGGACACACA 240
OY 241 CCCTGGATGCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 300
|||||
Db 241 CCCTGGATGCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 300
OY 301 ATACGGGCAAAAGTGTGCTCAGAGATGCTATACCTTAAGTGTCTATACGAATAT 360
|||||
Db 301 ATACGGGCAAAAGTGTGCTCAGAGATGCTATACCTTAAGTGTCTATACGAATAT 360
OY 361 CTAATCCCGAAACCTAACCTGCTTTTATGATACATACATGATGATGATGATG 420
|||||
Db 361 CTAATCCCGAAACCTAACCTGCTTTTATGATACATACATGATGATGATGATG 420
OY 421 GGTGAAATCATCGTATATGATGCTGATTTATTTCAATTAAGAGATGGTGTG 480
|||||

Db 421 GGNAAATCATCGTATGTATGTGCTCTGATTAATTCATTAAAAAGAGTGTGTTG 480
Qy 481 ATTAACATACATATGCTTTGGAGCTAGGTTTCTAAGTTTAAATCAGAACCTT 540
Db 481 ATTAACATACATATGCTTTGGAGCTAGGTTTCTAAGTTTAAATCAGAACCTT 540
Qy 541 AATGTCGGGTAAATGCGGCTTAAAGATCAAGTCAGCTTGGCTTGAATTAAT 600
Db 541 AATGTCGGGTAAATGCGGCTTAAAGATCAAGTCAGCTTGGCTTGAATTAAT 600
Qy 601 AATTGGCCCACTTTGTGGCAATCCCGATTAATATACAGTCTTGTGTAAGTCCGCT 660
Db 601 AATTGGCCCACTTTGTGGCAATCCCGATTAATATACAGTCTTGTGTAAGTCCGCT 660
Qy 661 GGTGCTCTACCACTACATGATGTATACCGAACAACCTGCGGCTTTTCATGCTGT 720
Db 661 GGTGCTCTACCACTACATGATGTATACCGAACAACCTGCGGCTTTTCATGCTGT 720
Qy 721 ATACTAATGTGGGTAATGCTATTTTGTCCATTTGGCTAATCCCAATGTCAACATGCTG 780
Db 721 ATACTAATGTGGGTAATGCTATTTTGTCCATTTGGCTAATCCCAATGTCAACATGCTG 780
Qy 781 TTCACTTAGCAAAATTTGGCGGCTATAAGGTAGAGTAATGATTAAGATGTTTGGAA 840
Db 781 TTCACTTAGCAAAATTTGGCGGCTATAAGGTAGAGTAATGATTAAGATGTTTGGAA 840
Qy 841 TTTCTTATGAAGCCAGCCAGAGATTATTAATACTTGAGGAAAAGTTTAACTCTA 900
Db 841 TTTCTTATGAAGCCAGCCAGAGATTATTAATACTTGAGGAAAAGTTTAACTCTA 900
Qy 901 GAAGAGGTCATAATAGTATGTTTCTTTGCTCCACTGTTGAGCCATATCAGACC 960
Db 901 GAAGAGGTCATAATAGTATGTTTCTTTGCTCCACTGTTGAGCCATATCAGACC 960
Qy 961 GCTGATTTGTCTTACCCAAACATCTCGGGAATGTTTAACTGCTGGGGTAATTCG 1020
Db 961 GCTGATTTGTCTTACCCAAACATCTCGGGAATGTTTAACTGCTGGGGTAATTCG 1020
Qy 1021 ATACCACTATGATGGGTAACTTCAATGAGGTCTATTTTTCACCTCAATCTTAAG 1080
Db 1021 ATACCACTATGATGGGTAACTTCAATGAGGTCTATTTTTCACCTCAATCTTAAG 1080
Qy 1081 CAATGCTATGCTTTTAAAGAACTTGTGTCAATTTTGTGCCAAGTGAATG 1140
Db 1081 CAATGCTATGCTTTTAAAGAACTTGTGTCAATTTTGTGCCAAGTGAATG 1140
Qy 1141 GCTGATTTGAAGCCAGCCGCCAGAGACCTTGAATGGGTGCTAAATTAAGAGCT 1200
Db 1141 GCTGATTTGAAGCCAGCCGCCAGAGACCTTGAATGGGTGCTAAATTAAGAGCT 1200
Qy 1201 CATGTTACGAGAAACACACAGCTGATTAATTTATGATCTTTGCTCACAATCTAT 1260
Db 1201 CATGTTACGAGAAACACACAGCTGATTAATTTATGATCTTTGCTCACAATCTAT 1260
Qy 1261 TTTCTGTTCCCATGATGCTTTTGTGCAATTTACCTTCAACACACCTCGGTCACCC 1320
Db 1261 TTTCTGTTCCCATGATGCTTTTGTGCAATTTACCTTCAACACACCTCGGTCACCC 1320
Qy 1321 GTCCTACTGATGCTGCTGACTTGCATTTGGAAGATCTTATCAATCCCTATATATG 1380
Db 1321 GTCCTACTGATGCTGCTGACTTGCATTTGGAAGATCTTATCAATCCCTATATATG 1380
Qy 1381 CGTAGTGAGAGTGTTAGGGTGTAGTCAATGCTGATGAATTAACCTATTTCTTCTG 1440
Db 1381 CGTAGTGAGAGTGTTAGGGTGTAGTCAATGCTGATGAATTAACCTATTTCTTCTG 1440
Qy 1441 AATCAATTTGGCCAAACGCTATGCTTAAGAAATGCGGTATACAAAACATTTGAGCTATG 1500
Db 1441 AATCAATTTGGCCAAACGCTATGCTTAAGAAATGCGGTATACAAAACATTTGAGCTATG 1500
Qy 1501 ACTGATATGATGATCAATTTGCGACACAGTAACTCTTATAGCAATGAATGAAGCT 1560
Db 1501 ACTGATATGATGATCAATTTGCGACACAGTAACTCTTATAGCAATGAATGAAGCT 1560

Qy 1561 ATGGAATAATGTTTCTGGGATCCAAATTAAGAAATCCGATGAAGTATACAGTGTGAAAT 1620
Db 1561 ATGGAATAATGTTTCTGGGATCCAAATTAAGAAATCCGATGAAGTATACAGTGTGAAAT 1620
Qy 1621 ATTAGTGAATGAATGAATGATGCTGCTGAATTAAGTAAAGATTAACAATGGAG 1680
Db 1621 ATTAGTGAATGAATGAATGATGCTGCTGAATTAAGTAAAGATTAACAATGGAG 1680
Qy 1681 TCGATGTTGAAAAACATAGACATTTATTTAG 1713
Db 1681 TCGATGTTGAAAAACATAGACATTTATTTAG 1713

RESULT 4
US-09-068-960-5
; Sequence 5, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rarch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068, 960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/RU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-5

Query Match 99.6%; Score 1706.6; DB 4; Length 1713;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGAATTTCAAGCTTATGTTGATGAGAAATTAATGGAAGATTAATGATGAAAT 60
Db 1 ATGAATTTCAAGCTTATGTTGATGAGAAATTAATGGAAGATTAATGATGAAAT 60
Qy 61 AAGTTTAACTATGCTTTAACTACCAATGAAGCGGTGATCTGAACTGAATATGCG 120
Db 61 AAGTTTAACTATGCTTTAACTACCAATGAAGCGGTGATCTGAACTGAATATGCG 120
Qy 121 AAAGTGAAGCGGTTAAACGTTTAACTGTGTAGATGATTTCTACTACAGTTTGAAGCT 180
Db 121 AAAGTGAAGCGGTTAAACGTTTAACTGTGTAGATGATTTCTACTACAGTTTGAAGCT 180
Qy 181 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAACACCCAGCAGCAACA 240
Db 181 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAACACCCAGCAGCAACA 240
Qy 241 CCCTGGGATGCTGCTGATGTTTGTGCAATCATTAAGATAAGTCAAGTGAATTTT 300
Db 241 CCCTGGGATGCTGCTGATGTTTGTGCAATCATTAAGATAAGTCAAGTGAATTTT 300
Qy 301 ATAAAGGGCAAGTGTGTGCTCAGAGATTTGTATACCTAAGTGTATAGCAATAT 360
Db 301 ATAAAGGGCAAGTGTGTGCTCAGAGATTTGTATACCTAAGTGTATAGCAATAT 360
Qy 361 CTAATCCCGCAAACTAAACGTCCTGTTTATGATATACATACATGCTGCTTATATATC 420
Db 361 CTAATCCCGCAAACTAAACGTCCTGTTTATGATATACATACATGCTGCTTATATATC 420
Qy 421 GGTGAATAATCATGATATGATGCTGCTGATTTATTTCAATTAAGAGATGTGCTG 480
Db 421 GGTGAATAATCATGATATGATGCTGCTGATTTATTTCAATTAAGAGATGTGCTG 480
Qy 481 ATTAACATACATATGCTTTGGAGCTAGCTTTTCTAATTTAATTTGAAGACCTT 540

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Db 481 ATTAACATACAAATATGTTGGAGCTGAGCTTTCTTAAGTTTAAATCAAGAACCTT 540
OY 541 AATGAGCCCGGTAATGCGGCTTAAAGTCAAGTACGCGCTTGGTTAAAT 600
Db 541 AATGAGCCCGGTAATGCGGCTTAAAGTCAAGTACGCGCTTGGTTAAAT 600
OY 601 AATGAGCCCGGTAATGCGGCTTAAAGTCAAGTACGCGCTTGGTTAAAT 600
Db 601 AATGAGCCCGGTAATGCGGCTTAAAGTCAAGTACGCGCTTGGTTAAAT 600
OY 661 GCTGCTCTACCCACTACATGATGTTAAACGAACAACTCGCGCTTTTCCATCGTGT 720
Db 661 GCTGCTCTACCCACTACATGATGTTAAACGAACAACTCGCGCTTTTCCATCGTGT 720
OY 721 ATACAAATGCGGGTAATGCTTTTGTCCATGCTTAATACCCATATGCAATGCTGTC 780
Db 721 ATACAAATGCGGGTAATGCTTTTGTCCATGCTTAATACCCATATGCAATGCTGTC 780
OY 781 TTCACCTTAAGCCAAATTTGGCGGCTATAAGGCTGAGATATGATTAAGATTTTGGAA 840
Db 781 TTCACCTTAAGCCAAATTTGGCGGCTATAAGGCTGAGATATGATTAAGATTTTGGAA 840
OY 841 TTTCTTAATGAAGCCAGGACAGATTTAATAAACTTGAGGAAAAAGTTTAACTTA 900
Db 841 TTTCTTAATGAAGCCAGGACAGATTTAATAAACTTGAGGAAAAAGTTTAACTTA 900
OY 901 GAAGAGCCGTAACAAATTAAGTCAATGTTTCTTTGCTCCACTGTTGAGCATATGAGACC 960
Db 901 GAAGAGCCGTAACAAATTAAGTCAATGTTTCTTTGCTCCACTGTTGAGCATATGAGACC 960
OY 961 GCTGATTTGCTTACCCAAATCTCGGGAATGTTAAACCTGCTGGGGTAATTCG 1020
Db 961 GCTGATTTGCTTACCCAAATCTCGGGAATGTTAAACCTGCTGGGGTAATTCG 1020
OY 1021 ATACCCACTATGATGAGTAACACTTCAATATGAGGCTATATTTTCACTTCAATTCCTAAG 1080
Db 1021 ATACCCACTATGATGAGTAACACTTCAATATGAGGCTATATTTTCACTTCAATTCCTAAG 1080
OY 1081 CAAATGCCATGCTTGTAAAGAAATTTGGAATCTGTCAATTTTGTGCAAGTGAATG 1140
Db 1081 CAAATGCCATGCTTGTAAAGAAATTTGGAATCTGTCAATTTTGTGCAAGTGAATG 1140
OY 1141 GCTGATTTGTAAGCAGCAGCCCGGACCTGGAATGCTGCTAAATTAAGGCT 1200
Db 1141 GCTGATTTGTAAGCAGCAGCCCGGACCTGGAATGCTGCTAAATTAAGGCT 1200
OY 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTATGATCTTGTCTCACAATCTAT 1260
Db 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTATGATCTTGTCTCACAATCTAT 1260
OY 1261 TTTCTGTTCCCATGATGCTTTTGTGCAATTTGCAATTTGCAACCTCGGTAACCC 1320
Db 1261 TTTCTGTTCCCATGATGCTTTTGTGCAATTTGCAATTTGCAACCTCGGTAACCC 1320
OY 1321 GCTCTACTGATGCTGCTGACCTTCAATTCGGAAGATCTTATCAATCCATATGATTAAG 1380
Db 1321 GCTCTACTGATGCTGCTGACCTTCAATTCGGAAGATCTTATCAATCCATATGATTAAG 1380
OY 1381 CGTAGTGAAGCTGTTAAAGGCTTATGATGCTGATGAATTAACCTATTTCTTGG 1440
Db 1381 CGTAGTGAAGCTGTTAAAGGCTTATGATGCTGATGAATTAACCTATTTCTTGG 1440
OY 1441 AATCAATTTGCGCAACGTAATGCTTAAGAAATGCGTGAATACAAACAAATTAACGTAAG 1500
Db 1441 AATCAATTTGCGCAACGTAATGCTTAAGAAATGCGTGAATACAAACAAATTAACGTAAG 1500
OY 1501 ACTGATATATGATACAAATTTGCGCAACGTAATGCTTATGCAATGAATTTAGAGT 1560
Db 1501 ACTGATATATGATACAAATTTGCGCAACGTAATGCTTATGCAATGAATTTAGAGT 1560
OY 1561 ATGAAAAATGTTTCTGAGATCAATTAAGAAATCCGATGAAGTATGAGTGTGAGT 1620
Db 1561 ATGAAAAATGTTTCTGAGATCAATTAAGAAATCCGATGAAGTATGAGTGTGAGT 1620

Db 1561 ATGAAAAATGTTTCTGAGATCAATTAAGAAATCCGATGAAGTATGAGTGTGAGT 1620
OY 1621 ATTAGATGATGATGAAATGATGATGCTGCGTGAAGATGATTAAGTAAACATGGAG 1680
Db 1621 ATTAGATGATGATGAAATGATGATGCTGCGTGAAGATGATTAAGTAAACATGGAG 1680
OY 1681 TCGATGTTTGAAGAAACATGAGATTTATTTAG 1713
Db 1681 TCGATGTTTGAAGAAACATGAGATTTATTTAG 1713

RESULT 5
US-08-669-524-1
; Sequence 1, Application US/08669524
; Patent No. 5843758
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, Robyn J.
; APPLICANT: NEWCOMB, Richard D.
; APPLICANT: ROBIN, Geoffrey C.
; APPLICANT: BOYCE, Thomas M.
; APPLICANT: CAMPBELL, Peter M.
; APPLICANT: PARKER, Anthony G.
; APPLICANT: OAKESHOT, John G.
; APPLICANT: SMYTH, Kerlie A.
; TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Love Price Leblanc & Becker
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,524
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Price, Robert L.
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 1451-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-669-524-1

Query Match 99.3%; Score 1701.8; DB 2; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 ATGAATTTCAACGTTAGTTGATGGAATTAAGAAATTAAGCAATTTGAAAT 60
Db 1 ATGAATTTCAACGTTAGTTGATGGAATTAAGAAATTAAGCAATTTGAAAT 60
OY 61 AAGTTTAACTATGCTTAACTACCAATGAACGCTGTAAGCTGAATTTGAGC 120
Db 61 AAGTTTAACTATGCTTAACTACCAATGAACGCTGTAAGCTGAATTTGAGC 120
OY 121 AAAGTGAAGGCGTTAAACGTTAACTGCTGATGATTTCTACTACAGTTTGAAGGT 180
Db 121 AAAGTGAAGGCGTTAAACGTTAACTGCTGATGATTTCTACTACAGTTTGAAGGT 180

QY 181 ATACCGTACGCCCAACCGCCAGTGGTGAGCTGAGATTTAAAGCACCCCGAGACCACA 240
 DB 181 ATACGTTAGGCCCAACCGCCAGTGGTGAGCTGAGATTTAAAGCACCCCGAGACCACA 240
 QY 241 CCTGGGATGGTGGCTGATGTTGCAATCAATAAGATCAAGTCAAGTGGATTTT 300
 DB 241 CCTGGGATGGTGGCTGATGTTGCAATCAATAAGATCAAGTCAAGTGGATTTT 300
 QY 301 ATACGGGCAAGTGGTGGCTGAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
 DB 301 ATACGGGCAAGTGGTGGCTGAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
 QY 361 CTAATCCCGAACTAAACGTCGCCCTTTAGTATACATACATGAGTGTATATATC 420
 DB 361 CTAATCCCGAACTAAACGTCGCCCTTTAGTATACATACATGAGTGTATATATC 420
 QY 421 GGTGAATATCATGCTGATATATATGCTCTATATTTCAATTAAGAGATGGTGTG 480
 DB 421 GGTGAATATCATGCTGATATATATGCTCTATATTTCAATTAAGAGATGGTGTG 480
 QY 481 ATTAACATACATATGCTTGGAGCTCTAGTCTTCTAATTTAAATTCAGAGACCTT 540
 DB 481 ATTAACATACATATGCTTGGAGCTCTAGTCTTCTAATTTAAATTCAGAGACCTT 540
 QY 541 AATGTCGCCGTAATGCGCGCTTAAAGATCAATGAGTGGCTTGCCTGATTTAAAT 600
 DB 541 AATGTCGCCGTAATGCGCGCTTAAAGATCAATGAGTGGCTTGCCTGATTTAAAT 600
 QY 601 AATGTCGCCGTAATGCGCGCTTAAAGATCAATGAGTGGCTTGCCTGATTTAAAT 660
 DB 601 AATGTCGCCGTAATGCGCGCTTAAAGATCAATGAGTGGCTTGCCTGATTTAAAT 660
 QY 661 GCTGCTCTACCACTACATGATGTTAAACGCAACAACTGCGGCTTTTCCATCTGT 720
 DB 661 GCTGCTCTACCACTACATGATGTTAAACGCAACAACTGCGGCTTTTCCATCTGT 720
 QY 721 ATACTATGTCGGGTAAATGCTATGCTATGCTAATGCTAATACCAATGCTCAATCTG 780
 DB 721 ATACTATGTCGGGTAAATGCTATGCTAATGCTAATGCTAATACCAATGCTCAATCTG 780
 QY 781 TTCACCTTACCAATTTGGCGGCTATAGGCTGAGATGATGATGATGATGATGAT 840
 DB 781 TTCACCTTACCAATTTGGCGGCTATAGGCTGAGATGATGATGATGATGATGAT 840
 QY 841 TTTCTTATGAAGCAACGCAAGCAAGATTTAATAAAGTGTGATGATGATGATGAT 900
 DB 841 TTTCTTATGAAGCAACGCAAGCAAGATTTAATAAAGTGTGATGATGATGATGAT 900
 QY 901 GAAGAGGCTCAAAATAGTATGCTATGCTTGTGCTGCTGCTGCTGCTGCTGCTG 960
 DB 901 GAAGAGGCTCAAAATAGTATGCTATGCTTGTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 961 GCTGATTTGCTTACCAAACTCTCGGGAATGTTAAACTGGTGGGTAATTCG 1020
 DB 961 GCTGATTTGCTTACCAAACTCTCGGGAATGTTAAACTGGTGGGTAATTCG 1020
 QY 1021 ATACCCACATGATGGGTAACTATGAGGCTATATTTTCACTTCAATTTCTTAAG 1080
 DB 1021 ATACCCACATGATGGGTAACTATGAGGCTATATTTTCACTTCAATTTCTTAAG 1080
 QY 1081 CAATGCTATGCTTGTAAAGAAATGGAACCTTGTGCTCAATTTTGTGCAAGTGAATG 1140
 DB 1081 CAATGCTATGCTTGTGTAAAGAAATGGAACCTTGTGCTCAATTTTGTGCAAGTGAATG 1140
 QY 1141 GCTGATTTGGAAGCAACGCGCCAGAGACCTTGGAAATGGTGTCTAAATTTAAAGGCT 1200
 DB 1141 GCTGATTTGGAAGCAACGCGCCAGAGACCTTGGAAATGGTGTCTAAATTTAAAGGCT 1200
 QY 1201 CATGTTACAGSAGAAACACCAACAGCTGATTAATTTATGAGCTTGTCTACATCTAT 1260
 DB 1201 CATGTTACAGSAGAAACACCAACAGCTGATTAATTTATGAGCTTGTCTACATCTAT 1260

QY 1261 TTTGCTTCCCATGATCGTTTGTGCAATTTACGTTTCAATTCACACCTCCGGTACACC 1320
 DB 1261 TTTGCTTCCCATGATCGTTTGTGCAATTTACGTTTCAATTCACACCTCCGGTACACC 1320
 QY 1321 GTCCTACTGTAATGCTTGTGATGCTTGTGCAATTTACGTTTCAATTTACGTTTATG 1380
 DB 1321 GTCCTACTGTAATGCTTGTGATGCTTGTGCAATTTACGTTTCAATTTACGTTTATG 1380
 QY 1381 CGTATGAGCTGCTGTTAAAGGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1440
 DB 1381 CGTATGAGCTGCTGTTAAAGGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1440
 QY 1441 AATCAATTTGCGCAACGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 1500
 DB 1441 AATCAATTTGCGCAACGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 1500
 QY 1501 ACTGCTATGATGATACATTTTCCACACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1560
 DB 1501 ACTGCTATGATGATACATTTTCCACACCTGCTGATGCTGATGCTGATGCTGATGCTGAT 1560
 QY 1561 ATGGAATATGCTTCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1620
 DB 1561 ATGGAATATGCTTCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1620
 QY 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 DB 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 QY 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713
 DB 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713

RESULT 6
 US-09-068-960-7
 ; Sequence 7, Application US/09068960A
 ; Patent No. 623515
 ; GENERAL INFORMATION:
 ; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
 ; TITLE OF INVENTION: MALATHION CARBOXYESTERASE
 ; FILE REFERENCE: Attorney Docket No. 623515 50179-051
 ; CURRENT APPLICATION NUMBER: US/09/068,960A
 ; EARLIER FILING DATE: 1998-05-20
 ; EARLIER APPLICATION NUMBER: PCT/AU96/00746
 ; EARLIER FILING DATE: 1996-11-22
 ; EARLIER APPLICATION NUMBER: AU 6751
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 1713
 ; TYPE: DNA
 ; ORGANISM: Lucilia cuprina
 US-09-068-960-7

Query Match 99.3%; Score 1701.8; DB 4; Length 1713;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGAATTTTCAAGTTAGTTGATGAGAAATTTAAATGGAAGATTAAATGCAATTTGAAAT 60
 DB 1 ATGAATTTTCAAGTTAGTTGATGAGAAATTTAAATGGAAGATTAAATGCAATTTGAAAT 60
 QY 61 AAGTTTAACTATGCTTAACTACCAATGAAAGGCTGCTGAAAGTAAATATGCTG 120
 DB 61 AAGTTTAACTATGCTTAACTACCAATGAAAGGCTGCTGAAAGTAAATATGCTG 120
 QY 121 AAAGTAAAGGCTTAAAGCTTAACTGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 AAAGTAAAGGCTTAAAGCTTAACTGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 181 ATACGCTACGCCCAACCGCACTGGGTGAGCTGAGATTTAAAGCAACCCAGACCAACA 240
 DB 181 ATACGCTACGCCCAACCGCACTGGGTGAGCTGAGATTTAAAGCAACCCAGACCAACA 240

Db 181 ATACCGTACGCCAACCCGACGAGTGGGTGAGCTGAGATTTAAAGCACCCGACGACCAACA 240
Qy 241 CCTGGGATGGTGGCCGATGTTGGCAATCAATAAAGTAAGTCAAGTCAGAGTTGATTTT 300
Db 241 CCTGGGATGGTGGCCGATGTTGGCAATCAATAAAGTAAGTCAAGTCAGAGTTGATTTT 300
Qy 301 ATACGGGCAAGTGTGGGCTCAGAGAGTGTCTATACCTAAGTGTCTATACCAATAT 360
Db 301 ATACGGGCAAGTGTGGGCTCAGAGAGTGTCTATACCTAAGTGTCTATACCAATAT 360
Qy 361 CTAAATCCGAACTAAACGTCGCCGTTTGTATATACATACATACATGAGTGTGTTTATATC 420
Db 361 CTAAATCCGAACTAAACGTCGCCGTTTGTATATACATACATACATGAGTGTGTTTATATC 420
Qy 421 GGTGAAATCATCGTATATGATGTCCTGATTTTCAATTAATAAAGAGTGTGTG 480
Db 421 GGTGAAATCATCGTATATGATGTCCTGATTTTCAATTAATAAAGAGTGTGTG 480
Qy 481 ATTAACATACATATCGTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT 540
Db 481 ATTAACATACATATCGTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT 540
Qy 541 AATGCGCCGGTAAATGCGGCTTAAAGATCAAGTCAAGTGGCTTGGATTAATAAT 600
Db 541 AATGCGCCGGTAAATGCGGCTTAAAGATCAAGTCAAGTGGCTTGGATTAATAAT 600
Qy 601 AATGCGCCGGTAAATGCGGCTTAAAGATCAAGTCAAGTGGCTTGGATTAATAAT 660
Db 601 AATGCGCCGGTAAATGCGGCTTAAAGATCAAGTCAAGTGGCTTGGATTAATAAT 660
Qy 661 GCTGCTTACCCATCATGATGTTAACCAACAACTCGGCGCTTTTCCATCGTGT 720
Db 661 GCTGCTTACCCATCATGATGTTAACCAACAACTCGGCGCTTTTCCATCGTGT 720
Qy 721 ATACTAATGTCGGGTAAATGCTATTTGTCATTTGCTAATACCAATGTCACATCGTCC 780
Db 721 ATACTAATGTCGGGTAAATGCTATTTGTCATTTGCTAATACCAATGTCACATCGTCC 780
Qy 781 TTCACCTAGCAATTTGGCGGCTATTAAGGTGAGATTAATGATTAAGATTTTGGAA 840
Db 781 TTCACCTAGCAATTTGGCGGCTATTAAGGTGAGATTAATGATTAAGATTTTGGAA 840
Qy 841 TTTCTTATGAAGCCCAACAGAGATTTAAATTAACCTTGAGGAAAGTTTAACTCTA 900
Db 841 TTTCTTATGAAGCCCAACAGAGATTTAAATTAACCTTGAGGAAAGTTTAACTCTA 900
Qy 901 GAGAGCGCTACAAATTAAGGTATGTTCTTTGCTCCACTGTGAGCCATATCAGACC 960
Db 901 GAGAGCGCTACAAATTAAGGTATGTTCTTTGCTCCACTGTGAGCCATATCAGACC 960
Qy 961 GCTGATGTCGTTTACCAACATCTCGGGGAAATGTTAAACGCTTGGGTAATTCG 1020
Db 961 GCTGATGTCGTTTACCAACATCTCGGGGAAATGTTAAACGCTTGGGTAATTCG 1020
Qy 1021 ATACCCATATGATGTTAGTACACTTATGAGGCTATTTTTCATCTTCAATCTTAAAG 1080
Db 1021 ATACCCATATGATGTTAGTACACTTATGAGGCTATTTTTCATCTTCAATCTTAAAG 1080
Qy 1081 CAATAGCTATGCTTTTAAGGAATGGAACCTTGTCAATTTTGTGCCAAGTCAATTTG 1140
Db 1081 CAATAGCTATGCTTTTAAGGAATGGAACCTTGTCAATTTTGTGCCAAGTCAATTTG 1140
Qy 1141 GCTGATGTTGAAGCGACGCGCCCAAGACCTTGAATGAGGCTGAAATTAAGAGCT 1200
Db 1141 GCTGATGTTGAAGCGACGCGCCCAAGACCTTGAATGAGGCTGAAATTAAGAGCT 1200
Qy 1201 CATGTTACAGGAAACCAACAGAGCTGATATTTTATGATCTTTCCTCACAATCTAT 1260
Db 1201 CATGTTACAGGAAACCAACAGAGCTGATATTTTATGATCTTTCCTCACAATCTAT 1260
Qy 1261 TTTGTTGTTCCCATGATGTTTGTGCAATTTAGCTTCAATCAGACCTCGGATACACC 1320
Db 1261 TTTGTTGTTCCCATGATGTTTGTGCAATTTAGCTTCAATCAGACCTCGGATACACC 1320

Qy 1321 GTCATCTGTATTCGCTTCGACTGTGATTCGGAAGATCTTATCATCCATTCATTAAT 1380
Db 1321 GTCATCTGTATTCGCTTCGACTGTGATTCGGAAGATCTTATCATCCATTCATTAAT 1380
Qy 1381 CGTATGACGCTGCTTAAAGGCTGTATGTCATGCTGATTAACCTATTTCTTCTG 1440
Db 1381 CGTATGACGCTGCTTAAAGGCTGTATGTCATGCTGATTAACCTATTTCTTCTG 1440
Qy 1441 AATCAATTTGCCAAACGATGCTTAAAGATTCGCTGATTAACCAAAATTTGAACGTATG 1500
Db 1441 AATCAATTTGCCAAACGATGCTTAAAGATTCGCTGATTAACCAAAATTTGAACGTATG 1500
Qy 1501 ACTGCTATGATGATCAATTTTCCGACCACTGCTATCTTATAGCAATGAATTTAAGT 1560
Db 1501 ACTGCTATGATGATCAATTTTCCGACCACTGCTATCTTATAGCAATGAATTTAAGT 1560
Qy 1561 ATGAAATGTTTCTGCGATTCATTAAGAAATCCGATGAAGTATACAGTGTGTAAT 1620
Db 1561 ATGAAATGTTTCTGCGATTCATTAAGAAATCCGATGAAGTATACAGTGTGTAAT 1620
Qy 1621 ATTAGTATGAATTTGAATGATGATGCTGCTGAATGATTAAGATTAACATGGAG 1680
Db 1621 ATTAGTATGAATTTGAATGATGATGCTGCTGAATGATTAAGATTAACATGGAG 1680
Qy 1681 TCGATGTTGAAATCATGATTTATTTAG 1713
Db 1681 TCGATGTTGAAATCATGATTTATTTAG 1713

RESULT 7

US-08-669-524-2

Sequence 2, Application US/08669524

Patent No. 5843758

GENERAL INFORMATION:

APPLICANT: RUSSELL, Robyn J.

APPLICANT: NEWCOMB, Richard D.

APPLICANT: BOYCE, Geoffrey C.

APPLICANT: CAMPBELL, Peter M.

APPLICANT: PARKER, Anthony G.

APPLICANT: OAKESHOTT, John G.

APPLICANT: SMYTH, Kerrie A.

TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESS: Lowe Price Leblanc & Becker

STREET: 99 Canal Center Plaza, Suite 300

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/669,524

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Price, Robert L.

REGISTRATION NUMBER: 22,685

REFERENCE/DOCKET NUMBER: 1451-021

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-684-1111

TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1713 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: Linear
MOLECULE TYPE: DNA (genomic)
US-08-669-524-2

Query Match 97.9%; Score 1676.6; DB 2; Length 1713;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAAATGCAATGAAAT 60
DB 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAAATGCAATGAAAT 60
QY 61 AAGTTTTAACTATGCTTTAACTACCAATGAACGGGTGATGCTGAAGTGAATATGCG 120
DB 61 AAGTTTTAACTATGCTTTAACTACCAATGAACGGGTGATGCTGAAGTGAATATGCG 120
QY 121 AAGTGAAGGCGTTAAAGCTTGAATGATGATGATGCTGCTCTACAGTTTGAGGGT 180
DB 121 AAGTGAAGGCGTTAAAGCTTGAATGATGATGATGCTGCTCTACAGTTTGAGGGT 180
QY 181 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCAGCACACA 240
DB 181 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCAGCACACA 240
QY 241 CCCTGGATGGTGGCGGATGTTGCAATGATAAAGTAAAGTAAAGTAAAGTAAAGT 300
DB 241 CCCTGGATGGTGGCGGATGTTGCAATGATAAAGTAAAGTAAAGTAAAGTAAAGT 300
QY 301 ATAAAGGCGCAAGTGTGTGCTCAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
DB 301 ATAAAGGCGCAAGTGTGTGCTCAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
QY 361 CTAAATCCCGAACTAAACGTCCTGTTTACTATATACATACATGCTGCTGTTTATATC 420
DB 361 CTAAATCCCGAACTAAACGTCCTGTTTACTATATACATACATGCTGCTGTTTATATC 420
QY 421 GGTAAATATCATGCTGATATGATGCTGCTGATATTTCAATTAAGAGTGGTGTG 480
DB 421 GGTAAATATCATGCTGATATGATGCTGCTGATATTTCAATTAAGAGTGGTGTG 480
QY 481 ATTAACATACATATGCTTTGGAGCTCTAGGTTTCTAAGTTTAAATGAGAAGCTT 540
DB 481 ATTAACATACATATGCTTTGGAGCTCTAGGTTTCTAAGTTTAAATGAGAAGCTT 540
QY 541 AATGTGGCCGCTAATGCGGCTTAAAGATCACTGCGCTTGGCTGATTTAAAT 600
DB 541 AATGTGGCCGCTAATGCGGCTTAAAGATCACTGCGCTTGGCTGATTTAAAT 600
QY 601 AATGTGGCCGCTTGGTGGCAATCCGATATATTTACAGTCTTTGGTGAAGTGGCGGT 660
DB 601 AATGTGGCCGCTTGGTGGCAATCCGATATATTTACAGTCTTTGGTGAAGTGGCGGT 660
QY 661 GCTGCTCTACCACTACATGATGTTAACCGAACAACCTGCGGTCTTTTCCATGCTGT 720
DB 661 GCTGCTCTACCACTACATGATGTTAACCGAACAACCTGCGGTCTTTTCCATGCTGT 720
QY 721 ATACTATATGCGGCTATGCTATTTGCTATGCTAATGCCAATGCTCAACATGCTGCT 780
DB 721 ATACTATATGCGGCTATGCTATTTGCTATGCTAATGCCAATGCTCAACATGCTGCT 780
QY 781 TTACCTTATGACCAATTTGGCGGCTATAAGGCTGAGGATTAAGTATGATTTTGGAA 840
DB 781 TTACCTTATGACCAATTTGGCGGCTATAAGGCTGAGGATTAAGTATGATTTTGGAA 840
QY 841 TTTCTTATGAAAGCCAGCACAGGATTTATTAACCTTGAGGAAAGTTTAACTCTTA 900
DB 841 TTTCTTATGAAAGCCAGCACAGGATTTATTAACCTTGAGGAAAGTTTAACTCTTA 900
QY 901 GAAGAGCGTACAAATAAGGCTATGCTTCTTGGTCCACGCTGAGCATATATGAGAC 960
DB 901 GAAGAGCGTACAAATAAGGCTATGCTTCTTGGTCCACGCTGAGCATATATGAGAC 960
QY 961 GCTGATTTGTCTTACCAACATCTCTCGGAATGTTAAACTCTTGGGATATTCG 1020

DB 961 GCTGATTTGTCTTACCAACATCTCTCGGAATGTTAAANNCTTGGGATTAATTCG 1020
QY 1021 ATACCACATATGATGGGTAAACACTTCAATATGAGGCTATTTTCACTCAATCTTAAG 1080
DB 1021 ATACCACATATGATGGGTAAACACTTCAATATGAGGCTATTTTCACTCAATCTTAAG 1080
QY 1081 CAATGCTATGCTTGTGAAGATTTGAAACTTGTCTCAATTTTGTGCCAAGTGAATG 1140
DB 1081 CAATGCTATGCTTGTGAAGATTTGAAACTTGTCTCAATTTTGTGCCAAGTGAATG 1140
QY 1141 GCTGATTTGAAGCCAGCCGCCAGAGACCTTGAATGGGTGCTTAATTTAAAGAGCT 1200
DB 1141 GCTGATTTGAAGCCAGCCGCCAGAGACCTTGAATGGGTGCTTAATTTAAAGAGCT 1200
QY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTTGCTCATCTAT 1260
DB 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTTGCTCATCTAT 1260
QY 1261 TTCTGTTCCCATGATGCTGTTGCTGATGCTTCAATCAACCTCCGCTACACCC 1320
DB 1261 TTCTGTTCCCATGATGCTGTTGCTGATGCTTCAATCAATCAACCTCCGCTACACCC 1320
QY 1321 GTCTACTTGTATGCTTGCACCTTGCATTCGAAAGATCTTATCAATCCCTATATTAAG 1380
DB 1321 GTCTACTTGTATGCTTGCACCTTGCATTCGAAAGATCTTATCAATCCCTATATTAAG 1380
QY 1381 CGTAGTGGAGCTGGTGTGAAGGCTGTAGTACATGCTGATGATTAACCTATTTCTGTG 1440
DB 1381 CGTAGTGGAGCTGGTGTGAAGGCTGTAGTACATGCTGATGATTAACCTATTTCTGTG 1440
QY 1441 ATCAATTTGGCCAAAGCTATAGCTTAAAGATTCGCGAATATCAACCAATTTGAAGCTAG 1500
DB 1441 ATCAATTTGGCCAAAGCTATAGCTTAAAGATTCGCGAATATCAACCAATTTGAAGCTAG 1500
QY 1501 ACTGCTATATGATATCAATTTGCCACCACTGCTGATTCCTTATGCAATGAATGAAGCT 1560
DB 1501 ACTGCTATATGATATCAATTTGCCACCACTGCTGATTCCTTATGCAATGAATGAAGCT 1560
QY 1561 ATGGAATAATGTTCTGGGATTCCTAATTAAGAAATCCGANGAATNTCAAGTGTGGAAT 1620
DB 1561 ATGGAATAATGTTCTGGGATTCCTAATTAAGAAATCCGANGAATNTCAAGTGTGGAAT 1620
QY 1621 ATTAGTATGATTAATGAATGATGATGCTGGAATGATTAAGTAAATGAATGGAG 1680
DB 1621 ATTAGTATGATTAATGAATGATGATGCTGGAATGATTAAGTAAATGAATGGAG 1680
QY 1681 TCGATGTTGAAAACATAGAGATTTATTTAG 1713
DB 1681 TCGATGTTGAAAACATAGAGATTTATTTAG 1713

RESULT 8
US-09-068-960-14
Sequence 14, Application US/09068960A
Patent No. 623515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
FILE REFERENCE: Attorney Docket No. 623515 50179-051
CURRENT APPLICATION NUMBER: US/09/068, 960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 1710
TYPE: DNA
ORGANISM: Musca domestica
US-09-068-960-14

Query Match 55.8%; Score 956.6; DB 4; Length 1710;
 Best Local Similarity 73.4%; Pred. No. 6.9e-268;
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

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QY 44 TTAATGATGAAATTAAGTTTAACTATCGTTTAACATCAACAAATGAACGGTGTAG 103
DB 44 TTAATGATGATGAAATTAAGTTTAACTATCGTTTAACATCAACAAATGAACGGTGTAG 103
QY 104 CTGAATCGAATATGCGAAAGTGAAGGCTTAAACGTTTAACTGTACATGATTTCT 163
DB 104 TCGATACGAAATATGCGAAATTAAGGTTTAAACGAAATGACCGTCAAGTATTTCT 163
QY 164 ACTACAGTTTGGAGGTTATACCGTACGCCCAACCGCGTGTAGGTAGGATTTAAG 223
DB 164 ACTACAGTTTGGAGGTTATACCGTACGCCCAACCGCGTGTAGGTAGGATTTAAG 223
QY 224 CACCCCAAGCAACCAACCGTGGAGTGTGCTGATTTGCAATCAAAAGATAAGT 283
DB 224 CACCCCAAGCAACCAACCGTGGAGTGTGCTGATTTGCAATCAAAAGATAAGT 283
QY 284 CAGTCCAGTTGATTTTAAACGGCAAGTGTGCTGACAGAGATTTGTATACCTAA 343
DB 284 CAGTCCAGTTGATTTTAAACGGCAAGTGTGCTGACAGAGATTTGTATACCTAA 343
QY 344 GTGCTATACGAATTAATCCGGAACCTAAACGTCGCCGTTTGTATATACATACATG 403
DB 344 GTGCTATACGAATTAATCCGGAACCTAAACGTCGCCGTTTGTATATACATACATG 403
QY 404 GTGCTATACGAATTAATCCGGAACCTAAACGTCGCCGTTTGTATATACATACATG 463
DB 404 GTGCTATACGAATTAATCCGGAACCTAAACGTCGCCGTTTGTATATACATACATG 463
QY 464 AAAAGATGTGTGTATTAACATACATATCGTTTGGAGCTCTAGTTTCTAAGTT 523
DB 464 AAAAGATGTGTGTATTAACATACATATCGTTTGGAGCTCTAGTTTCTAAGTT 523
QY 524 TAAATTCAGAAAGACCTTAATGTCGCGTAATGCGGCTTAAAGATCAAGTACGCT 583
DB 524 TAAATTCAGAAAGACCTTAATGTCGCGTAATGCGGCTTAAAGATCAAGTACGCT 583
QY 584 TGAATTCGAAATATCAATGTCGCGTAATGCGGCTTAAAGATCAAGTACGCT 643
DB 584 TGAATTCGAAATATCAATGTCGCGTAATGCGGCTTAAAGATCAAGTACGCT 643
QY 644 TGGTGAAGTGGCGGTCTACCCACTACATGATGTTAAGCAACCAAGTCCG 703
DB 644 TGGTGAAGTGGCGGTCTACCCACTACATGATGTTAAGCAACCAAGTCCG 703
QY 704 GTCTTTCCATCGTGTATTAATGTCGCGTAATGCTATTGTCATTTGCTTAATACCC 763
DB 704 GTCTTTCCATCGTGTATTAATGTCGCGTAATGCTATTGTCATTTGCTTAATACCC 763
QY 764 AATGTCACATCGTGTATTAATGTCGCGTAATGCTATTGTCATTTGCTTAATACCC 823
DB 764 AATGTCACATCGTGTATTAATGTCGCGTAATGCTATTGTCATTTGCTTAATACCC 823
QY 824 ATAAGCATGTTTGAATTTCTTATGAAGCAACGACAGATTTAATAAATCTTGAGG 883
DB 824 ATAAGCATGTTTGAATTTCTTATGAAGCAACGACAGATTTAATAAATCTTGAGG 883
QY 884 AAAAGATATCTCGAATTCCTAAATGAAGCAACGACAGATTTAATAAATCTTGAGG 943
DB 884 AAAAGATATCTCGAATTCCTAAATGAAGCAACGACAGATTTAATAAATCTTGAGG 943
QY 944 TTAGACCATATACAGACCGCTGATTTGCTTACCCAAACATCTCTGGGAAATGTTAA 1003
DB 944 TTAGACCATATACAGACCGCTGATTTGCTTACCCAAACATCTCTGGGAAATGTTAA 1003
QY 1004 CTGCTTGGGATTAATGATACCAATGATGATGGTAAACATTTCAATGAGGTCTAATTT 1063
DB 1004 CTGCTTGGGATTAATGATACCAATGATGATGGTAAACATTTCAATGAGGTCTAATTT 1063

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QY 1064 TCACCTCAATCTTATAGCAAAATGCTATGCTTAAAGCAATTTGCAAACTGTGCAAT 1123
DB 1064 CCAATCAATTTCCCAAAATATATCCGAGGTTTAAAGAGTTGCAATTTCTGTGCAAT 1123
QY 1124 TTGTCACAGTGAATTTGCTGATTTGAACGACCGCCCAAGACCTTGAATGCGTG 1183
DB 1124 ATGTCTCTGGAGTGTGCTGACAGTGAACGACGAGTCCCGGAACCTCTGAGAGGCTG 1183
QY 1184 CTAAATTAATAAGGCTCATGTTACAGAGAAACCAACCACTGATATTTTATGATC 1243
DB 1184 CATTGTATAAAGGCTCATGTTACAGAGAAACCAACCACTGATATTTTATGATC 1243
QY 1244 TTGCTCTACATCTATTTCTGTTCCCATGCTATGTTGCAATTTATGCTTCAATC 1303
DB 1244 TTGCTCTATTTCTATTTCTGTTCCCATGCTATGTTGCAATTTATGCTTCAATC 1303
QY 1304 ACACCTCCGATACACCGCTCTACTGTTATGCTTGCATTTGCAATTTGCAATTTATCA 1363
DB 1304 ACACAGTGGGACCTCCATTTATTTGATGCTTGCATTTGCAATTTGCAATTTATCA 1363
QY 1364 ATCCCTATGCTATTTATGCTGATGACGCTGTTAAGGTTTATGCTATGCTGATGAT 1423
DB 1364 ACCCTATGCTATTTATGCTGATGACGCTGTTAAGGTTTATGCTATGCTGATGAT 1423
QY 1424 TAACCTATTTCTTGAATCAATTTGCCCAACGATGCTTAAAGATGCGTGAATACA 1483
DB 1424 TAACCTATTTCTTGAATCAATTTGCCCAACGATGCTTAAAGATGCGTGAATACA 1483
QY 1484 AAACATTTGAACGATGACGCTATATGATACAAATTTGCCCAACGATGCTTAAATCCTTAA 1543
DB 1484 AAACATTTGAACGATGACGCTATATGATACAAATTTGCCCAACGATGCTTAAATCCTTAA 1543
QY 1544 GCAATGAATTTGAAGTATGCAAAATGTTTCTGCGATTCATTTAAGAAATCCGATGAG 1603
DB 1544 GCAATGAATTTGAAGTATGCAAAATGTTTCTGCGATTCATTTAAGAAATCCGATGAG 1603
QY 1604 TATACAGTGTGTAATATTAATGATGATTAATAATGATGATGCTGCTGAATGATA 1663
DB 1604 TATACAGTGTGTAATATTAATGATGATTAATAATGATGATGCTGCTGAATGATA 1663
QY 1664 AGATTAACATGAGATGATGATTTGAAAAACATGAGATTTATTT 1710
DB 1664 AGATTAACATGAGATGATGATTTGAAAAACATGAGATTTATTT 1710

```

RESULT 9
 US-08-747-221B-51
 ; Sequence 51, Application US/08747221B
 ; Patent No. 6063610
 ; GENERAL INFORMATION:
 ; APPLICANT: Silver, Gary W.
 ; TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
 ; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; ADDRESSER: Heska Corporation
 ; STREET: 1825 Sharp Point Drive
 ; CITY: Fort Collins
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80525
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: WordPerfect for Windows, Version 7.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/747,221B
 ; FILING DATE: No. 6063610e1ember 12, 1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

RESULT 10
US-08-747-221B-52/C
; Sequence 52, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.

QY	116	ATGGCAAGGTGAAGAGCGTTTAACGTTTAACGTGTACGATGATTCTTACAGCTTTTG	175
Db	1556	AAGGTACTTAAAGAAAGAAAGAGCAAAATTAAGAAAAAGAAATGTTCCACTAGTATT	1497
QY	176	AAGGATATACCGTAGACGCCAACCGCAGTAGTGGAGCTGATTTTAAAGCACCCAGCGAC	235
Db	1496	CTGGATTTCCATATATGCCAATACCTCCTGTAGGTATCTAAGATTTTAAGCCACTCAACCTG	1437
QY	236	CAACACCCCTGGAGTGGTGTGCGTGTATTTGTCATCATAAAGATAAGTCAGTGCACATTG	295
Db	1436	CAGAACCCTTGGTCAGGTGTTCTTGATGCTAGTAAGAAAGAAATAGTTTACATCAGTAC	1377
QY	296	ATTTTATATACGGGGCAAAAGTGTGGCTGAGAGATTGTGTATACCTAAAGTCTATACGA	355
Db	1376	ATTTTATTAATAAAATTAATAAGTAGGGGCTGAAGATTGTTTATACCCATATGCTATAGTAC	1317
QY	356	ATATCTTAATCCCGCAACTAAACGTCGCCGTTTAACTATATACATACATGCTGTGTTTAA	415
Db	1316	CAAAAAACATCAGAGAAATCACTTCTCCAGTATGATGATACATGAGAGAGCGCTTCT	1257
QY	416	TATATCGGTAAATATCTCGTATATGTATGAGTCCTATTAATTTTCATTAATAAAGATGTG	475
Db	1256	TCATGGGATCTGGAAATATAGTATATCTATGGTCTGAATATTTTGATGGATTAATGAAATG	1197
QY	476	TGTTGATTAACATACAAATATCGTTTGGAGACTCTAGCTTTTCTAAGTTTAAATTCGAAG	535
Db	1196	TTCGTGTACTTTCATTAATTCGATTAAGGTGTTGGATTTTGAACCTGGGAATGAAG	1137
QY	536	ACCTTAATATGCGCCGATATGCGGCTTAAGATATGAAGCATGAGCGCTTGCCTGGATTA	595
Db	1136	AA-----GCGCTGGCAATGTGGTTTGATGAGCAGAGGTTGAAGCTCTAAATGGGTAA	1083

OY 116 ATGCAAGATGAAAGCGCTTAAAGCTTTAACTGTGTACGATGATTCCTACTACAGTTTG 175
 Db 29 AAGGACTCTTTAAAGAAAGAAAGCAAAATTAAGTAAAAAGCAAAATGTCTCCATAGTTATT 88
 OY 176 AGGATTAACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTTAAAGCAACCCAGCGAC 235
 Db 89 CTGGAAATTCATATGCCCAAACTCTCTGTAGGTGTATCTTAAGATTTTAAACCCACGCTCAACTG 148

1 AFFILIANT: WISCONSIN, MADC
2 TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
3 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
4 NUMBER OF SEQUENCES: 66
5
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Carol Talkington Verser, Ph.D.
8 ADDRESSEE: Heska Corporation
9 STREET: 1825 Sharp Point Drive
10 CITY: Fort Collins
11 STATE: Colorado
12 COUNTRY: USA
13
14 ZIP: 80525
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: Windows 95
20 SOFTWARE: Wordperfect for Windows, Version 7.0
21
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/09/005, 051
24 FILING DATE:
25 CLASSIFICATION:
26
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: 08/747,221
29 FILING DATE: No. 6291222e1 12, 1996
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Verser, Carol Talkington
32 REGISTRATION NUMBER: 37,459
33 REFERENCE/DOCKET NUMBER: FC-1
34
35 TELECOMMUNICATION INFORMATION:
36

TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1584 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-005-051-52

Query Match 10.5%; Score 179.6; DB 4; Length 1584;
 Best Local Similarity 56.2%; Pred. No. 2.3e-42;
 Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

QY 116 ATGCAAGTGAAGCGCTTAACGTTTAACGTGTACGATGATTCCTACAGATTG 175
 DB 1556 AAGGTACTTTAAAGGAAAGCAAAATTAAGGAAAGAAATGTTCCATAGTTAT 1497
 QY 176 AGGTATACCGTACCGCCCAACGCCAGTGGTGAGCTGATTTAAAGCACCAGCAG 235
 DB 1496 CTGGAAATTCATATGCCAAACCTCCTGTAGTGATCTAAAGATTAAAGCACCCTCAACCTG 1437
 QY 236 CAACACCCCTGGAGTGTGCTGATTTGTTCATCAATGAATGAATAGTCAGGCAAGTGTG 295
 DB 1436 CAGAACCTTGTCAGGTGTTCTTGAATGCTAGTAAAGAAAGGAATGTTGTAGATCAGTAC 1377
 QY 296 ATTTTATTAACGGGCAAAAGTGTGTGCTCAGAGATTTGCTATACCTAAGTGTCTATACGA 355
 DB 1376 ATTTTATTAAGAAATTAAGTGAAGGCGCTGAAGATTGTTTATACCTCAATGCTATAGTAC 1317
 QY 356 ATATCTAATCCCGAACTAAGCTCCGTTTGTAGTATACATACATGTGTGTTTGA 415
 DB 1316 CAAAACATCAGAAATCACTCTTCCAGTAAATGATATGATACATGAGAGAGGCTTCT 1257
 QY 416 TTATCGTGAAATATCATGATATGATGTGCTGATTTATTCATTTAAAGAGATGTG 475
 DB 1256 TCAATGGATCTGAAATATGATATGATGTGCTGATTTATTCATTTATGATATG 1197
 QY 476 TGTGATTAACATACATATGCTTTGGAGCTGATGTTTCTAAGTTTAATTACAGAG 535
 DB 1196 TTCTGTTACTTTCATTTATGATTTAGTGTGTTGGGATTTTGAACCTGGGAATAGAG 1137
 QY 536 ACCTTAATGTCCCGGTAATGCCGCTTAAAGATCAAGTATCATATTTACGCTTTGGTGAAGTG 595
 DB 1136 AA-----GCGCTGGCAATGTGTTGATGAGCAGAGTTGAGCTTAATAATGGGTTAA 1083
 QY 596 AAATTAATGGCCCACTTTGGTGGCAATCCGATATATTACGCTTTGGTGAAGTG 655
 DB 1082 AAAACATATTGCAATCTTTGGTGTGACCCCAACATGTGACTATTTTGGAGNAATCAG 1023
 QY 656 CCGGTGCTGCTTACCCACTACATGATGTATTAACCAACAACTCGCGTCTTTTCATC 715
 DB 1022 CAGGTGGAGAGTGTTCATTTATTTGATGTATTCAGATCTTTCCAAAGAGCTTTTTCATA 963
 QY 716 GTGTATACATATGTCGGTAAATGCTATTTGTCATTGGC 755
 DB 962 AAGCATCTCAAAAGTGAAGTCTTTTATCTTGGGC 923

RESULT 13
 US-08-747-221B-36
 Sequence 36, Application US/08747221B
 Patent No. 6063610
 GENERAL INFORMATION:
 APPLICANT: Silver, Gary W.
 APPLICANT: Misnewski, Nancy
 TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
 TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Heska Corporation

STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747,221B
 FILING DATE: No. 6063610e1ember 12, 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: FC-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2007 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 11..1594
 US-08-747-221B-36

Query Match 10.5%; Score 179.6; DB 3; Length 2007;
 Best Local Similarity 56.2%; Pred. No. 2.6e-42;
 Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

QY 116 ATGCAAGTGAAGCGCTTAACGTTTAACGTGTACGATGATTCCTACAGATTG 175
 DB 39 AAGGTACTTTAAAGGAAAGCAAAATTAAGTGAAGAAATGTTCCATAGTTAT 98
 QY 176 AGGTATACCGTACCGCCCAACGCCAGTGGTGAGCTGAGATTTAAAGCACCAGCAG 235
 DB 99 CTGGAATTCATATGCAACCTCTGTAGTGATCTAAAGATTAAAGCCACTCAACCTG 158
 QY 236 CAACACCCCTGGAGTGTGCTGATTTGTGCAATCATATGAATGAAGTGAAGTGTG 295
 DB 159 CAGAACCTTGTCAGGTGTTCTTGAATGCTAGTAAAGAAAGGAATAGTGTAGATCAGTAC 218
 QY 296 ATTTTATTAACGGGCAAAAGTGTGCTCAGAGATTTGCTATACCTAAGTGTCTATACGA 355
 DB 219 ATTTTATTAAGAAATTAAGTGAAGGCGCTGAAGATTGTTTATACCTCAATGCTATGATAC 278
 QY 356 ATATCTAATCCCGAACTAAGCTCCGTTTGTAGTATACATACATGTGTGTTTGA 415
 DB 279 CAAAACATCAGAAATCACTCTTCCAGTAAATGATGTATGATGAGAGAGGCTTCT 338
 QY 416 TTATCGTGAAATATCATGATATGATGTGCTGATTTATTCATTTAAAGAGATGTG 475
 DB 339 TCATGGATCTGAAATATGATATGATGTATGTCGATATTTGATGATATGATGAAATG 398
 QY 476 TGTGATTAACATACATATGCTTTGGAGAGCTCTGAGTTTCTAAGTTTAATTACAGAG 535
 DB 399 TTCTGTTACTTTCATTTATGATTTAGTGTGTTGGGATTTTGAACCTGGGAATAGAG 458
 QY 536 ACCTTAATGTCCCGTATGCGGCTTAAAGATCAAGTCAATGCTTGGCTGAGTTA 595
 DB 459 AA-----GCGCTGGCAATGTGTTGATGAGACAGAGTTGAAGCTCTTAATAGGGTTAA 512
 QY 596 AAATTAATTTGGCCCACTTTGGTGGCAATCCCGATTAATATTATACAGTCTTTGGTGAAGTG 655
 DB 513 AAACATATTTGCAATCTTTGGTGTGACCCCAACATGTGACTATTTTGGAGAAATCAG 572

NAME/KEY: CDS
LOCATION: 11..1594
US-09-005-051-36

Query Match 10.5%; Score 179.6; DB 4; Length 2007;
Best Local Similarity 56.2%; Pred. No. 2.6e-42;
Matches 360; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

QY 116 ATGGCAAAAGTGAAGGCTTAAAGCTTTAAGTGTAGCATGATGATTCCTACTACAGTTTG 175
DB 39 AAGGTACTTTAAAGCAAGCAAGCAATTAAGTGAAGAAAGAAAGTGTTCATAGTTATT 98
QY 176 AAGGTATACCGTACGCCCAAGCCAGTGGTGGAGCTGAGATTAAAGCAAGCCAGCGAC 235
DB 99 CTGGAATTCATATGCCCAAGCTCCTGTAGTGATCTAAGATTAAAGCCAGCTCAACCTG 158
QY 236 CAACACCCCTGGGATGGTGGCGGTGATGTTGTCATATAAGTAAAGTCAAGTCAAGTTG 295
DB 159 CAGAACCTTGGTCAAGTGTCTTGTAGTGTAGTAAAGAGGAGTATGTTGATCAGTAC 218
QY 296 ATTTTAAAGGCAAGTGTGGCTCAGAGAGATTGTCTATACCTAAGTGTCTATACGA 355
DB 219 ATTTTAAAGGCAAGTGTGGCTCAGAGAGATTGTCTATACCTAAGTGTCTATACGA 278
QY 356 ATAACTAAATCCCGAAGTAAAGTCCCGTTTAAATACATACATAGTGTGGTTTA 415
DB 279 CAAGAACATCAGAAATCATCTCTTCCAGTAAAGTATGATACATGAGAGAGCTTCT 338
QY 416 TTATCGGTGAATCATCGTATGATGATGATGATGATGATGATGATGATGATGATG 475
DB 339 TCATGGGATCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATG 398
QY 476 TGTGATTAACATACATATCGTTTGGAGCTCTAGTTTCTAAGTTTAAATTCAGAG 535
DB 399 TTCTGTTACTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATG 458
QY 536 ACCTTAATGTCCCGGTAAATGCGGCTTAAAGATCAAGTCAAGTCAAGTCAAGTCA 595
DB 459 AA-----GCGCTGGCAATGTTGTTGATGAGCCAGGTGAAGCTCTAAATGGTAA 512
QY 596 AAATTAATGGCCCACTTGGTGGCAATGCCGATATATATACAGTCTTGGTGAAGTG 655
DB 513 AAACAAATATGATCTCTTGGTGGCAATGCCGATATATATACAGTCTTGGTGAAGTG 572
QY 656 CCGGTCTCTCTTACCTACCATATGATGATGATGATGATGATGATGATGATGATGATG 715
DB 573 CAGGTGTGCAAGTGTCAATATGATGATGATGATGATGATGATGATGATGATGATG 632
QY 716 GTGTATACTAATGTCGGTAAATGCTATTTGTCATTGGC 755
DB 633 AAGCATCTCACAAGTGAAGTCTTTAATCCTTGGGC 672

Search completed: April 11, 2003, 08:51:10
Job time : 47.5118 secs

GenCore version 5.1.4 p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 01:07:17 ; Search time 94.5276 Seconds
(Without alignments)
15895.765 Million cell updates/sec

Title: US-09-776-910-1

Perfect score: 1713

Sequence: 1 atgaattcaacgttagttt.....aacatagagattatttttag 1713

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCOT_NEM_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEM_PUB.seq:*
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- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88.8	5.2	1691	9	US-10-083-590-13
2	77.2	4.5	1611	9	US-09-738-626-1254
3	62.2	3.6	1967	10	US-09-748-739A-1
4	62.2	3.6	2381	10	US-09-880-107-2271
5	62.2	3.6	2416	10	US-09-748-739A-3
6	62.2	3.6	2416	10	US-09-748-739A-5
7	62.2	3.6	2416	10	US-09-748-739A-7
8	62.2	3.6	2416	10	US-09-748-739A-16
9	62.2	3.6	2444	9	US-09-893-519A-112
10	57.8	3.4	657	10	US-09-974-300-1107
11	57.6	3.4	2508	10	US-09-934-323-3
12	57.6	3.4	4667	10	US-09-934-323-1
13	56.8	3.3	2191	9	US-09-954-531-1038
14	56.8	3.3	2191	10	US-09-880-107-3854
15	56.8	3.3	2484	9	US-10-103-806-271
16	55.4	3.2	1641	10	US-09-895-860-3
17	55.4	3.2	2087	10	US-09-895-860-1
18	55.4	3.2	2428	9	US-09-418-176-1
19	55.4	3.2	2428	10	US-09-969-347-220

20	55.4	3.2	3824	9	US-10-036-041-22	Sequence 22, Appl
21	55.4	3.2	3824	9	US-10-028-072-541	Sequence 541, App
22	55.4	3.2	3824	9	US-10-035-855-22	Sequence 22, Appl
23	55.4	3.2	3824	9	US-10-121-049-541	Sequence 541, App
24	55.4	3.2	3824	9	US-10-123-904-541	Sequence 541, App
25	55.4	3.2	3824	9	US-10-140-470-541	Sequence 541, App
26	55.4	3.2	3824	9	US-09-931-836-22	Sequence 22, Appl
27	55.4	3.2	3824	9	US-10-175-746-541	Sequence 541, App
28	55.4	3.2	3824	9	US-10-176-921-541	Sequence 541, App
29	55.4	3.2	3824	9	US-10-176-921-541	Sequence 541, App
30	55.4	3.2	3824	9	US-10-227-884-209	Sequence 209, App
31	55.4	3.2	3824	9	US-10-036-214-22	Sequence 22, Appl
32	55.4	3.2	3824	9	US-10-137-865-541	Sequence 541, App
33	55.4	3.2	3824	9	US-10-140-474-541	Sequence 541, App
34	55.4	3.2	3824	9	US-10-035-719-22	Sequence 22, Appl
35	55.4	3.2	3824	9	US-10-142-431-541	Sequence 541, App
36	55.4	3.2	3824	9	US-10-143-114-541	Sequence 541, App
37	55.4	3.2	3824	9	US-10-230-163-209	Sequence 209, App
38	55.4	3.2	3824	9	US-10-140-002-541	Sequence 541, App
39	55.4	3.2	3824	9	US-10-036-160-22	Sequence 22, Appl
40	55.4	3.2	3824	9	US-10-142-419-541	Sequence 541, App
41	55.4	3.2	3824	9	US-10-218-631-209	Sequence 209, App
42	55.4	3.2	3824	9	US-10-230-338-209	Sequence 209, App
43	55.4	3.2	3824	9	US-10-035-958-22	Sequence 22, Appl
44	55.4	3.2	3824	9	US-10-036-150-22	Sequence 22, Appl
45	55.4	3.2	3824	9	US-10-123-262-541	Sequence 541, App

ALIGNMENTS

RESULT 1
US-10-083-590-13

Sequence 13, Application US/10083590
Publication No. US20030027257A1

GENERAL INFORMATION:

APPLICANT: IATROU, Kostas

APPLICANT: FARRELL, Patrick J.

APPLICANT: BEHRE, Leo A.

TITLE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF

FILE REFERENCE: 028722-207

CURRENT FILING DATE: 2002-02-27

PRIOR FILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/136,421

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/056,871

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 13

TYPE: DNA

LENGTH: 1691

ORGANISM: Heliothis virescens

US-10-083-590-13

Query Match

Best Local Similarity 53.6%; Pred. No. 7.2e-13;

Matches 211; Conservative 0; Mismatches 177; Indels 6; Gaps 1;

QY	368	CCGAACCTAAGCTCCGCTTTAGTATACATACATGCTGCTTTTATATCGGTAA	427
DB	380	CCACACCTTTAGCGCTATCCGCTGCTTATACATGCTGAGAGATTGGCTTCGCTCG	439
QY	428	ATCATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	487
DB	440	GCCACGAGAGACCTACACGAGACAGATATTTGCTCCTAAGATATGATCATCATACCT	499
QY	488	TACATATGTTGGAGCTAGCTAGCTTTCTAAGTTTAAATTCAGAACGCTTAATGTC	547
DB	500	TTAATATGAGATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	553

QY	548	CCGGTAATGCCGGCCTTAACATCAAGCATGGCCCTTGCGTTGATTAATAAATAATATGGC	607
Db	554	CCGGTAATGCCGGCTTCCTCGGGATCAGGTAACCCCTTTGGCCGTGGGTCAAAAGGAAAGCCA	613
QY	608	CCAACTTTGGTGGCAATCCCGATTAATAATTACAGCTTTTGGGAAGTGCCTGCTCCT	667
Db	614	AGAAATTTGGAGAGAAACCCACGACATCACACATAGGGGGGACAAAGCGCTGGTCAATCAG	673
QY	668	CTACCCACTACATGATGTGTAACCAACAACACTCGCGGCTCTTTTCCATCGTGGTAATCAA	727
Db	674	CTGGGCATCTACTACCTCTTTCTTAAGCTACTGAAGGCTCTTTTCAAAAGAGCATCTCGA	733
QY	728	TGTCGGGTAAATGCTAATTTGCTCAATGGCTAATAC	761
Db	734	TGACGGACAGGAAATGAGCTACTTCTTTACTAC	767

RESULT 2

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Sequence 1254, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 1254
LENGTH: 1611
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1254

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Query Match	4.5%	Score 77.2	DB 9	Length 1611
Best local similarity	50.2%	Pred. No. 7e-10	Mismatches 283	Indels 12
Matches 277	Conservative	0	Mismatches 283	Indels 12
			Gaps	3
QY	177	GGGTATACGGTACGCCCAACGCCAGTGGGTGAGCTGAGATTAAAGCACCACCGAGCACC	236	
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QY	237	AACACCCCTGGGATGGTGTGCGGTGATTTGTCAC---ATCATTAAGATTAAGTCAGTCACGT	293	
Db	138	CAGAAGATGGGACGCGCGTGGGATTTGTCATGTTGGGTGAATACCTTCTCAGCCAAC	197	
QY	294	TGATTTTATTAAGGGGCAAAAGTGTGTGGCTCAGAGAGATTGTATACCTAAGTGTCTATAC	353	
Db	198	GTACCTCTGGACAGATTAAGATTGCGGGTTACAGAAAGACGCTTAACTCGATGTCTGGCG	257	
QY	354	GAAATATCTAAATCCCGAAACTAAACGTCGCCGTTTATGATATCATACATGGGTGGGTTT	413	
Db	258	G-----CCTGTATTCGGAAGAAACCTCTGTTGTGTGTATCTCCACGCGGTTCTCT	311	
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Db	312	CATCATGGGCGTCATCAACCGA	AAAGCGCTCGGGGATATTAAC	TCTGCACAAACATGMA	371
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Db	492	GCTCAGCGCTTAATATCGAAG	ATTTCGTTGGGATCTCGACAC	GTCACTCCCTCATGGGCGA	551
Qy	651	AAGTCGCGTGCTCCCTCTAC	CCCACTACATGATTTAAACGA	AAACAACTGCGCGCTTTT	710
Db	552	ATTCGCGGGGCGCTCGACAG	TGGTTCACATCATGTGTGTC	CGCGCTCGACGAGAGCATTT	611
Qy	711	CCATCGTGTGTAT	722		
Db	612	CCACCGCGGCAT	623		

RESULT 3

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US-09-/48-739A-1
? Sequence 1, Application US/09748739A
? Patent No. US20020119489A1
? GENERAL INFORMATION:
? APPLICANT: Lockridge, Oksana
? APPLICANT: Watkins, Jeffrey D.
? TITLE OF INVENTION: Butyrylcholinesterase Variants and
? TITLE OF INVENTION: Methods of Use
? FILE REFERENCE: P-IX 4143
? CURRENT APPLICATION NUMBER: US/09/748,739A
? CURRENT FILING DATE: 2000-12-06
? NUMBER OF SEQ ID NOS: 31
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 1967
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Human Butyrylcholinesterase variantt
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (86)...(1891)
? US-09-/48-739A-1

```

[illegible]

Db 721 AATCCTAAAGTGAATCTCTTTGGAGAAAGTGCAGAGACGCTTC 777

RESULT 4
US-09-880-107-2271

Sequence 2271, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-NO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2271
LENGTH: 2381
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474
US-09-880-107-2271

Query Match 3.6%; Score 62.2; DB 10; Length 2381;
Best Local Similarity 54.8%; Pred. No. 6.7e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

Qy 325 GAGAGTTGCTATACCTAGTGTCTATACGAATAATCCCGAAACTAAAGTCC 384
Db 427 GAGAGCTGTTATATCTAATGTATGATTCAGACCTAAAC--AAATAATGCCACT 483
Qy 385 GTTTAGTATACATACATGCTGCTTTTATATCGTGGAATCATCGTATGTAT 444
Db 484 GTATTGATATGATTTAGTGCTGTTTCAACTGGAACATCTTTTACATGTTAT 543
Qy 445 GTCCTGATTTATTCATTAATAAAGA--TGCGTGTGATTAACTAATCATATGCTTG 501
Db 544 GATGCAAGTTCTGCTCGGCTTAAGAGATTATGTATGATCATATGATAGGCTG 603
Qy 502 GAGCTGATGTTTCTAGATTAAATTCAGAAAGCTTAATGTGCCCGGTAATGCCGC 561
Db 604 GGTGCCCTAGATCTCTAGCTT--GCCAGGAATCCTGAGGCTCCAGGAAATGAGGT 660
Qy 562 CTTAAGATCAAGTATGCGCTTGCTTGATTAATAAATATGCGCACTTTGCTGC 621
Db 661 TTATTGATCAACAGTGTGCTTCTAGTGCTTCAAAAAAATATAGACGCTTTGCTGA 720
Qy 622 AATCCGATTAATATTAACAGTCTTTGCTGAAGTCCGCTGCTGCCTC 668
Db 721 AATCCTAAAGTGAATCTCTTTGGAGAAAGTGCAGAGACGCTTC 767

RESULT 5
US-09-748-739A-3

Sequence 3, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Mackins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2416
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
NAME/KEY: CDS
LOCATION: (214)...(1935)
US-09-748-739A-3

Query Match 3.6%; Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6.8e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

Qy 325 GAGAGTTGCTATACCTAGTGTCTATACGAATAATCCCGAAACTAAAGTCC 384
Db 481 GAGAGCTGTTATATCTAATGTATGATTCAGACCTAAAC--AAATAATGCCACT 537
Qy 385 GTTTAGTATACATACATGCTGCTTTTATATCGTGGAATCATCGTATGTAT 444
Db 538 GTATTGATATGATTTAGTGCTGTTTCAACTGGAACATCTTTTACATGTTAT 597
Qy 445 GTCCTGATTTATTCATTAATAAAGA--TGCGTGTGATTAACTAATCATATGCTTG 501
Db 598 GATGCAAGTTCTGCTCGGCTTAAGAGATTATGTATGATCATATGATAGGCTG 657
Qy 502 GAGCTGATGTTTCTAGATTAAATTCAGAAAGCTTAATGTGCCCGGTAATGCCGC 561
Db 658 GGTGCCCTAGATCTCTAGCTT--GCCAGGAATCCTGAGGCTCCAGGAAATGAGGT 714
Qy 562 CTTAAGATCAAGTATGCGCTTGCTTGATTAATAAATATGCGCACTTTGCTGC 621
Db 715 TTATTGATCAACAGTGTGCTTCTAGTGCTTCAAAAAAATATAGCACTTTGCTGA 774
Qy 622 AATCCGATTAATATTAACAGTCTTTGCTGAAGTCCGCTGCTGCCTC 668
Db 775 AATCCTAAAGTGAATCTCTTTGGAGAAAGTGCAGAGACGCTTC 821

RESULT 6
US-09-748-739A-5

Sequence 5, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Mackins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2416
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
NAME/KEY: CDS
LOCATION: (214)...(1935)
US-09-748-739A-5

Query Match 3.6%; Score 62.2; DB 10; Length 2416;
Best Local Similarity 54.8%; Pred. No. 6.8e-06;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

Qy 325 GAGAGTTGCTATACCTAGTGTCTATACGAATAATCCCGAAACTAAAGTCC 384
Db 481 GAGAGCTGTTATATCTAATGTATGATTCAGACCTAAAC--AAATAATGCCACT 537


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QY 385 GTTTAGTATACATACATGCTGCTTTTATATCGTGGAATAATCATCGTATATGAT 444
    || || || || || || || || || || || || || || || || || || || || ||
Db 538 GTATTGATATGATTTATGCTGCTTTTCAAACTGGAACATCATGTTTACATGTTAT 597
QY 445 GGTCTGATTTATTCATTAATAAGAA--TGCTGCTGATTAATCAATACATGCTTGG 501
    || || || || || || || || || || || || || || || || || || || || ||
Db 598 GATGGCAAGTTTCTGGCTCGGGTGAAGAGTTATTTAGTCAATGCAATATAGGCTG 657
QY 502 GGACCTAGCTTTTCTAAGTTTAATTGAGAACCTTATGTCCTGATATGCGGC 561
    || || || || || || || || || || || || || || || || || || || || ||
Db 658 GGTGCTCCTAGATTTCTTACCTT---GCCAGGAATCCTGAGCTCCAGGGAACATGGGT 714
QY 562 CTAAAGATCAAGTCATGCGCTTGCCTTGAATTAATGCGCAACTTTGCTGGC 621
    || || || || || || || || || || || || || || || || || || || || ||
Db 715 TTATTGATCAACAGTTGGCTCTTCACTGAGGCTCAAAAAATATAGCAAGCTTTGGTGA 774
QY 622 AATCCGATATATATACAGTCTTTGGTGAAGTCCGCTGCTGCTC 668
    || || || || || || || || || || || || || || || || || || || || ||
Db 775 AATCTTAAAGTGTACTCTCTTTGGAGAAAGTGCAGAGACAGCTTC 821

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RESULT 7

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US-09-748-739A-7
; Sequence 7, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1935)
US-09-748-739A-7

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Query Match

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Best Local Similarity 3.6%; Score 62.2; DB 10; Length 2416;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

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QY 325 GAGGATTTCTATACCTAGTCTCTATACGAATATCTAATCCGAAACTAAGCTGCC 384
    || || || || || || || || || || || || || || || || || || || || ||
Db 481 GAAGACTGTTTATATCTAATATGATGATTCACGACCTAATACC---AAAAATGCCACT 537
QY 385 GTTTAGTATACATACATGCTGCTTTTATATGCGGAATCATGCTGATATGAT 444
    || || || || || || || || || || || || || || || || || || || || ||
Db 538 GTATTGATATGATTTATGCTGCTTTTCAAACTGGAACATCATGTTTACATGTTAT 597
QY 445 GGTCTGATTTATTCATTAATAAGAA--TGCTGCTGATTAATCAATACATGCTTGG 501
    || || || || || || || || || || || || || || || || || || || || ||
Db 598 GATGGCAAGTTTCTGGCTCGGGTGAAGAGTTATTTAGTCAATGCAATATAGGCTG 657
QY 502 GGACCTAGCTTTTCTAAGTTTAATTGAGAACCTTATGTCCTGATATGCGGC 561
    || || || || || || || || || || || || || || || || || || || || ||
Db 658 GGTGCTCCTAGATTTCTTACCTT---GCCAGGAATCCTGAGCTCCAGGGAACATGGGT 714
QY 562 CTAAAGATCAAGTCATGCGCTTGCCTTGAATTAATGCGCAACTTTGCTGGC 621
    || || || || || || || || || || || || || || || || || || || || ||
Db 715 TTATTGATCAACAGTTGGCTCTTCACTGAGGCTCAAAAAATATAGCAAGCTTTGGTGA 774
QY 622 AATCCGATATATATACAGTCTTTGGTGAAGTCCGCTGCTGCTC 668
    || || || || || || || || || || || || || || || || || || || || ||

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Db 775 AATCTTAAAGTGTACTCTCTTTGGAGAAAGTGCAGAGACAGCTTC 821

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RESULT 8

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US-09-748-739A-16
; Sequence 16, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-748-739A-16

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Query Match

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Best Local Similarity 3.6%; Score 62.2; DB 10; Length 2416;
Matches 190; Conservative 0; Mismatches 148; Indels 9; Gaps 3;

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QY 325 GAGGATTTCTATACCTAGTCTCTATACGAATATCTAATCCGAAACTAAGCTGCC 384
    || || || || || || || || || || || || || || || || || || || || ||
Db 481 GAAGACTGTTTATATCTAATATGATGATTCACGACCTAATACC---AAAAATGCCACT 537
QY 385 GTTTAGTATACATACATGCTGCTTTTATATGCGGAATCATGCTGATATGAT 444
    || || || || || || || || || || || || || || || || || || || || ||
Db 538 GTATTGATATGATTTATGCTGCTTTTCAAACTGGAACATCATGTTTACATGTTAT 597
QY 445 GGTCTGATTTATTCATTAATAAGAA--TGCTGCTGATTAATCAATACATGCTTGG 501
    || || || || || || || || || || || || || || || || || || || || ||
Db 598 GATGGCAAGTTTCTGGCTCGGGTGAAGAGTTATTTAGTCAATGCAATATAGGCTG 657
QY 502 GGACCTAGCTTTTCTAAGTTTAATTGAGAACCTTATGTCCTGATATGCGGC 561
    || || || || || || || || || || || || || || || || || || || || ||
Db 658 GGTGCTCCTAGATTTCTTACCTT---GCCAGGAATCCTGAGCTCCAGGGAACATGGGT 714
QY 562 CTAAAGATCAAGTCATGCGCTTGCCTTGAATTAATGCGCAACTTTGCTGGC 621
    || || || || || || || || || || || || || || || || || || || || ||
Db 715 TTATTGATCAACAGTTGGCTCTTCACTGAGGCTCAAAAAATATAGCAAGCTTTGGTGA 774
QY 622 AATCCGATATATATACAGTCTTTGGTGAAGTCCGCTGCTGCTC 668
    || || || || || || || || || || || || || || || || || || || || ||
Db 775 AATCTTAAAGTGTACTCTCTTTGGAGAAAGTGCAGAGACAGCTTC 821

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RESULT 9

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US-09-893-519A-112
; Sequence 112, Application US/09893519A
; Publication No. US20030027243A1
; GENERAL INFORMATION:
; APPLICANT: ANADYS PHARMACEUTICALS, INC.
; APPLICANT: THOMPSON, Craig
; APPLICANT: MOORE, Jeffrey
; APPLICANT: BURMAN, Ed T.
; APPLICANT: BRADLEY, John
; APPLICANT: DESTIVA, Thameara
; APPLICANT: HARRIS, Sandra
; APPLICANT: KOMARNITSKY, Svetlana
; APPLICANT: MENDILLO, Marc
; APPLICANT: MOORE, Daniel
; APPLICANT: MCCOY, Melissa
; APPLICANT: SANDERSON, Karen
; APPLICANT: HAQ, Tariq
; APPLICANT: ZHU, Shuhao
; APPLICANT: LONG, Fan
; APPLICANT: DAVIDOV, Eugene

```


RESULT 12
US-09-934-323-1

Sequence 1, Application US/09934323
Patent No. US20020150910A1
GENERAL INFORMATION:
APPLICANT: Curtiss, Roy A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYL ESTERASE
FILE REFERENCE: 10448-081001
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4667
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (420)...(2924)
US-09-934-323-1

Query Match 3.4%; Score 57.6; DB 10; Length 4667;
Best Local Similarity 54.2%; Pred. No. 0.00015;
Matches 117; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 530 CAGAACCTTAAATGTCGGGTAATGCGGCTTAAGATCAAGTGCCTTGGCT 589
DB 1090 CCGGGACCGAGCTGCAAAAGGCACTATGCGCTCTGACCGAGATCCAGCCCTGGCT 1149
QY 590 GATTAATAATTAATGCGCAACTTTGGTGCAATCCGCAATATTAATTAAGTCTTTGGTG 649
DB 1150 GGCCTACATGAAGACATGCGCACTTTGGGGGCGACCCGAGCATATCACCATTCTTGGT 1209
QY 650 AAGTGGCGGTGCTGCTTACCACTACATGATGATTAACCGAACAACCTGGCTTTT 709
DB 1210 CCGGGGCGAGGGGCTCTGCTGCTTACCACTTCTCTCCACCATTCAGAAAGGCTGT 1269
QY 710 TCCATGCTGATCTACTATGTCGGGTAAATGCTATTT 745
DB 1270 TCCAGAAAGCCATGCGCCAGAGTGGCACCGCATTT 1305

RESULT 13

US-09-954-531-1038

Sequence 1038, Application US/09954531

Patent No. US20020165180A1

GENERAL INFORMATION:

APPLICANT: Weaver, Zoe

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand

FILE REFERENCE: 689290-77

CURRENT APPLICATION NUMBER: US/09/954,531

CURRENT FILING DATE: 2002-05-02

PRIOR APPLICATION NUMBER: US/60/233,133

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/60/234,009

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US/60/234,034

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US/60/234,509

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: US/60/234,567

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 1392

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1038

LENGTH: 2191

TYPE: DNA

ORGANISM: Homo sapiens

US-09-954-531-1038

Query Match 3.3%; Score 56.8; DB 9; Length 2191;

Best Local Similarity 53.2%; Pred. No. 0.00016;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

QY 322 TCAGAGATGTCCTATACCTAAGTGTCTATACGATATCTAATCCGAA---ACTAA 378
DB 436 TCTGAGAGCTGCTGTACTGACATCTACGCGGCCATAGCCATGAGAGCTCTAAC 495
QY 379 CGTCCGCTTTTGTATACATACATGATGATGTTTATATATGCGTGAATATCGTAT 438
DB 496 CTGCGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 553
QY 439 ATGATAGTCTGATATTTTCAATTAAGATGATGATGATGATGATGATGATGATGAT 498
DB 554 ATGATAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 612
QY 499 TTGGAGCTCTAGCTTTTCTAAGTTAATTCAGAAAGCTTAATGCGGCTATGCG 558
DB 613 CTGGGCTCTGCTGGCTT-----CTTACAGCTGAGAGACAGCAGCAACCGCACTG 666
QY 559 GGCCTTAAGATCAAGTCAATGCGCTTGCCTGATTAATAATTAATTAATTAATTAAT 618
DB 667 GGCCTACCTGAGCAAGTGGCTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
QY 619 GGCATCCCGATATATTTACAGCTTTTGTGAAAGTCCGCGCTGCTGCTGCTGCTGCT 678
DB 727 GGCATCCCGATATATTTACAGCTTTTGTGAAAGTCCGCGCTGCTGCTGCTGCTGCT 786
QY 679 ATGATGTTAAGCAACAACCTGCGCTTTTCTGATGATGAT 722
DB 787 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 830

RESULT 14

US-09-880-107-3854

Sequence 3854, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3854

LENGTH: 2191

TYPE: DNA

ORGANISM: Homo sapiens

OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y09616

US-09-880-107-3854

Query Match 3.3%; Score 56.8; DB 10; Length 2191;
Best Local Similarity 53.2%; Pred. No. 0.00016;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;

QY 322 TCAGAGATGTCCTATACCTAAGTGTCTATACGATATCTAATCCGAA---ACTAA 378
DB 436 TCTGAGAGCTGCTGTACTGACATCTACGCGGCCATAGCCATGAGAGCTCTAAC 495
QY 379 CGTCCGCTTTTGTATACATACATGATGATGATGATGATGATGATGATGATGATGAT 438
DB 496 CTGCGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 553
QY 439 ATGATAGTCTGATATTTTCAATTAAGATGATGATGATGATGATGATGATGATGATGAT 498

Db	554	ATGANGGTTCCATCTGGCTGCTT-TGGAGAACGTGGTGGTCATCATTCACGTAACCGC	612
Qy	499	TTGGAGAGCTCTAGGTTTTTCTTAAGTTTAAATTCCAGAAACCTTAATGTGCCCGGTAATGCC	558
Db	613	CTGGGTGTCCTGGGCTT-----CTTGAGACATGGAGAACAGCAGCAGAACCGGCAACTGG	666
Qy	559	GGCCTTAAAGATCTCAAGTCATGAGCCCTTGCCCTGGATTAAATAATATGGCCGCACTTGGT	618
Db	667	GGCTACCTGGAGCAAAAGTGGGCTGCACACTACCGTGGGTCCAGAGAAATATCGGCCACTTTGGA	726
Qy	619	GGCAATCCCGATTAAATTATACAGTCTTTGGTGAAGTCCGGTGTGCTCTTACCCACTAC	678
Db	727	GGCAACCTGTGACCTGTGCACCATTTTGGCGAGCTGTCGGGTGGCAGCAAGTGTGTCTCG	786
Qy	679	ATGATGTTAACCGAACAACCTGGGGCTTTTCCATGCTGGTAT	722
Db	787	CTTGTTGTGTCCTCCCATATCCCAAGAGACTCTTCCACGAGCAACT	830

RESULT 15
HE-10-103

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Sequence 771. Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103PICI
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
Seq ID NO 271
LENGTH: 2484
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (194)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (623)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (2396)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (2484)
OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-271

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Query Match	Score	DB	Length
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QY 322 TCAGAGGATTTGTGATATACCAAGTGTCTTACGAATAATCTAAATCCGAA---ACTAAA 378
 Db 950 TCTGAGGATCTCCGCTAGCCACACATCTACACGCCGCCCATAGCCATGAGGCTTTAAC 1009
 QY 379 CGTCCCTTTTACATATACATACATATGGTGTGGTGTATTTATTCGGTGAATAATCATCGTAT 438
 Db 1010 CTGCGGCGATAGGTGTGTGATCCACGGGTGGCGCTTGTTTTG--GCATGGCTTCTTGCT 1067
 QY 439 ATGTATGTCCTGATTATTTTCATTTAAAGAAGATGTGGTGTATTAAACATACATATATGCT 498
 Db 1068 ATGATGGTTCACATCTGGTGGCT-TGGAGAAAGTGTGTGTGCATATCCAGTAGACGC 1126
 QY 499 TTGGGACCTCTAGGTTTTCTAAGTTTAAATTCAGAAAGACTTAAATGTGGCCGGTATGCC 558

Db 1127 CTGGGTGTCTCTGGGCTT-----CTTCAGACACTGGAGACAGCAACGACCGGCAACTGG 1180
 QY 559 GGCCTTAAAGATCAAGCATGCGCCCTGCGCTGGATTAAATAATATGGCCCAACTTGGT 618
 Db 1181 GGCCTACTGGACCAAGTGGCTGCATCACTGGGTCCAGACAAATATGCCCCACTTTGGA 1240
 QY 619 GGCATCCCGCATATATATTACAGCTCTTGGTGAAGGCGCGGTCTGCCCTTACCCACTAC 678
 Db 1241 GGCACCCCTGACCGTGTGCACCATTTTGGCGAGTCTGGGGGTGGCAGCAGTGTGTCTCG 1300
 QY 679 ATGATGTTAACCGAACAACCTCGCGGCTCTTTCCATCGTGAT 722
 Db 1301 CTGTGTGTGTCGCCCATATGCCAAGACCTTCCACAGGACCAT 1344

Search completed: April 11, 2003, 13:23:19
Job time : 106.528 secs

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:59:47 ; Search time 294.03 Seconds

(without alignments)
16933.650 Million cell updates/sec

Title: US-09-776-910-3

Perfect score: 1713
Sequence: 1 atgaattcaccgttagttt.....aacatagagattatttttag 1713Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: gb.ov:*
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40: em.htgo.mus:*
41: em.htgo.other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1713	100.0	1713	6	AR153439 Sequence
2	1711.4	99.9	1713	6	AR153442 Sequence
3	1709.8	99.8	1713	6	AR153438 Sequence
4	1706.6	99.6	1713	6	AR153440 Sequence
5	1701.8	99.3	1713	6	AR062837 Sequence
6	1701.8	99.3	1713	6	AR153441 Sequence
7	1701.8	99.3	2240	3	LCU56636 Sequence
8	1676.6	97.9	1713	6	AR062838 Sequence
9	985.6	57.5	2160	3	AF133341 Musca dom
10	959.4	56.0	2175	3	AF139082 Haematobi
11	955	55.8	1710	6	AR153445 Sequence
12	680.4	39.7	2017	3	AY051473 Drosophila
13	378.6	22.1	2660	3	AT121675 Drosophila
14	377	22.0	2820	3	DMU51050 Drosophila
15	372.2	21.7	5735	2	AC015272 Drosophila
16	372.2	21.7	18459	3	AC008312 Drosophila
17	372.2	21.7	197597	3	AC011253 Drosophila
18	372.2	21.7	309023	3	AE003671 Drosophila
19	365.4	21.3	1962	3	AY051497 Drosophila
20	323	18.9	2122	3	AY058637 Drosophila
21	304.6	17.8	1906	3	AY058345 Drosophila
22	300.4	17.5	13044	2	AC014297 Drosophila
23	300.4	17.5	117743	2	AC008098 Drosophila
24	300.4	17.5	173373	3	AC008349 Drosophila
25	300.4	17.5	307363	3	AE003457 Drosophila
26	289.8	16.9	2050	3	AF216210 Drosophila
27	278.4	16.3	1205	3	AF216215 Drosophila
28	270	15.8	1809	6	AX260182 Sequence
29	241.4	14.1	1630	3	COESPA2EA Drosophila
30	240.4	14.0	3946	3	DMU51044 Drosophila
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32	238.2	13.9	188459	3	AC008312 Drosophila
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35	229.6	13.4	1724	3	AY069743 Drosophila
36	227.6	13.3	2401	3	DMU51054 Drosophila
37	224.2	13.1	933	3	AF216216 Drosophila
38	224.2	13.1	1836	3	CQSERES1 Drosophila
39	224	13.1	3447	3	DMU51052 Drosophila
40	219.2	12.8	1630	2	CQSERES2 Drosophila
41	214	12.5	84252	2	AC009207 Drosophila
42	212	12.4	1401	3	CPU43544 Culex pipie
43	207.4	12.1	6028	3	AF177382 Culex tri
44	204.8	12.0	1401	3	CPU43546 Culex pipie
45	199.8	11.7	1401	3	CPU43545 Culex pipie

ALIGNMENTS

RESULT 1
LOCUS AR153439
DEFINITION Sequence 3 from patent US 6235515.
ACCESSION AR153439
VERSION AR153439.1 GI:15120971
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
Roblin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.A.,
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
TITLE Malathion carboxylesterase

JOURNAL Patent: US 6235515-A 3 22-MAY-2001;
 FEATURES Location/Qualifiers
 Source 1..1713
 BASE COUNT 515 a 306 c 370 g 522 t
 ORIGIN

Query Match 100.0%; Score 1713; DB 6; Length 1713;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTTTCAACGTTACTTTGATGAGAAATTAATGAGATTAAATGCAATGAAAT 60
 DB 1 ATGATTTTCAACGTTACTTTGATGAGAAATTAATGAGATTAAATGCAATGAAAT 60
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 DB 121 AAGGTGAAGCGCTTAAACGTTTAACTGTAGATGATCTTAACTAGTTTGAAGGT 180
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DB 901 GAAGAGCGTACAAATTAAGTCAATGTTTCTTGGTCCCACTGTTGAGCCATATCAGACC 960
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 DB 1441 AATCAATTTGCCCAACGATGCTTAAAGAAATGCGGTGAATACAAAACAATTAAGCTATG 1500
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 DB 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTTGA 1713

RESULT 2
 AR153442 1713 bp DNA Linear PAT 08-AUG-2001
 LOCUS AR153442
 DEFINITION Sequence 9 from patent US 6235515.
 ACCESSION AR153442
 VERSION AR153442.1 GI:15120974
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1713)
 AUTHORS Russell,R.,Joyce,,Newcomb,R.,David,,Campbell,P.,Malcolm,,
 Robin,G.,Charlesde,,Queteville,,Claudioanos,C.,Smyth,K.,-A.,
 Boyce,T.,Mark,,Oakesholt,J.,Graham,,and Brownlie,J.,Collin.
 TITLE Malachion carboxylesterase
 JOURNAL Patent: US 6235515-A 9 22-MAY-2001;
 FEATURES Location/Qualifiers
 Source 1..1713

BASE COUNT 515 a 305 c 370 g 523 t
ORIGIN

Query Match 99.9%; Score 1711.4; DB 6; Length 1713;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAAATTCACACCTTATGATGAGAGAAATTAATAAGAGATTAAATGATGAAAT 60
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DB 1081 CAATGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
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DB 1441 AATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
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DB 1561 ATGGAATAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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DB 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 TCGATGTTGAAAAACATGAGATTTATTTAG 1713
DB 1681 TCGATGTTGAAAAACATGAGATTTATTTAG 1713
RESULT 3
ARI53438
LOCUS ARI53438 1713 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6235515.
ACCESSION ARI53438
VERSION ARI53438.1 GI:15120970
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Robinson, G. Charlesde., Quetleville., Claudianos, C., Smyth, K. A.,
Boyce, T. Mark., Oakeshot, J. Graham. and Brownlie, J. Colin.
TITLE Malation carboxylesterase
JOURNAL Patent: US 6235515-A 1 22-MAY-2001;
FEATURES Location/Dualifiers
source 1. 1713
BASE COUNT 515 a 304 c 370 g 524 t
ORIGIN

Query Match 99.8%; Score 1709.8; DB 6; Length 1713;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAATTCACACGTTAGTTGATGAGAAATTAATAAGAGATTAAATGCAATGAAAT 60
 Db 1 ATGAAATTCACACGTTAGTTGATGAGAAATTAATAAGAGATTAAATGCAATGAAAT 60
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 Db 181 ATACCGTACCGCCCAACCGCCAGTGGGTGAGCTGAGATTAAAGCACCACCGACCA 240
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RESULT 4
 ARI53440 1713 bp DNA linear PAT 08-AUG-2001
 LOCUS ARI53440
 DEFINITION Sequence 5 from patent US 6235515.
 ACCESSION ARI53440
 VERSION ARI53440.1 GI:15120972
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1713)
 AUTHORS Russell, R. Joyce, R. Newcomb, R. David, Campbell, P. Malcolm, Rodin, G. Charlesde, Quetleville, C. Claudianos, C. Smyth, K. A., Boyce, T. Mark, J. Oakesholt, J. Graham, and Brownlie, J. Colin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 6235515-A 5 22-MAY-2001;
 FEATURES location/qualifiers
 source 1..1713
 BASE COUNT 516 a 305 c 369 g 523 t
 ORIGIN
 Query Match 99.8%; Score 1706.6; DB 6; Length 1713;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 5
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LOCUS AR062837
DEFINITION Sequence 1 from patent US 5843758.
ACCESSION AR062837
VERSION AR062837.1 GI:5990528
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Robin, G. Charlesde. Quetleville.,
Boyce, T. Mark., Campbell, P. Malcolm.,
Oakeshott, J. Graham. and Smyth, K. A.
TITLE Enzyme based bio remediation
JOURNAL Patent: US 5843758-A 1 01-DEC-1998;
FEATURES
source Location/Qualifiers
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BASE COUNT 516 a 305 c 370 g 522 t
ORIGIN
Query Match 99.3%; Score 1701.8; DB 6; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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AR153441 1713 bp DNA Linear PAT 08-Aug-2001
LOCUS AR153441
DEFINITION Sequence 7 from patent US 6235515.
ACCESSION AR153441
VERSION AR153441.1 GI:15120973
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce, Newcomb, R. David, Campbell, P. Malcolm, Robin, G. Charlesde, Quetleville, Claudianos, C., Smyth, K. A., Boyce, F. Mark, Oakeshott, J. Graham, and Brownlie, J. Colin.
TITLE Malathion carboxylesterase
JOURNAL Patent: US 6235515-A 7 22-MAY-2001;
FEATURES Location/Qualifiers
source 1..1713
BASE COUNT 516 a 305 c 370 g 522 t
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Query Match 99.3%; Score 1701.8; DB 6; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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 ACCESSION
 U56636
 VERSION
 U56636.1 GI:1336079
 KEYWORDS
 SOURCE
 ORGANISM
 Lucilia cuprina.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Oestroidea; Calliphoridae; Lucilia.
 REFERENCE
 1 (bases 1 to 2240)
 Newcomb, R.D., East, P.D., Russell, R.J. and Oakeshott, J.G.
 Isolation of alpha cluster esterase genes associated with
 organophosphate resistance in *Lucilia cuprina*
 Insect Mol. Biol. 5 (3), 211-216 (1996)
 MEDLINE
 PUBMED
 8799740
 REFERENCE
 2 (bases 1 to 2240)
 Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
 cDNA cloning, baculovirus-expression and kinetic properties of the
 esterase, E3, involved in organophosphorus resistance in *Lucilia*
 cuprina
 Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)
 MEDLINE
 PUBMED
 9061925
 REFERENCE
 3 (bases 1 to 2240)
 Newcomb, R.D., Campbell, P.M., Ollis, D.L., Cheah, E., Russell, R.J. and
 Oakeshott, J.G.
 A single amino acid substitution converts a carboxylesterase to an
 organophosphorus hydrolase and confers insecticide resistance on a

JOURNAL blowfly
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997)
PUBMED 97352821
AUTHORS 4 (bases 1 to 2240)
TITLE Campbell, P.M., Newcomb, R.D., Russell, R.J. and Oakeshott, J.G.
JOURNAL Two different amino acid substitutions in the alpha-esterase, E3,
confer alternative types of organophosphorus insecticide resistance
in the sheep blowfly
Unpublished
5 (bases 1 to 2240)
REFERENCE Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
AUTHORS Direct Submission
TITLE Submitted (24-Apr-1996) Richard D. Newcomb, Molecular Genetics,
HortResearch, Private Bag 92 169, Auckland, New Zealand
FEATURES
Source Location/Qualifiers
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1..2240
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Db 1558 TTCTGTTTCCCATGATCGCTTTGTCATTTACGTTTCAATCAACCTCCGATACACC 1617
Qy 1321 GTCACCTGATGCTGCTTCGATTTGATTCGGAATCTTATCATCTCCATCTATATG 1380
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Qy 1621 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Db 1918 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1977
Qy 1681 TCGATGTTTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1713
Db 1978 TCGATGTTTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 2010

RESULT 8
LOCUS AR062838 1713 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5843758.
ACCESSION AR062838
VERSION AR062838.1 GI:5990529
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Robin, G. Charlesde. Quetreville.,
Boyce, J. Mark., Campbell, P. Malcolm., Parker, A. Gerard.,
Okeshott, J. Graham, and Smyth, K. A.
TITLE Enzyme based bioremediation
JOURNAL Patent: US 5843758-A 2 01-DEC-1998;
FEATURES
source location/Qualifiers
BASE COUNT 506 a 299 c 363 g 515 t 30 others
ORIGIN

Query Match 97.9%; Score 1676.6; DB 6; Length 1713;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy 121 AAGTGAAGGCGTTAAAGCTTTAACTGATGATGATGATGATGATGATGATGATGATG 180
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Db 1141 GCTGATNCTGAAACGACGCGCCGACAGACCTGGAAATGGGTGCTAAATTAAGAGCT 1200
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QY 1681 TCGATGTTTGAACAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1713
Db 1681 TCGATGTTTGAACAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1713

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RESULT 9
 AF133341 2160 bp mRNA linear INV 17-AUG-2000
 LOCUS AF133341 Musca domestica carboxylesterase MdaE7 (MdaE7) mRNA, complete cds.
 DEFINITION AF133341
 ACCESSION AF133341
 VERSION AF133341.1 GI:4768932
 KEYWORDS
 SOURCE Musca domestica.
 ORGANISM Musca domestica
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscidae; Muscidae; Musca.
 REFERENCE 1 (bases 1 to 2160)
 AUTHORS Claudiños, C., Russell, R.J. and Oakeshott, J.G.
 TITLE The same amino acid substitution in orthologous esterases confers organophosphate resistance on the house fly and a blowfly
 JOURNAL Insect Biochem. Mol. Biol. 29 (8), 675-686 (1999)
 MEDLINE 99381228
 PUBMED 10451921
 JOURNAL 2 (bases 1 to 2160)
 TITLE Claudiños, C., Russell, R.J. and Oakeshott, J.G.
 AUTHORS Direct Submission
 REFERENCE Submitted (07-MAR-1999) Entomology, CSIRO, Clunies Ross, Canberra, ACT 2601, Australia
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 /chromosome="11"
 /dev_stage="4 day third instar larvae"
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 /gene="MdaE7"
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aE7 alpha esterase; organophosphate resistance"
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/protein_id="A029685.1"
/db_xref="GI:4768933"
/translacion="MNFKVSQMERLSMKLKCNVKNRYNRLSTNETOIIDREYGOIK
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VAVOYRGLVGLSLKSEMLNYPNAGLKDOYMAIRWKSINATNGRVDNITVFES
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SAMGNSIPLNGTSTYEGLEFKSIKAKOPEVVKELSCVNVVPELADERSABETLE
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polya_signal
2115..2120
/gene="MdaE7"
BASE COUNT 661 a 440 c 466 g 593 t
ORIGIN
Query Match 57.5%; Score 985.6; DB 3; Length 2160;
Best Local Similarity 73.5%; Pred. No. 8.2e-211;
Matches 1258; Conservative 0; Mismatches 454; Indels 0; Gaps 0;
QY 1 ARGAAATTCACGGTATGTTGATGAGAAATTAATGGAATTAATGATGATGATGATGATGATGATG 60
Db 217 ATGGAATTTCAAGTTATGCAATGAGAGAGGCTCTCTGGAATCTAATGATGATGATGATGATG 276
QY 61 AAGTTTAACTATGCTTAACTACCAATGAAACGGTGTAGTGAACCTGAATATGATGATGATGATG 120
Db 277 AATATCACAACTACCGCTGTGATCAATGAAACCAATTAATGATGATGATGATGATGATGATG 336
QY 121 AAAGTGAAGGCGTTAAAGCTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
Db 337 CAAATTTAAGGCTGTATTAAGCGAATGACCGCTTACGATGATGATGATGATGATGATGATGATG 396
QY 181 ATACGCTACGCCCAACCGCCAGTGGTGAAGCTGATGATTTAAAGCAACCCAGCAGCAACA 240
Db 397 ATACCCCTATGCTAAGCCCTCAGTGGTGTAGATTTCAAGGCAACCCAGCAGCAGCTGTA 456
QY 241 CCTGGATGAGTGGCGGATGTTGTCATATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 300
Db 457 CCATGGAGGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 516
QY 301 ATACGGGCAAAAGTGTGCTCAGAGAGATGCTATACCTAAGTGTCTATACGATTAAT 360
Db 517 ATAGTGTGCAAAACCCAGAGGTTGCGAGAGATGCTATACCTGATGATGATGATGATGATGATGATG 576
QY 361 CTAATCCCGGAACCTAAACGCTCCGTTTACTATACATACATACATACATACATACATACATACAT 420
Db 577 TTGAACCCAGCAAAACCCGCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 636
QY 421 GGTGAATTCATCGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
Db 637 GGCGAAGCAATTCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 696
QY 481 ATTAACATACATATGCTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAGACCTT 540
Db 697 GTAACCCGTGCAATATCGTTGGGTGTGTTGCTTACCTTGAACCTGAATGGAATATCTC 756
QY 541 AATGCGCGGTATGCGCGGCTTAAGATCAAGTCAATGCGCTTGGCTGGATTAATAAT 600
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QY 601 AATGCGCAACTTGGTGGCAATCCGATATATTAACGCTTGGTGAAGATGCGCGG 660
Db 817 AATATGCCAATTTGCGTGGCGATGAGCAATATTAACGCTTGGCGCAAGATGCGTGG 876

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Oy	661	GCACCTCTACCCACTCTACATGATGTTAACCGAAACAACCTCGCGCTTTCATCTGCGT	720
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Oy	721	ATTACTAATGTCGGGTAAATGCTATTTCCTCATTTGGCTTAATPACCAATGTCACATCTGCGC	780
Db	937	ATCATGATGTCGGTATTCGATTTCGATCTGCTCATGCGCTCTACAGAAATGCCAAAGTCGTCG	996
Oy	781	TTTACCTTTAGCAAAATTGGCCGGCTTAAGGGGTAGAGATTAATGATMAAGATGTTTGGAA	840
Db	997	CTCACCATGGCCAAACGTTGGCTTAAGGGGAGAGACATGAAGAAAGATATCCTGGAA	1056
Oy	841	TTTTCTTTAGAAAGCCAAAGCCACAGGATTTATATAAACTTGAAGAAAAAGTTTAACTCTA	900
Db	1057	TTTCTTAATGAAGAACCAATCCCTATGATTTATGATCAAGAGAACCCAAAGTTTGGACACC	1116
Oy	901	GAAGAGGCTACAAATFAAGTCATGTTCCCTTTGGTCCACTGTTGAGCCATATACAGCC	960
Db	1117	GAAGAAATGCAAAATTAAGTCATGTTCTTTTGGACCCACTGTATGAACATACCAGCA	1176
Oy	961	GCTGATTTGTCTTTACCCAAACATCTCTGGGAAATGTTAAAACTGCTTGGGGTAATTCG	1020
Db	1177	GCCACACTGTGGTACCCAAACCAATCAGAGAAATGTTGAAGAGCGCTGGGGAATATCG	1236
Oy	1021	ATACCCCACTAATGAGGGTAACTCTCATATGAGGGCTATTTTCTACTTCATCTCTTAAG	1080
Db	1237	ATPCCCACTATTGAGCAATPACCTCTCTAGAAAGTTTCTTTTAAATCAATATGCCAAA	1296
Oy	1081	CAAAATGCCATATGCTTTTAAAGAAATTTGAACCTTGTCTCAATTTTGTGCCAAGTAATTC	1140
Db	1297	CAATATCCGGAGGTTTGAATAAGATTTGGAAATCCTGTGTCAATATATGTCTCTGGAGTTG	1356
Oy	1141	GCTGATGCTGAAGCCACCGCCCCAGAGACCTTGGAAATGGTGTCTAAATTTAAAAAGCT	1200
Db	1357	GCTACACGTGAACCACTGAGCCCGCGGAACCCCTGGAAGGGCTGCCATTGTGAAAAAGGCC	1416
Oy	1201	CATGTTACAGGAAACAACCAACAGCTGATTAATTTATGATCTTTGCTCTACATCTAT	1260
Db	1417	CATGTGATGGGGAACCACTACTCTGGAATAATTTATGACCTTTGCTCTATTTCTAT	1476
Oy	1261	TTTCTGTTCCCAATGCATATCGTTTGTGGCAATPACGTTTCAATCACACCTCGGTACACC	1320
Db	1477	TTTCTCTTCCCAATGCATCTCTTCTCTCAATTTGCGTTTAAACACACAGCTGGCACTCC	1536
Oy	1321	GTTACTATTGATCGCTTGCATTCGATTTGGAAGATCTTATCAATCCTATCGTATTAATG	1380
Db	1537	ATTATATTGTATCGTTTCGATTTGATTCGGAAGAAATTAATTAACCCATATGATTAATG	1596
Oy	1381	CGTATGAGACTGGTGTAAAGGGTGTATGATCATGCTGATGAATTAACGATATTTCTTCCG	1440
Db	1597	CGTTTGTGCGCTGGCGTTAAAGGTGTAAAGCAACCGGATTAACCTATCTCTTCCG	1656
Oy	1441	AATCAATATGGCCAAACCTATAGCCTAAAGAAATGCGTGAATPACAAAACATTTGAACGTATG	1500
Db	1657	AACATTTTGTGGAAGACCTGTGCCAAAGGAAGCCGGGAATACAAAACCTTAAGCGCATG	1716
Oy	1501	ACTGCTATATGATPACAAATTTGCCACACTGTATCTCTTAATAGCAATGAATGAAGT	1560
Db	1717	GTTGGCATTTGAGAGGAATTTGCCACACCGCAACCACTACAGCAATGATPATAACCGCCG	1776
Oy	1561	ATGGAATAATGTTTCTCTGGGATCCCAATTAAGAAATCCGATGAAGTATACAGTGTGAT	1620
Db	1777	ATGGAATAACCTCACCTGGGATTCCTATPAAAAATTCGATGATGTCTATPAAAAATGTAAT	1836
Oy	1621	ATTAGTATGAATGAATAATGATTAATGATGCTCGAAGTGAATGATTAACAAATGGAG	1680
Db	1837	ATTCGCGATGATTAAGAAATTTAGATTTGCCGAAGATGATTAATTAACAAATGGGCA	1896
Oy	1681	TCGATGTTGAATAACATATAGATTAATTTTA	1712
Db	1897	AGTATATTTCGATTAAGAAGGAATGTGTTTA	1928

RESULT 10					
AF139082		2175 bp	mRNA	linear	INV 20-OCT-2000
LOCUS	AF139082				
DEFINITION	Haemacobia irritans irritans alpha E7 esterase (ae7) mRNA, complete cds.				
ACCESSION	AF139082				
VERSION	AF139082.1	GI:5502938			
KEYWORDS					
ORGANISM	Haematobia irritans irritans. Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Haematobia.				
REFERENCE	1 (bases 1. to 2175) Guerrero, F.D. Cloning of a horn fly cDNA, H1alphae7, encoding an esterase whose transcript concentration is elevated in diazinon-resistant flies				
AUTHORS	Insect Biochem. Mol. Biol. 30 (11), 1107-1115 (2000)				
TITLE					
JOURNAL	20445807				
MEDLINE	10989298				
PUBMED	2 (bases 1 to 2175)				
REFERENCE	Guerrero, F.D. Direct Submission				
AUTHORS	Submitted (30-MAR-1999) USDA-ARS, Knippling-Bushland U.S. Livestock Insects Research Laboratory, 2700 Fredericksburg Rd., Kerrville, TX 78028, USA				
JOURNAL					
FEATURES	Location/Qualifiers				
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gene					
CDS					
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ORIGIN					
Query Match	56.0%; Score 959.4; DB 3; Length 2175;				
Best Local Similarity	72.5%; Pred. No. 6.3e-205;				
Matches 1242; Conservative	0; Mismatches 471; Indels 0; Gaps 0;				
1	ATGAATTCACAGTGAAGTGGAGAAATTTAAATGGAAGATTAATGATTCATGAAAT 60				
282	ATGATTTTCAATGTCAGCTCTTGAGAAATTAAGATGGAATAATTAAGTGTGTAATA 341				
61	AAGTTTAACTATGTTAACTACCAATGAACGGTGTGAGTGTGAAACTGCAATATGGC 120				
342	AAATTTTAACTACCGCTTATACCAATGAACGCAATATGTCGATACGGAATATGGA 401				
121	AAAGTGAAGGCGTTAAACGTTAACTGTGTCGATGATTCCTACTACAGTTTGAAGGT 180				
402	AAATTAAGGTTTAAAGGTTTGAACGTTGACGTACGATGACTCATCTACAGCTTGAAGGT 461				


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Db 522 CCTTGGATGAGTAAAGATTTGTCATGTCGCCCTCCGTTGGTTCAACAGATTTG 581
QY 301 ATACGGGCAAGTGTGTGTCAGAGATTTGTCATACCTAAGTGTCTATACGAAT 360
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Db 582 ATATCCGGCACTCAAGTGTGAGGATTTGTTATTTGAATGCTATACGAATAT 641
QY 361 CTAAATCCCGAACTAAACCTCCGTTTATATACATACATGAGTGTGTTTATATC 420
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Db 642 TTAATACTGATCAAAAGCTCCGTTTGTGTTCTTCATGAGTGTGTTTCAATTTG 701
QY 421 GGTGAATACTGATGATATGTCCTGATTTATTTCAATAAAGATGCTGTG 480
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Db 702 GGGGAAGCTAATAGAAATTAATGCGGCTGATTAATTTCAATAAAGAGACGTTGCTTC 761
QY 481 ATTAACATACATATGCTTTGGAGCTAGCTTTCTAAGTTTAATTCAGAAAGCTT 540
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Db 762 ATACCTGCAATATGCTTTAGGGGTGTTAGTTTCTAAGTTTAATTCGGAATTC 821
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QY 721 ATACTAATGCTGCTATGCTATTTGCTCATTTGGCTAATACCAATGTCACATCTGCT 780
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Db 1002 GTTTGATGCTGGAACCTGATGCTATGCTATGAGGCCCATACCAATGTCACATCTGCT 1061
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QY 1141 GCTGATGCTGAACGACGCGCCAGAGACTTGAATGGGTGCTAATAATTAAGAGCT 1200
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Db 1422 GATGTTGAAGATCGAGTTCTCCAGAACTCTTGAATTTGATGATCTTAAGAAATTTG 1481
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QY 1261 TTCTGTTTCCCATGCTGCTTTGTCATATGCTTTTACATGACACTCCGTTACACC 1320
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QY 1321 GTCCTACTTGTATGCTGCTGCACTTCGATTTGCGAGATCTTATCAATCCCTATTTATG 1380
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Db 1602 ATCTACCTATATGCTTTTGAATTTGATTCGAAAGATTTTATATCCCTATGCAATTTATG 1661
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Db 1962 AGTGTTCATTAATGAACAGCGGGAATGTTTATG 1994

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RESULT 11
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LOCUS AR153445 1710 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 14 from patent US 6235515.
ACCESSION AR153445
VERSION AR153445.1 GI:15120977
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1710)
Russell, R. Joyces., Newcomb, R. David., Campbell, P. Malcolm.,
Roblin, G. Charles., Quetleville., Claudianos, C., Smyth, K. -A.,
Boyce, T. Mark., Oakeshort, J. Graham. and Brownlie, J. Colin.
Malathion carboxylesterase
Patent: US 6235515-A 14 22-MAY-2001;
Location/Qualifiers
1..1710
source
BASE COUNT 498 a 369 c 394 g 449 t
ORIGIN

Query Match 55.8%; Score 955; DB 6; Length 1710;
Best Local Similarity 73.3%; Pred. No. 6.2e-204;
Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

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RESULT 12
 AY051473
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 DEFINITION
 Drosophila melanogaster GH13950 full length cDNA.
 AY051473
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 2017)
 Stapleton, M., Broksstein, P., Hong, L., Abdayani, A., Carlson, J.,
 Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,
 Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J.,
 Nunoo, J., Pacleby, J., Paragas, V., Park, S., Phoumanavong, S., Wan, K.,
 Yu, C., Lewis, S. E., Rubin, G. M. and Celisner, S.
 Direct Submission
 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA
 Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Berkeley, CA 94720
 This clone was sequenced as part of a high-throughput process to
 sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
 Science 2000). The sequence has been subjected to integrity checks
 for sequence accuracy, presence of a poly A tail and contiguity
 within 100 kb in the genome. Thus we believe the sequence to
 reflect accurately this particular cDNA clone. However, there are
 artifacts associated with the generation of cDNA clones that may
 have not been detected in our initial analyses such as internal
 priming, priming from contaminating genomic DNA, retained introns
 due to reverse transcription of unsliced precursor RNAs, and
 reverse transcriptase errors that result in single base changes.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our web site
 (<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.

FEATURES
 source
 1..2017
 location=Qualifiers
 /organism="Drosophila melanogaster"
 /strain="y; cn bw sp"
 /db_xref="taxon:7227"
 /map="84D5-84D5"

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1. 2017
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MKDLF"

BASE COUNT 522 a 487 c 519 g 489 t
ORIGIN

Query Match 39.7%; Score 680.4; DB 3; Length 2017;
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Matches 1075; Conservative 0; Mismatches 636; Indels 3; Gaps 1;

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Db 511 GGTGAATCAATCGTATGATGATGATGATGATGATGATGATGATGATGATG 570
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RESULT 13
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DEFINITION Drosophila melanogaster 2660 bp mRNA linear INV 18-JUN-2002
ACCESSION AY121675
VERSION AY121675.1 GI:21464397
KEYWORDS
SOURCE FLI CDNA.
ORGANISM fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2660)
Stapleton, M., Brokstein, P., Hong, L., Abmayyan, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guadri, H., Krommiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C. J., Nuno, J., Pacle, J., Paragas, V., Park, S.,
Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M.,
and Celisner, S.
REFERENCE
AUTHORS
TITLE Direct Submission
JOURNALS Submitted (13-JUN-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
COMMENT
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila gene collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unsplined precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu

FEATURES
SOURCE
1. 2660
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/strain="y; cn bw sp"
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ORIGIN

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QY 145 ACTGTGTACGATGATTCTACAGCTTGTGAGGATCCGTACGCCACCGCCAGCG 204
DB 606 TCCATCTTCACGACAACTACTACAGCTTGTGAGGATCCGTTCGCCAAGCGCGG 665
QY 205 GGTGACCTGAGATTAAAGCACCCGACGCCAACACACCTGGGATGTGTGGCGATTTGT 264
DB 666 GCGACGCTCCGCTTCAAGCGCGCCGCGGAGCCAGACACTGGTGCAGATCTCAAGCGCTGC 725
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QY 745 TGTCCATGCTAATACCAATGTCACATGCTTACCTTACCAATATGCGC 801
DB 1206 GCACCTGCGGCGCAGACCCCAACCAACCAATATGCGCCTTATGCGCAGACGCACT 1265
QY 802 GCGTATTAAGGTTGAGATATGATTAAGATGTTTGAATTTCTTATGAAGCCAGCA 861
DB 1266 GCGTATTAAGGTTGAGATATGATTAAGATGTTTGAATTTCTTATGAAGCCAGCA 1325
QY 862 CAGGATTTAATAAAGTTGAGATTAAGATGTTTGAATTTCTTATGAAGCCAGCA 920
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D	b	1610	ATCCCACTGCATCACTGTTTGGAGAGATGCTGGAGGCCCTCCACTACATCATGA	1669
Q	y	683	TGTTAAACCGAACAACCTCGCGGTCTTTCCATGCTGTATCTAATGTCCGGTATGCTA	742
D	b	1670	TGCTAACCGGTACAGACCCAAAGGGCTCTTTCATGCGGGCACTGTGAGTGGGGAGTGC	1729
Q	y	743	TTTTTCATTGGC---TAATACCCAATGTCAACATGCTGCGCTCCACTTACCAATTTG	799
D	b	1730	TTTTCTCTTGCGCTTACACGGCGACATTTACCCATATTCCTACAGGATATGCCAACTGG	1789
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D	b	1790	TTGCTACAAAGGGGAGAGAACAGACAGATGATGTGCTGAGTCTTGCAAGACTTAAG	1849
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D	b	1910	TAAATGTTCCCTTTGGGCCATCCCTGGAACATCTCCACGCGCGAATGTGATATCCA	1969
Q	y	980	AACATCTCGGGAAATGTTTAAACTCTTTGGGGTAATTCGATACCCACTATGATGGTA	1039
D	b	1970	AGCTCCAAAGAGATGATGAAGACCGCTGGAGTAATCCATCCCATGTTTATAGSAA	2029
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Q	y	1243	-----CTTTGCTCTCACATCTATTTTCGTTCCCATGCAATCGTT	1282
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D	b	2390	TGGTCACTTCCCGACAGCGCTAGCGGGTGGAGCTCCATATATTTCTATGATGATGACT	2449
Q	y	1343	TCGATTTGGGAAGATCTTATATATCCCTATGCGATTTATGCGTGTGGAGCTGATGAAG	1402
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Db	2810	ATTATTTT 2818	
RESULT 15			
AC015272/c			
LOCUS			
DEFINITION			
AC015272			
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pieces.			
AC015272			
AC015272.1 GI:6436063			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Drosophila melanogaster.			
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
Ephydroidea; Drosophilidae; Drosophila.			
1 (bases 1 to 57335)			
AUTHORS			
Adams,M. and Venter,J.C.			
TITLE			
Direct Submission			
JOURNAL			
Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,			
Rockville, MD, USA			
COMMENT			
This sequence was identified as CDM:10213452 by the submitter.			
For further information on this sequence e-mail to fly@celera.com.			
* NOTE: This is a 'working draft' sequence.			
* This sequence will be replaced			
* by the finished sequence as soon as it is available and			
* the accession number will be preserved.			
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/organism="Drosophila melanogaster"			
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BASE COUNT			
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ORIGIN			
Query Match			
Best Local Similarity			
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54.6%; Pred. No. 2.8e-73;			
Mismatches 613; Indels 263; Gaps 5;			
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Db	36421	GACACGAGATAGCGCAATGAGGGGTATCAACGCGTATCTCTACATGATGCGCTAC	36362
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Db	36301	CCTCAGAGGCCATTCCTCCGAGGAGGAGTTCGCACTGACGACGACGCAAGATAAGGCC	36242
QY	286	GTCGAGTTGATTTTATAACGGGCAAGTGTGTGCTCAGCAGATTTGCTATTAAGT	345
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[illegible]

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QY	1403	GTTGTATGTCATGCTGATGATTAATTAACCTATTCTTGTGATATCAATTTGGCCAAACGTATGC	1462
Db	34861	GGGTGACGCATCCGACCATTTTGACTTACCAATTTAGCAGCCTCGTGGCTCGCCGGTTGC	34802
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QY	1523	CCACGACGTGTAACTCTTATACCAATGAAATTTGAAGTATGGAATAATGTTTCTCGGGATTC	1582
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QY	1583	CATTAAAGAAATCCGATTAAGTATCAAGGTGTTGAATATTAGTATGATTAATTTGAAATAGA	1642
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Search completed: April 11, 2003, 06:03:00
Job time : 3045.03 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:58:21 ; Search time 246.905 Seconds
(without alignments)
15624.094 Million cell updates/sec

Title: US-09-776-910-3

Perfect score: 1713
Sequence: 1 atgaattcaacgtagttt.....aacatagagattatttttag 1713

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1701.8	99.3	1713	AAQ91561	OP-sensitive ester
2	1701.8	99.3	1713	AAAT68596	Lc-alpha-E7 malath
3	1681	98.1	1713	AAQ91566	OP-resistant ester
4	1677.8	97.9	1713	AAQ91564	OP-resistant ester
5	1677.8	97.9	1713	AAQ91565	OP-resistant ester
6	1676.2	97.9	1713	AAQ91563	OP-resistant ester
7	1674.6	97.8	1713	AAQ91562	OP-resistant ester
8	955	55.8	1710	AAAT68597	Md-alpha-E7 gene.
9	680.4	39.7	2001	ABLO2067	Drosophila melanog

10	381.8	22.3	1704	23	ABLO2081	Drosophila melanog
11	372.2	21.7	6175	23	ABLO2066	Drosophila melanog
12	368.2	21.5	1665	23	ABLO2099	Drosophila melanog
13	365.4	21.3	1792	23	ABLO4689	Drosophila melanog
14	323.6	18.9	1593	23	ABLO2103	Drosophila melanog
15	323	18.9	1863	23	ABLO1859	Drosophila melanog
16	311.4	18.2	1791	23	ABLO1033	Drosophila melanog
17	305.8	17.9	1719	23	ABLO2101	Drosophila melanog
18	304.6	17.8	1878	23	ABLO1947	Drosophila melanog
19	300.4	17.5	3856	23	ABLO1032	Drosophila melanog
20	300.4	17.5	67279	23	ABLO7668	Drosophila melanog
21	270	15.8	1809	24	ABA90480	Drosophila cell cy
22	238.2	13.9	4320	23	ABLO4688	Drosophila melanog
23	229.6	13.4	1727	23	ABLO1943	Drosophila melanog
24	228.6	13.3	4242	23	ABLO2102	Drosophila melanog
25	224	13.1	5008	23	ABLO2080	Drosophila melanog
26	198.8	11.6	4294	23	ABLO2098	Drosophila melanog
27	198.8	11.6	4294	23	ABLO2100	Drosophila melanog
28	196	11.4	1987	19	AAVA0762	C. fellis esterase,
29	196	11.4	1987	19	AAVA0763	C. fellis esterase,
30	194.4	11.3	1626	23	ABLO1945	Drosophila melanog
31	193.2	11.3	2613	23	ABLO1906	Drosophila melanog
32	191.8	11.2	5132	23	ABLO1858	Drosophila melanog
33	185.8	10.8	1590	19	AAVA0764	C. fellis esterase,
34	185.8	10.8	1590	19	AAVA0765	C. fellis esterase,
35	178	10.4	1540	19	AAVA0756	C. fellis esterase,
36	178	10.4	1584	19	AAVA0757	C. fellis esterase,
37	178	10.4	2007	19	AAVA0754	C. fellis esterase,
38	178	10.4	2007	19	AAVA0755	C. fellis esterase,
39	178	10.4	2007	22	AAD21174	Ctenocephalides fe
40	167.6	9.8	4288	23	ABLO1942	Drosophila melanog
41	164.2	9.6	1783	23	ABLO2029	Drosophila melanog
42	148	8.6	4283	23	ABLO1946	Drosophila melanog
43	143.8	8.4	1488	19	AAVA0767	C. fellis esterase
44	143.8	8.4	1590	19	AAVA0743	C. fellis esterase
45	143.8	8.4	1590	22	AAD21169	Ctenocephalides fe

ALIGNMENTS

RESULT 1	
ID	AAQ91561 standard; CDNA: 1713 BP.
AC	AAQ91561;
AC	22-DEC-1995 (first entry)
DT	OP-sensitive esterase E3 Lc743 clone.
DE	
XX	
KW	Esterase; E3; bioremediation; organophosphate; carbamate;
KW	Insecticide; pesticide; water decontamination; meat decontamination;
KW	ss.
XX	
OS	Lucilia cuprina.
XX	
FT	Key
FT	CDS
XX	Location/Qualifiers
XX	1..1713
XX	/*tag= a
XX	
PN	W09519440-A1.
XX	
PD	20-JUL-1995.
XX	
PF	13-JAN-1995; 95W0-AU00016.
XX	
PR	13-JAN-1994; 94AU-0003347.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
XX	
PI	Boyce TM, Campbell PM, Newcomb RD, Oakeshott JC;
PI	Parker AG, Robin GC, Russell RJ, Smyth K;

XX LC-alpha-E7 malathion susceptible esterase clone Lc743.
XX Malathion carboxylesterase; organophosphate; insecticide;
KW pesticide; remediation; bioremediation; decontamination; esterase;
KW ss.
XX Lucilia cuprina.
XX
FH Key Location/Qualifiers
FT primer_bind complement (1..26)
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FT /note- "Lc743 5' primer"
FT primer_bind 1686..1713
FT /*tag- b
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FT mutation 752
FT /*tag- c
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(Trp to Leu mutation)"
FT mutation 1344
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FT mutation 1362
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FT mutation 1629
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XX 29-MAY-1997.
XX 22-NOV-1996; 96WO-AU00746.
XX 23-NOV-1995; 95AU-0006751.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX Boyce T, Brownlie JC, Campbell PM, Claudianos C;
PI Newcomb RD, Oakshott JG, Robin GC, Russell RJ, Smyth K;
XX WPI: 1997-298113/27.
DR P-PSDB; AAM17765.
XX
XX DNA encoding enzyme that degrades organophosphate pesticides-
PT useful for decontamination of soil, water, food etc
XX
PS Claim 4; Fig 1; 52pp; English.
XX
XX DNA molecule Lc743 (AAT68596) codes for an esterase (AAM17765) from
CC a malathion susceptible strain of Lucilia cuprina. Comparison
CC with a consensus sequence from derived from clones of the
CC Lc-alpha-E7 resistant allele (see also AAM17768) indicated only one
CC replacement site difference, a Trp to Leu substitution at amino
CC acid position 251 (nucleotide position 752). This mutation is an
CC excellent candidate for the malathion resistance mutation. The
CC resistant enzyme acts as a malathion carboxylesterase and can be
CC formulated for use in degrading environmental carboxylester or
CC dimethyl general organophosphates.
XX
SQ Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;

Query Match 99.3%; Score 1701.8; DB 18; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 ATGATTTTCACGCTTACTTTGATGAGAAATTTAAATGAGATTAATGCAATTAAT 60
DB 1 ATGATTTTCACGCTTACTTTGATGAGAAATTTAAATGAGATTAATGCAATTAAT 60
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DB 1021 ATACCACTATGATGATGATACATCTCATATGAGGCTATTTTCACTCAATCTTAAG 1080


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QY 721 ATACTAATGTCGGTAAATGCTATTGTCATTTGGCTAATACCAATGTCACATGTCGCC 780
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    |||||||
Db 841 TTCTTTTGAAGCCAGGCCAGAGATTATTAATACTTGAGGAAAAAGTTTAACTCTA 900
QY 901 GAAGAGGCTACAAATTAAGGTATGTTCTTTGTCCTCCACTGTGAGCCATATCAGACC 960
    |||||||
Db 901 GAAGAGGCTACAAATTAAGGTATGTTCTTTGTCCTCCACTGTGAGCCATATCAGACC 960
QY 961 GCTGATGTCGCTTACCACCAATCCTCGGGAATGTTAAACTGCTTGGGGTAATTGCG 1020
    |||||||
Db 961 GCTGATGTCGCTTACCACCAATCCTCGGGAATGTTAAACTGCTTGGGGTAATTGCG 1020
QY 1021 ATACCCACTATGATGGGTAACACTTCATATAGGGTCTATTTTTCACCTCAATCTTAA 1080
    |||||||
Db 1021 ATACCCACTATGATGGGTAACACTTCATATAGGGTCTATTTTTCACCTCAATCTTAA 1080
QY 1081 CAATAGCCTATGCTTGTTAAGGAATGGAACCTTGTCATTTTGTGCGCAAGTGAATG 1140
    |||||||
Db 1081 CAATAGCCTATGCTTGTTAAGGAATGGAACCTTGTCATTTTGTGCGCAAGTGAATG 1140
QY 1141 GCTGATGTCGTAACGACCGCCCGCAGAGACCTTGGAATAGGGTCTAAATTAAGAGCT 1200
    |||||||
Db 1141 GCTGATGTCGTAACGACCGCCCGCAGAGACCTTGGAATAGGGTCTAAATTAAGAGCT 1200
QY 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTTTGTCTCACATCTAT 1260
    |||||||
Db 1201 CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTTTGTCTCACATCTAT 1260
QY 1261 TTCTGGTTCCTCCATGATGCTTTGTCATTTAGCTTTCATTCACCTCGGTAACACC 1320
    |||||||
Db 1261 TTCTGGTTCCTCCATGATGCTTTGTCATTTAGCTTTCATTCACCTCGGTAACACC 1320
QY 1321 GTCGTAATGTAATGCTTGCATTCGATTCGAGAGATCTTATCAATCCCTATCGATTA 1380
    |||||||
Db 1321 GTCGTAATGTAATGCTTGCATTCGATTCGAGAGATCTTATCAATCCCTATCGATTA 1380
QY 1381 CGTAGTGGACCTGGTGTAAAGGGTGTAGTATGCTGATGAATTAACCTATTTCTTGG 1440
    |||||||
Db 1381 CGTAGTGGACCTGGTGTAAAGGGTGTAGTATGCTGATGAATTAACCTATTTCTTGG 1440
QY 1441 AATCAATTTGGCCAAACGATGCTTAAGAAATCGCGTGAATCAAAACAAATGAACGTAT 1500
    |||||||
Db 1441 AATCAATTTGGCCAAACGATGCTTAAGAAATCGCGTGAATCAAAACAAATGAACGTAT 1500
QY 1501 ACTGGTATATGATTAACAATTTGCCACCACTGTAATCCTTATAGCAATGAATTTGAAG 1560
    |||||||
Db 1501 ACTGGTATATGATTAACAATTTGCCACCACTGTAATCCTTATAGCAATGAATTTGAAG 1560
QY 1561 ATGGAATAATGTTTCTCGGATCCCAATTAAGAAATCCGATGAAGTATCAAGTGTGAT 1620
    |||||||
Db 1561 ATGGAATAATGTTTCTCGGATCCCAATTAAGAAATCCGATGAAGTATCAAGTGTGAT 1620
QY 1621 ATTAGTGAATGAATTAAGAAATGATGATGCTGAAATGATTAAGATTAAGATGAGAG 1680
    |||||||
Db 1621 ATTAGTGAATGAATTAAGAAATGATGATGCTGAAATGATTAAGATTAAGATGAGAG 1680
QY 1681 TCGATGTTTGAATAACATAGAGATTATTTAG 1713
    |||||||
Db 1681 TCGATGTTTGAATAACATAGAGATTATTTAG 1713

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RESULT 4
AA091564
ID AA091564 standard; cDNA; 1713 BP.

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XX XX
AC AA091564;
XX XX
DT 22-DEC-1995 (first entry)
XX XX
DE OP-resistant esterase Lc7LI03C allele.
XX XX
KW Esterase; E3; bioremediation; organophosphate; carbamate;
KW insecticide; pesticide; water decontamination; meat decontamination;
KW ss.
XX XX
OS Lucilia cuprina.
XX XX
FH Key 1.1713
FT CDS /tag- a
FT
XX PN W09519440-A1.
XX PD 20-JUL-1995.
XX XX
PF 13-JAN-1995; 95WO-AU00016.
XX PR 13-JAN-1994; 94AU-0003347.
XX XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX DR WPI, 1995-263870/34.
XX XX
PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
PT eliminate residues of organo:phosphate and carbamate pesticides from
PT water, meat etc.
XX XX
PS Example 4; Page 12-17; 38pp; English.
XX XX
CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC Op-susceptible esterase E3 of L. cuprina) from a diazinon
CC resistant strain, Ilandilol 103. 4 Isolated clones were
CC sequenced (Lc7LI03 A-D, AA091562-65) that encoded diazinon-resistant
CC esterases. The esterases, or cells expressing them, are used
CC in bioremediation.
XX XX
SO Sequence 1713 BP; 512 A; 308 C; 368 G; 525 T; 0 other;
Query Match 97.9%; Score 1677.8; DB 16; Length 1713;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1691; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATAAGAGATTAAATGCAATTGAAT 60
    |||||||
Db 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATAAGAGATTAAATGCAATTGAAT 60
QY 61 AAGTTTAACTATCGTTTAACTACCAATGAAGGAGGTTGAGCAATGAATATGCG 120
    |||||||
Db 61 AAGTTTAACTATCGTTTAACTACCAATGAAGGAGGTTGAGCAATGAATATGCG 120
QY 121 AAAGTGAAGCGGTTAAAGCTTTAACTGTAGATGATATTCCTACTACAGTTTGAAGGT 180
    |||||||
Db 121 AAAGTGAAGCGGTTAAAGCTTTAACTGTAGATGATATTCCTACTACAGTTTGAAGGT 180
QY 181 AAAGTGAAGCGGTTAAAGCTTTAACTGTAGATGATATTCCTACTACAGTTTGAAGGT 240
    |||||||
Db 181 AAAGTGAAGCGGTTAAAGCTTTAACTGTAGATGATATTCCTACTACAGTTTGAAGGT 240
QY 241 CCCTGGATGATGATGCGGATTTGCAATCATTAAGATTAAGTCAAGTGAATTTT 300
    |||||||
Db 241 CCCTGGATGATGATGCGGATTTGCAATCATTAAGATTAAGTCAAGTGAATTTT 300
QY 301 ATAAAGGCAAAAGTGTGCTCAAGAGATGCTATATCTTAAGTGTCTATACGAATAT 360
    |||||||

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Db 301 ATTACAGCAAGTGTGGCTCAGAGATTGCTATACCTAAGGCTATACGAATAAT 360
Qy 361 CTAAATCCGGAATAAAGTCCGTTTGTATATACATACATAGTGTGTTTATPAC 420
Db 361 CTAAATCCGGAATAAAGTCCGTTTGTATATACATACATAGTGTGTTTATPAC 420
Qy 421 GGTGAATAATCATCGTATATGATGTCTGATATATTTTCATTAATAAAGATGTGTTG 480
Db 421 GGTGAATAATCATCGTATATGATGTCTGATATATTTTCATTAATAAAGATGTGTTG 480
Qy 481 ATTAACATACATATGTTGGAGCTCTAGTGTTCATTAATTTTAAATTCAGAGACTT 540
Db 481 ATTAACATACATATGTTGGAGCTCTAGTGTTCATTAATTTTAAATTCAGAGACTT 540
Qy 541 AATGTCGCGGTAATGCGGCTTAAGATCAAGTCATGCGCTTGCCTGGATTAAAAAT 600
Db 541 AATGTCGCGGTAATGCGGCTTAAGATCAAGTCATGCGCTTGCCTGGATTAAAAAT 600
Qy 601 AATGTCGCGCACTTGGTGGCAATCCGATATATATACAGTCTTGGTGAAGTCCGCT 660
Db 601 AATGTCGCGCACTTGGTGGCAATCCGATATATATACAGTCTTGGTGAAGTCCGCT 660
Qy 661 GCTGCTCTACCACTACATGATGTTAACGCAAACTCGCGTCTTTCCATCGTGT 720
Db 661 GCTGCTCTACCACTACATGATGTTAACGCAAACTCGCGTCTTTCCATCGTGT 720
Qy 721 ATACTAATGCGGTATGCTATGTTGCTATGCTATACCAATGCTCAACATCGTGC 780
Db 721 ATACTAATGCGGTATGCTATGTTGCTATGCTATACCAATGCTCAACATCGTGC 780
Qy 781 TTCACCTTAAGCAAAATGCGCGCTATAGGATGATGATGATGATGATGATGATGAT 840
Db 781 TTCACCTTAAGCAAAATGCGCGCTATAGGATGATGATGATGATGATGATGATGAT 840
Qy 841 TTTCTTTGAAGCAAGCCACAGAGATTATTAACCTGAGAAAAAGTTTAACTCTA 900
Db 841 TTTCTTTGAAGCAAGCCACAGAGATTATTAACCTGAGAAAAAGTTTAACTCTA 900
Qy 901 GAAGAGCGTCAAAATAGTGCATGTTCTTTGTCCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 GAAGAGCGTCAAAATAGTGCATGTTCTTTGTCCTGCTGCTGCTGCTGCTGCTGCT 960
Qy 961 GCTGATGTTGCTTTACCAAAATCCTCGGGAATGTTTAAACTGCTGGGCTAATTG 1020
Db 961 GCTGATGTTGCTTTACCAAAATCCTCGGGAATGTTTAAACTGCTGGGCTAATTG 1020
Qy 1021 ATACCACTATGATGGGTAACTTCAATGAGGCTCATTTTTCATCTCAATCTTAA 1080
Db 1021 ATACCACTATGATGGGTAACTTCAATGAGGCTCATTTTTCATCTCAATCTTAA 1080
Qy 1081 CAAATGCTATGCTTGTAAAGAAATGGAACCTGTGCAATTTTGTGCAAGTGAATTG 1140
Db 1081 CAAATGCTATGCTTGTAAAGAAATGGAACCTGTGCAATTTTGTGCAAGTGAATTG 1140
Qy 1141 GCTGATGCTGAAGCAAGCCGCTGAGACCTTGAAGATGGTCTTAAATTAAGAGCT 1200
Db 1141 GCTGATGCTGAAGCAAGCCGCTGAGACCTTGAAGATGGTCTTAAATTAAGAGCT 1200
Qy 1201 CATGTTACAGAGAAACACCAACCGCGATTAATTTATGATCTTGTCTCACATCTAT 1260
Db 1201 CATGTTACAGAGAAACACCAACCGCGATTAATTTATGATCTTGTCTCACATCTAT 1260
Qy 1261 TTTCTGTTCCCATGATGATGCTTGTGCAATACGTTTCAACACACCTCCGCTACACC 1320
Db 1261 TTTCTGTTCCCATGATGATGCTTGTGCAATACGTTTCAACACACCTCCGCTACACC 1320
Qy 1321 GCTCTACTGATATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1380
Db 1321 GCTCTACTGATATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1380
Qy 1381 GCTAGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 GCTAGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440

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Qy 1441 AATCAATTTGGCCAAACGATATGCTTAAGAAATGCGCTGAATACAAAACAATTTGAACGTATG 1500
Db 1441 AATCAATTTGGCCAAACGATATGCTTAAGAAATGCGCTGAATACAAAACAATTTGAACGTATG 1500
Qy 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Db 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Qy 1561 ATGGAATAATGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1561 ATGGAATAATGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Qy 1621 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Qy 1681 TCGATGTTTGAAGAAACATAGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Db 1681 TCGATGTTTGAAGAAACATAGATGATGATGATGATGATGATGATGATGATGATGAT 1740

RESULT 5
AA091565
ID AA091565 standard; cDNA; 1713 BP.
XX
AC AA091565;
XX
DT 22-DEC-1995 (first entry)
XX
DE Op-resistant esterase Lc7L103D allele.
XX
KW Esterase; E3; bioremediation; organophosphate; carbamate;
KW insecticide; pesticide; water decontamination; meat decontamination;
KW ss.
XX
OS Lucilia cuprina.
XX
FH Key 1.1713
FT CDS /*tag= a
FT
PN W09519440-A1.
XX
PD 20-JUL-1995.
XX
PF 13-JAN-1995; 95MO-AU00016.
XX
PR 13-JAN-1994; 94AU-0003347.
XX
(CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PA Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX
PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX
DR WPI: 1995-263870/34.
XX
PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
PT eliminate residues of organo:phosphate and carbamate pesticides from
PT water, meat etc.
XX
PS Example 4; Page 12-17; 38pp; English.
XX
CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC Op-susceptible esterase E3 of L. cuprina) from a diazinon
CC resistant strain, Llandillo 103. 4 isolated clones were
CC sequenced (Lc7L103 A-D. AA091562-65) that encoded diazinon-resistant
CC esterases. The esterases, or cells expressing them, are used
CC in bioremediation.
XX
SQ Sequence 1713 BP; 513 A; 307 C; 369 G; 524 T; 0 other;
Query Match 97.9%; Score 1677.8; DB 16; Length 1713;

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Best Local Similarity 98.7%; Pred. No. 0;
Matches 1691; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY 1 ATGAATTCACAGTTAGTTGATGAGAAATTAATGAGATTAAATCATTGAAAT 60
Db 1 ATGAATTCACAGTTAGTTGATGAGAAATTAATGAGATTAAATCATTGAAAT 60
QY 61 AAGTTTAACTAGTGTAACTACCAATGAACGGGTGAGTGAATGATATAGGC 120
Db 61 AAGTTTAACTAGTGTAACTACCAATGAACGGGTGAGTGAATGATATAGGC 120
QY 121 AAGTGAAGGCGTTAAAGCTTAACTGTAGATGATTCCTACTACATTTTGAGGGT 180
Db 121 AAGTGAAGGCGTTAAAGCTTAACTGTAGATGATTCCTACTACATTTTGAGGGT 180
QY 181 ATAACCGTACCCCAACCGCCAGTGGGTGAGCTGAGATTAAAGCCACGACCAACA 240
Db 181 ATAACCGTACCCCAACCGCCAGTGGGTGAGCTGAGATTAAAGCCACGACCAACA 240
QY 241 CCTGGGATGTGGCGCGATTTGTGCAATCATAAAGTAAAGTCAAGTGGATTTT 300
Db 241 CCTGGGATGTGGCGCGATTTGTGCAATCATAAAGTAAAGTCAAGTGGATTTT 300
QY 301 ATAAAGGCGAAAGTGTGGCTCAGAGATTGCTATACCTAAGTCTATACGAATAAT 360
Db 301 ATAAAGGCGAAAGTGTGGCTCAGAGATTGCTATACCTAAGTCTATACGAATAAT 360
QY 361 CTAAATCCCAAACTAAAGCTCCGTTTGTATACATACATGATGATTTATATTC 420
Db 361 CTAAATCCCAAACTAAAGCTCCGTTTGTATACATACATGATGATTTATATTC 420
QY 421 GGTGAATAATCATGCTGATGATGATGCTGATTTCTAATTAAGGATGGTGTG 480
Db 421 GGTGAATAATCATGCTGATGATGATGCTGATTTCTAATTAAGGATGGTGTG 480
QY 481 ATTAACATACAAATATCTTTGGGAGCTCTAGGTTTCTAAGTTTAAATGAGAAGCTT 540
Db 481 ATTAACATACAAATATCTTTGGGAGCTCTAGGTTTCTAAGTTTAAATGAGAAGCTT 540
QY 541 AATGTGCGCGGTAATGCGCGCTTAAAGATCAAGTCAATGCGCTTGGATTAAAT 600
Db 541 AATGTGCGCGGTAATGCGCGCTTAAAGATCAAGTCAATGCGCTTGGATTAAAT 600
QY 601 AATTGCGCAACTTGGTGGCAATCCGATTAATTTACAGCTTGGTGAAGGCGCGT 660
Db 601 AATTGCGCAACTTGGTGGCAATCCGATTAATTTACAGCTTGGTGAAGGCGCGT 660
QY 661 GCTGCTCTACCCACTACATGATGTTAAACGCAACAACTGCGGCTTTTCCATCGTGT 720
Db 661 GCTGCTCTACCCACTACATGATGTTAAACGCAACAACTGCGGCTTTTCCATCGTGT 720
QY 721 ATACTAATGTCGGGTATGCTATTTGTCATTTGCTAATACCATATCAATCGTGC 780
Db 721 ATACTAATGTCGGGTATGCTATTTGTCATTTGCTAATACCATATCAATCGTGC 780
QY 781 TTACCTTAGCCAAATATGGCGGCTATTAAGGATGAATGAATGATTTTGGAA 840
Db 781 TTACCTTAGCCAAATATGGCGGCTATTAAGGATGAATGAATGATTTTGGAA 840
QY 841 TTTCTTGAAGCCAAAGCCACAGATTTAATAAACTTGAGAAAAAGTTTAACTCTA 900
Db 841 TTTCTTGAAGCCAAAGCCACAGATTTAATAAACTTGAGAAAAAGTTTAACTCTA 900
QY 901 GAAGAGGCTACAAATAGGATCATGTTTCTTTTGTCCCACTGTGAGCCATACAGAC 960
Db 901 GAAGAGGCTACAAATAGGATCATGTTTCTTTTGTCCCACTGTGAGCCATACAGAC 960
QY 961 GCTGATTTGTCTTACCCAAACATCTCGGGAATGGTTAAATGCTGGGGAATTCG 1020
Db 961 GCTGATTTGTCTTACCCAAACATCTCGGGAATGGTTAAATGCTGGGGAATTCG 1020
QY 1021 ATACCACTATGATGGTAAACACTTCAATATGAGGCTATTTTTCACCTCAATTCCTAAG 1080
Db 1021 ATACCACTATGATGGTAAACACTTCAATATGAGGCTATTTTTCACCTCAATTCCTAAG 1080

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Db 1021 ATACCACTATGATGGTAAACACTTCAATATGAGGCTATTTTTCACCTCAATTCCTAAG 1080
QY 1081 CAAATGCCCTATGCTGTGTAAGGAATTTGAAACTTGTGTCAATTTTGTGCCAAGGAATG 1140
Db 1081 CAAATGCCCTATGCTGTGTAAGGAATTTGAAACTTGTGTCAATTTTGTGCCAAGGAATG 1140
QY 1141 GCTGATCTGAGCAGCCGCCGCCAGAGACCTTGGAAATGGGTGCTAAATTAAGAAAGGCT 1200
Db 1141 GCTGATCTGAGCAGCCGCCGCCAGAGACCTTGGAAATGGGTGCTAAATTAAGAAAGGCT 1200
QY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTTGCTCTACATCAT 1260
Db 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTTGCTCTACATCAT 1260
QY 1261 TTCTGTGCCCATGATCGTTTGTGCAATTTACGTTTCAATTCACACCTCCGGTACACC 1320
Db 1261 TTCTGTGCCCATGATCGTTTGTGCAATTTACGTTTCAATTCACACCTCCGGTACACC 1320
QY 1321 GTCTACTTGTATGCTTGCAGCTTCGATTCGAGATCTTATCAATCCCTATCGTATATG 1380
Db 1321 GTCTACTTGTATGCTTGCAGCTTCGATTCGAGATCTTATCAATCCCTATCGTATATG 1380
QY 1381 CGTAGTGAGCTGCTGTTAAGGCTGTAGTATGATGATGATTAACCTATTTCTCTG 1440
Db 1381 CGTAGTGAGCTGCTGTTAAGGCTGTAGTATGATGATGATTAACCTATTTCTCTG 1440
QY 1441 AATCAATTTGCCAAAGCTATGCTTAAAGATCGCTGATATCAAAACATTTGAACGTATG 1500
Db 1441 AATCAATTTGCCAAAGCTATGCTTAAAGATCGCTGATATCAAAACATTTGAACGTATG 1500
QY 1501 ACTGTATATGATGATATGATTTGCCACCACTGATGATCTTATACCAATGAATGAAGGT 1560
Db 1501 ACTGTATATGATGATATGATTTGCCACCACTGATGATCTTATACCAATGAATGAAGGT 1560
QY 1561 ATGGAATAATGTTTCTGGATCAATTAAGAATCCGATGAAGATTAACAAGTGTGAT 1620
Db 1561 ATGGAATAATGTTTCTGGATCAATTAAGAATCCGATGAAGATTAACAAGTGTGAT 1620
QY 1621 ATTAGTATGATGATTAAGAAATGATGATGCTGCTGAATGATTAAGATTAACAATGGAG 1680
Db 1621 ATTAGTATGATGATTAAGAAATGATGATGCTGCTGAATGATTAAGATTAACAATGGAG 1680
QY 1681 TCGATTTTGAAGAAACATAGAGATTTATTTAG 1713
Db 1681 TCGATTTTGAAGAAACATAGAGATTTATTTAG 1713

RESULT 6
AA091563
ID AA091563 standard; cDNA; 1713 BP.
XX
AC AA091563;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103B allele.
XX
KW Esterase; E3; bioremediation; organophosphate; carbamate;
KW insecticide; pesticide; water decontamination; meat decontamination;
KW ss.
XX
OS Lucilia cuprina.
XX
FH Key location/Qualifiers
FT CDS 1..1713
FT /tag= a
XX
PN MO9519440-A1.
XX
PD 20-JUL-1995.
XX
PF 13-JAN-1995; 95MO-AU00016.
XX

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PR 13-JAN-1994; 94AU-0003347.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Roblin GC, Russell RJ, Smyth K;
 XX WPI: 1995-263870/34.
 DR
 XX
 PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 PS Example 4: Page 12-17; 38pp; English.
 CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
 CC OP-susceptible esterase E3 of *L. cuprina*) from a diazinon
 CC resistant strain, Llandillo 103. 4 isolated clones were
 CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
 CC esterases. The esterases, or cells expressing them, are used
 CC in bioremediation.
 XX
 SQ Sequence 1713 BP; 513 A; 308 C; 368 G; 524 T; 0 other;
 Query Match 97.9%; Score 1676.2; DB 16; Length 1713;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 1690; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 1 ATGATATTCACGTTAGTTGATGAGAAATTAATAATGAAATTAATGATGAAAT 60
 DB 1 ATGATATTCACGTTAGTTGATGAGAAATTAATAATGAAATTAATGATGAAAT 60
 QY 61 AAGTTTTTAACATGATGTTAACTACCATGAACGGTGTAGCTGAACCTGAATGCG 120
 DB 61 AAGTTTTTAACATGATGTTAACTACCATGAACGGTGTAGCTGAACCTGAATGCG 120
 QY 121 AAGTGAAGGCGTTAAAGCTTAACTGTGATGATGATGATGATGATGATGATG 180
 DB 121 AAGTGAAGGCGTTAAAGCTTAACTGTGATGATGATGATGATGATGATGATG 180
 QY 181 ATACCGTACGCGCCCAACCGCCAGTGGGTGAGTGAATTAAGCAACCCGAGCAACA 240
 DB 181 ATACCGTACGCGCCCAACCGCCAGTGGGTGAGTGAATTAAGCAACCCGAGCAACA 240
 QY 241 CCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 DB 241 CCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 QY 301 ATACGCGCAAGAGTGTGCTCAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
 DB 301 ATACGCGCAAGAGTGTGCTCAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
 QY 361 CTAAATCCCGAAGTAAAGCTCCCTTTTATGATATACATACATGCTGTGTTTATATC 420
 DB 361 CTAAATCCCGAAGTAAAGCTCCCTTTTATGATATACATACATGCTGTGTTTATATC 420
 QY 421 GGTGAAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 DB 421 GGTGAAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 QY 481 ATTAACATCAATATCGTTTGGAGCTCTAGTTTCTAAGTTTAAATTCGAAGACTT 540
 DB 481 ATTAACATCAATATCGTTTGGAGCTCTAGTTTCTAAGTTTAAATTCGAAGACTT 540
 QY 541 AATGTCGCGGTAATGCGGCTTAAAGATCAACATGCGCTGCTGCTGATTAATAAT 600
 DB 541 AATGTCGCGGTAATGCGGCTTAAAGATCAACATGCGCTGCTGCTGATTAATAAT 600
 QY 601 AATTGCGCAACTTGTGTGCAATCCGATATATTAACAGTCTTGTGTAAGGCGCGT 660
 DB 601 AATTGCGCAACTTGTGTGCAATCCGATATATTAACAGTCTTGTGTAAGGCGCGT 660
 QY 661 GCTGCTCTACCCACTACATGATGTTAACCGAACAACCTGCGGCTTTTCCATGCTGT 720

DB 661 GCTGCTCTACCCACTACATGATGTTAACCGAACAACCTGCGGCTTTTCCATGCTGT 720
 QY 721 ATACTAATGTGGGTAATGCTATTTGCTATGCTGTAATACCAATGCAATGCTGCG 780
 DB 721 ATACTAATGTGGGTAATGCTATTTGCTATGCTGTAATACCAATGCAATGCTGCG 780
 QY 781 TTACACCTTACCAATTTGGCGGCTATTAAGGTGAGATTAATGAAGATGTTTGGAA 840
 DB 781 TTACACCTTACCAATTTGGCGGCTATTAAGGTGAGATTAATGAAGATGTTTGGAA 840
 QY 841 TTCTTATGAAGCCCAAGCCAGGATTAATTAATTAACCTGAGAAAAGTTTAACTCTA 900
 DB 841 TTCTTATGAAGCCCAAGCCAGGATTAATTAATTAACCTGAGAAAAGTTTAACTCTA 900
 QY 901 GAAGACGTAACAATTAAGTCTATGTTCTTCTTGGTCCACGTTGAGCATATGAGACC 960
 DB 901 GAAGACGTAACAATTAAGTCTATGTTCTTCTTGGTCCACGTTGAGCATATGAGACC 960
 QY 961 GGTGATGTTGCTTACCCCAACATCTCGGGAATGTTAAACTGCTTGGGGTAATTCG 1020
 DB 961 GGTGATGTTGCTTACCCCAACATCTCGGGAATGTTAAACTGCTTGGGGTAATTCG 1020
 QY 1021 ATACCCATATGATGGGTAACTCATATGAGGGCTATTTTCACTTCAATTTCTTAAG 1080
 DB 1021 ATACCCATATGATGGGTAACTCATATGAGGGCTATTTTCACTTCAATTTCTTAAG 1080
 QY 1081 CAATGCTGATGCTTGTAAAGATTAAGAACTTGTCAATTTTGTGCCAAGTAATG 1140
 DB 1081 CAATGCTGATGCTTGTAAAGATTAAGAACTTGTCAATTTTGTGCCAAGTAATG 1140
 QY 1141 GGTGATGCTGAAGCAGCCGCCAGAGACCTGGAATAGGGTCTAAATTAATAAGGCT 1200
 DB 1141 GGTGATGCTGAAGCAGCCGCCAGAGACCTGGAATAGGGTCTAAATTAATAAGGCT 1200
 QY 1201 CATGTTACAGAGAACAACAACAGCTGATTAATTTATGATCTTTGCTCTACATCTAT 1260
 DB 1201 CATGTTACAGAGAACAACAACAGCTGATTAATTTATGATCTTTGCTCTACATCTAT 1260
 QY 1261 TTCTGTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 DB 1261 TTCTGTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 QY 1321 GTTACTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 DB 1321 GTTACTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 QY 1381 CGTATGAGAGTGTGTTAAGGCTGTTAGTCAATGCTGATGAATTAACCTATCTCTG 1440
 DB 1381 CGTATGAGAGTGTGTTAAGGCTGTTAGTCAATGCTGATGAATTAACCTATCTCTG 1440
 QY 1441 AATTAATGGCAAGTATGCTTAAGAAATCCGCTGCAATACAAACATTTGACGTATG 1500
 DB 1441 AATTAATGGCAAGTATGCTTAAGAAATCCGCTGCAATACAAACATTTGACGTATG 1500
 QY 1501 ACTGATATATGATATCAATTTGACCACTGTAATCTTATAGCAATGAATGAAGT 1560
 DB 1501 ACTGATATATGATATCAATTTGACCACTGTAATCTTATAGCAATGAATGAAGT 1560
 QY 1561 ATGGAAGATTTTCTGGGATTTCAATTAAGAAATCCGATGAGTATACAGTGTGTAAT 1620
 DB 1561 ATGGAAGATTTTCTGGGATTTCAATTAAGAAATCCGATGAGTATACAGTGTGTAAT 1620
 QY 1621 ATTAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATG 1680
 DB 1621 ATTAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATG 1680
 QY 1681 TCGATGTTGAAGAAACATAGAGATTTATTTAG 1713
 DB 1681 TCGATGTTGAAGAAACATAGAGATTTATTTAG 1713
 RESULT 7

AA091562
ID AA091562 standard: cDNA; 1713 BP.
XX
AC AA091562:
XX
XX 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103A allele.
XX
XX Esterase; E3; bioremediation; organophosphate; carbamate;
KW Insecticide; pesticide; water decontamination; meat decontamination;
KW ss.
XX
XX Lucilia cuprina.
FH Key Location/Qualifiers
FT CDS 1..1713
FT /tag- a
XX
XX MO9519440-AI.
XX
XX 20-JUL-1995.
XX
XX 13-JAN-1995; 95MO-AU00016.
XX
XX 13-JAN-1994; 94AU-0003347.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX Parker AG, Robin GC, Russell RJ, Smyth K;
XX
XX WPI; 1995-263870/34.
XX
XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
PT eliminate residues of organo:phosphate and carbamate pesticides from
PT water, meat etc.
XX
XX Example 4; Page 12-17; 38pp; English.
XX
XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
CC resistant strain, Llandillo 103. 4 isolated clones were
CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
CC esterases. The esterases, or cells expressing them, are used
CC in bioremediation.
XX
XX
SQ Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;
Query Match 97.8%; Score 1674.6; DB 16; Length 1713;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1689; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 301 ATACGGCAAAAGTGTGGCTCAGAGATTTGCTATACCTAGTGTCTATACGAATAT 360
DB 301 ATTACAGGCAAAAGTGTGGCTCAGAGATTTGCTATACCTAGTGTCTATACGAATAT 360
QY 361 CTAAATCCCGAACTAAACGTCCTTTAGTATACATACATGCTGTTTATATATC 420
DB 361 CTAAATCCCGAACTAAACGTCCTTTAGTATACATACATGCTGTTTATATATC 420
QY 421 GGTGAAATCATGCTGATATGATGCTGATTTATTTCAATTAAGAGATGCTGTG 480
DB 421 GGTGAAATCATGCTGATATGATGCTGATTTATTTCAATTAAGAGATGCTGTG 480
QY 481 ATTACATACATATGCTTTGGAGCTCTAGCTTTCTAAGTTTAAATTCGAAGACCTT 540
DB 481 ATTACATACATATGCTTTGGAGCTCTAGCTTTCTAAGTTTAAATTCGAAGACCTT 540
QY 541 AATGTCGGGTAAATGCGCGCTTAAAGATCAATGCGCTTGTGATTAATAAT 600
DB 541 AATGTCGGGTAAATGCGCGCTTAAAGATCAATGCGCTTGTGATTAATAAT 600
QY 601 AATGTCGGGTAAATGCGCGCTTAAAGATCAATGCGCTTGTGATTAATAAT 660
DB 601 AATGTCGGGTAAATGCGCGCTTAAAGATCAATGCGCTTGTGATTAATAAT 660
QY 661 GCTGCTCTACACCTATGATGATGATTAACGCAAACTCGCGCTTTTCCATCGTGT 720
DB 661 GCTGCTCTACACCTATGATGATGATTAACGCAAACTCGCGCTTTTCCATCGTGT 720
QY 721 ATACTAATGTCGGTAAATGCTATTTGTCATGTCCTAATACCAATGTCAATCGTGC 780
DB 721 ATACTAATGTCGGTAAATGCTATTTGTCATGTCCTAATACCAATGTCAATCGTGC 780
QY 781 TTACCTTAGCCAAATGCGCGCTATTAAGGTCAGATTAATGAATGATTTTGAA 840
DB 781 TTACCTTAGCCAAATGCGCGCTATTAAGGTCAGATTAATGAATGATTTTGAA 840
QY 841 TTCTTATGAAGCCAAAGCCACAGATTTAATAAATCTGAGAAAAGTTTAACTTA 900
DB 841 TTCTTATGAAGCCAAAGCCACAGATTTAATAAATCTGAGAAAAGTTTAACTTA 900
QY 901 GAAGAGGCTCAATTAAGTATGCTATTTGCTTGTGCTGCTGATGATGATGATG 960
DB 901 GAAGAGGCTCAATTAAGTATGCTATTTGCTTGTGCTGCTGATGATGATGATG 960
QY 961 GCTGATGCTGCTTACCAATCAATCCTGGAATGTTAAACGCTGTTGGGTAATTCG 1020
DB 961 GCTGATGCTGCTTACCAATCAATCCTGGAATGTTAAACGCTGTTGGGTAATTCG 1020
QY 1021 ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 CAATGCTATGCTTGTGAAGAAATGGAATCTGTCAATTTTGTGCCAAGTGAATG 1140
DB 1081 CAATGCTATGCTTGTGAAGAAATGGAATCTGTCAATTTTGTGCCAAGTGAATG 1140
QY 1141 GCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 1141 GCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1201 CATGTTACAGAGAGAACCAACAGCTGATATTTATGATCTTTGCTCATCATCTAT 1260
DB 1201 CATGTTACAGAGAGAACCAACAGCTGATATTTATGATCTTTGCTCATCATCTAT 1260
QY 1261 TTTGTTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 TTTGTTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
DB 1321 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
QY 1381 CGTAGTGGAGTGTGTTAAGGTTAGTATGATGATGATGATGATGATGATGATGATG 1440

QY 1004 CTGCTGGGGGAATTGCATCCCATATGATGGGTAACTTCATATGAGGCTATTTT 1063
 Db 1004 GCGCTGGGGAATTGCATCCCATATGATGGGTAACTTCATATGAGGCTATTTT 1063
 QY 1064 TCACCTCAATTCCTTAAGCAATGCTATGCTTGAAGAATTTGAACCTTGTCTCAAT 1123
 Db 1064 CCAATCAATTTGCCAACAATATCCGAGGTGTAAAGAGTTGATTCCTGTGTGATTT 1123
 QY 1124 TTGTGCAAGTGAATTTGGCTGATGCTGACGACCCGCCAGAGACTTGGAAATGGCT 1183
 Db 1124 ATGTGCTTGGAGCTGACGACGACGACGACGACGACGACGACGACGACGACG 1183
 QY 1184 CTAATTAATTAAGGCTCATGTTTACAGAGAAACCAACAGCTGATTAATTTTATGATC 1243
 Db 1184 CCAATTTGAAAAAGGCCCATGTGATGGAGAAACCACTACTCTGATTAATTTTATGAGC 1243
 QY 1244 TTGTGCTCAATTCCTTAAGCAATGCTATGCTTGAAGAATTTGAACCTTGTCTCAAT 1303
 Db 1244 TTGTGCTCAATTCCTTAAGCAATGCTATGCTTGAAGAATTTGAACCTTGTCTCAAT 1303
 QY 1304 ACACCTCCGGTACACCCGCTACTGATGCTGCTGACCTGATGCTGATGCTGATGCT 1363
 Db 1304 ACACAGCTGGACCTCCATTTATTTATGCTGCTGATGCTGATGCTGATGCTGAT 1363
 QY 1364 ATCCCTATTCATATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1423
 Db 1364 ACCCTATTCATATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1423
 QY 1424 TAACCTATTCCTGATGATCAATTTGGCCAAACCTATGCTGATGCTGATGCTGATG 1483
 Db 1424 TAACCTATTCCTGATGATCAATTTGGCCAAACCTATGCTGATGCTGATGCTGATG 1483
 QY 1484 AAACATTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
 Db 1484 AAACATTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
 QY 1544 GCAATGAAATGAAAGTATGAAAGTATGAAAGTATGAAAGTATGAAAGTATGAAAG 1603
 Db 1544 GCAATGAAATGAAAGTATGAAAGTATGAAAGTATGAAAGTATGAAAGTATGAAAG 1603
 QY 1604 TATCAAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
 Db 1604 TATCAAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
 QY 1664 AGATTAACAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1710
 Db 1664 AAATTAACAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1710
 RESULT 9
 ABL02067
 ID ABL02067 standard; cDNA; 2001 BP.
 AC ABL02067;
 XX
 XX 26-MAR-2002 (first entry)
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 683;
 KM Drosophila: developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US09231.
 PF 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PR

XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 XX
 XX P-PDB; ABB57964.
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 683; 21bp + Sequence Listing; English.
 CC
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SQ Sequence 2001 BP; 502 A; 488 G; 521 G; 490 T; 0 other:
 Query Match 39.7%; Score 680.4; DB 23; Length 2001;
 Best Local Similarity 62.7%; Pred. No. 6.9e-177;
 Matches 1075; Conservative 0; Mismatches 636; Indels 3; Gaps 1;
 QY 1 ATGATTTTCAACGTTAGTTGATGAGCAATTAATGAAGATTAATGATGAAAT 60
 Db 95 ATGATTAAGAACTCCGCTTGTGAGGCTTGGGCTCCCTCAAAACCATGAGCAT 154
 QY 61 AAGTTTAACTATCGTTTAACATGAAACGAGGTGAGGCAAGCAATGAAATGAGC 120
 Db 155 AAAGTCCAGCATATCGCCAGTCCGACCATGAAACAGTTGTCGCCGACAGGATGAGGC 214
 QY 121 AAAGTGAAGGCGTTAAACGTTAACTGATGATGATGATGATGATGATGATGATGAT 180
 Db 215 CAAGTGAAGGCGTTAAACGTTAACTGATGATGATGATGATGATGATGATGATGAT 274
 QY 181 ATACCTGACGCGCAACGCGGAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
 Db 275 ATCCCGTACGCGCAACGCGGAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 334
 QY 241 CCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 Db 335 CCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 394
 QY 301 ATAAAGGCGCAAGTGTGCTGACAGGATGCTATACCTAAGTCTATACGAATAT 360
 Db 395 GTCTTGCATAGTGAAGGCTCCGAGGATGCTATACCTAAGTCTATACGAATAT 454
 QY 361 CTAATCCGCAATTAACGTCGCTTGTATATACATACATACATACATACATACATAC 420
 Db 455 GTGAAGCGCGCAAGGCTCCGCTGCTGATGATGATGATGATGATGATGATGATGAT 514
 QY 421 GGTAAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 Db 515 GGTAAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 574
 QY 481 ATTAACATACATATGCTTGGAGCTTATGATGATGATGATGATGATGATGATGATGAT 540
 Db 575 GTCAAGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 634
 QY 541 AATGTCGCGGTAATGCGGCTTAAAGATCAAGTATGATGATGATGATGATGATGATGAT 600
 Db 635 AATGTCAGGAAATGCTGCGCTCAAGGATCAAGTATGATGATGATGATGATGATGATGAT 694
 QY 601 AATGTCGCGGTAATGCTGCGCTCAAGGATCAAGTATGATGATGATGATGATGATGATGAT 660

Db 695 AATTCGCTAGTTCGGGCGAGATCCCAACATGACATGTTTGGAGAGAGTGTGGA 754
 661 GCTGCTCTACCCACATACATGATGTTAAACCAACAACTGGGTCCTTTCATCTGTG 720
 755 GGGGCTCCACTACATACATGATGATGCTAAGCATGACAGCCCAAGGCTCTTTCATCGGGC 814
 721 ATACTAATGCGGTAAGCTATTTGTCATTTGGC--TAATACCAATGTCAACATCT 777
 815 ATCTGACATCGGAGCTCCATTTGCTTGGCCCTACAAAGGCGACATTTACCATAT 874
 778 GCCTTACCTTAAACCAATTTGGCCGCTATAGGCTGAGGTAATAGATAGATGTTTG 837
 875 CCTACAGATACCAAGCTGCTGCTCAAGGGGAGGACACAGACAGATGCTGTG 934
 838 GAATTTCTTTGAAGACCAAGCCACAGATTTAATTAACCTTGAGAAAATTTTACT 897
 935 GAGTTCTTGACAGACGTAAGGCAAGGATCTTATTCGGTGAGAGAAAATGCTCTGACA 994
 898 CTAGAAGAGCGTACAAATAGTCAATGTTCTTTGTCCTCCATGAGCCATATCAG 957
 995 CTGAGAGAACCATGAAAGATAGTGTGCTTGGCCATCCCTGGAACCATTTCTCC 1054
 958 ACCGCTGATGCTGCTTACCAACATCTTCGGGAAATGTTAAACTGCTTGGGTAT 1017
 1055 ACGCCGGAATGTGATATCCAAAGCTCCAAAGGAGATGTAAGACCGCTGAGATAC 1114
 1018 TCGATACCCACTATGATGGGTAAACATCATATGAGGCTATATTTTCACTCAATCT 1077
 1115 TCCATCCCCATGTTATAGGAACCTTCACAGAGGCGCTGCTGGTTCACAGAGTA 1174
 1078 AAGCAATGCTATGCTTGAAGAAATGGAATTTGTGCAATTTTGGCCAAAGTAA 1137
 1175 AAGCTTATCCGACAGTGTGACAGACTGATGCTGACACCTTTCATTTCCAAAGAA 1234
 1138 TTGGCTGATGCTGAACGCCACCCCGCCAGAGACCTTGAATGCTGCTAAATTTAAAG 1197
 1235 TTGCTGGCCACGAGCCGTAAGAAAACGATGCTGAGAGTGCACAGATTCGAGAT 1294
 1198 GCTCATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATCTTGTCTCACATC 1257
 1295 GTTCATCGCATGCTGCACAAAGACCCAGATTAATTAATGATGATCTGTTCCATTTAC 1354
 1258 TATTTGCTGCTCCCATGATGCTGTTGTCATTAAGCTTCAATACACACTCCGTACA 1317
 1355 TACTTCGTTTCCGGCCCTGAGGGTGTCCATTTCCGACACAGCGTACCGCTGAGCT 1414
 1318 CCGCTACATGATGCTGCTTCGATTCGATTCGAAAGATCTTATCAATCCCATGAT 1377
 1415 CCAATATTTCTATGATATGATTCGATTCGATTCGAGAGACTCAATTTTCCGATCCGAT 1474
 1378 ATGCGTACGAGCTGCTGTTAAGGCTGATGATGCTGATGATGATTAATTTCTTC 1437
 1475 ATGCGTGGGAGCGCGGTGTAAGGGGCTGACGATCCGAGATTTGAGCTACCAATTC 1534
 1438 TGGATCAATTTGGCCAAACGATATCCCTAAGATCCGCTAATACAAACAAATGAAC 1497
 1535 AGCAGCTGCTGCTGCGCGGCTGCGAAGGAAAGTGCAGAGTACAGACATCGAACA 1594
 1498 ATGACTGATATGATATCAATTTGGCCACACATGCTGATATCCCTTATACCAATGAAT 1557
 1595 ACCGTTGGGATCTGAGACCAAGTTTGTCTTCAAGGGTAAATCCCTACAGAGAGATC 1654
 1558 GGTATGAATAATGTTTCTGAGATCAATTAAGAAATCCGATGAGATTAACAAAGT 1617
 1655 GGTATGACACTCTGACATTTGATTCAGTTCGAATCCGAGAGGCTATCAATGATGCTC 1714
 1618 AATATATGATGATTAATTAATGATGATGCTGAAATGATGATTAATTAACATG 1677
 1715 AATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1774
 1678 GAGTCAATGTTGAATAAATAGATTAATTTT 1711

Db 1775 GAGAGCCTATGACGACACAAAGATTTATGCT 1808
 RESULT 10
 ID ABL02081
 ABL02081 standard; cDNA: 1704 BP.
 AC ABL02081;
 XX 26-MAR-2002 (first entry)
 XX 26-MAR-2002 (first entry)
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 725.
 XX Drosophila: developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX Drosophila melanogaster.
 OS MO200171042-A2.
 XX 27-SEP-2001.
 PD 23-MAR-2001; 2001MO-US09231.
 PE 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PA (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI: 2001-656860/75.
 DR P-PSDB; ABB57978.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Claim 1: SEQ ID NO 725; 21bp + Sequence Listing: English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB12072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_Pct_sequences.
 XX Sequence 1704 BP; 417 A; 445 C; 460 G; 382 T; 0 other;
 SQ
 Query Match 22.3%; Score 381.8; DB 23; Length 1704;
 Best Local Similarity 54.0%; Pred. No. 11e-94;
 Matches 879; Conservative 0; Mismatches 727; Indels 21; Gaps 4;
 Db 85 ACCAATGAACGGTGTGATGCTGAATGATGATGATGATGATGATGATGATGAT 144
 64 AGCAATGACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 123
 145 ACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 204
 124 TCCATCTGACCAACACTACTACTACTACTACTACTACTACTACTACTACTACTACT 183
 205 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 264
 184 GCGAGCTCCGCTTCAGGCGCGCTGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
 265 TGCATCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 324
 244 ACAATGTTGCGCCCAAGCCCTGCGAGTCAACATGCTTGAAGACGAGTGAAGGAGC 303

QY	325	GAGATGTGCTATATCCCTAAGTGGCTCTATACGAATAATCTAAATCCCGAAGCTAAAGCTGCC	384
Db	304	GAGACTGTCTGTACCTCAATGTCTACACAGGGAATTCATCTACACAGACTTTGGCG	363
QY	385	GTTTTAGTATACATACATGCTGGTGGTTTTATATTCGTGGAATAATCATCTGATATGAT	444
Db	364	GTTCGTGTTGGANTATATGCGCGGTGGATTCGAATGGAGAAAGCATCGGGGATCTGAC	423
QY	445	GCTCCTATATTTCATTAAAAAGATGTGGTGTGGATTAACTATCAATATCTGTTGGGA	504
Db	424	AGCCGGACTACATTTATGATGAAACATGTCTACTGTGTAAATTCATGCGTTAGGA	483
QY	505	GCTCTAGTTTTCTAAGTTTAATTCAGAAAGACTTAATGTGCCGGTAATGCCGCTT	564
Db	484	GCCCTGGGAATTCCTTACTCTTGGCAGACGAAGAATCGATGTCTCTGGAAACCGGGACTA	543
QY	565	AAATCATACATCAAGGCGCTTGCCTGGATTAATAAATTAATGGCGCACTTTGGTGGCAT	624
Db	544	AAGGATTAAGTTATGGCTCTTGGCTGGTCAAAACGAAATGGCAAGTCTTTGGTGGCAT	603
QY	625	CCCGATTAATATACAGTCTTTGGTGAAGTCCCGGCTGCTTACCACATCATATGAG	684
Db	604	CCGATTAATTAACCGTTTGGTGAAGTGGTGGAGTGATCCACATATATATGATG	663
QY	685	TTAACCAACAACACTGCGGCTCTTTTCCATCGTGATATCATATGTGGGTAATGTATTT	744
Db	664	CTGACGATACAGGCAAGGCGCTTATTCACAAGACATATTAATATGTGGGATCCGACTG	723
QY	745	TGTCCATGGCTAATACCAATGTCA--ACATCGTCTTACTTACCTTACCCAAATGGCC	801
Db	724	GCACCTCTGGGGCAGACCCCAACCCACATTAATTTGGCTTATCGCTGGCACAGGCCACT	783
QY	802	GGCTATTAAGGCTGAGATTAATGATAAGATGTTTTGGAATTTCTTATGAAGCCAAAGCA	861
Db	784	GGCTACACAGAGATGCTAACGATCGGGACATTTTGGCCATCTCAAGAAATGTAAAGCC	843
QY	862	CAGATTTAATTAACCTTGAGAAAAATTTTACTCTAGAAGCGTACAAATTAAGT-	920
Db	844	AGTAGCATGTCTGAAGGTGGCGGAGATATCATCACCATGGAAGACACACAGCGGTTG	903
QY	921	--CATGTTCCTTTGGTCCACTGTGTGAGCATATCACACCGCGTATGTCTTACC	978
Db	904	ACCATGTTCAGCTTTGGACCCACATCAGACCCCTAATTTACATCTCATTTGTGTGATTTCC	963
QY	979	AAACATCTCGGGAAGATGTTAAACACTGCTGGGGTAATTCATACCCACATATGATGGT	1038
Db	964	AAGTCGCCACTGGAATGATGCGGGACTGTTGGGGCAACAGACTTCCATGTCTATCGGA	1023
QY	1039	AACACTTCATATGAGGCTATATTTTCACTTCATTTCTTAACCAATGCCTATGCTGTT	1098
Db	1024	GGAATCTCTCGAAGGTCTCTCATGTTTCCGAAGTGAACAACTGGCCGGAATCGTT	1083
QY	1099	AAGAAATGGAACTGTGTCAATTTTGTGCCAAGTGAATTTGGCTGATGTGAACGCACC	1158
Db	1084	TGCCAGTGGGTGACTGCGGAACCTGGCCCTCAAGATGGCCACAGTGAATGACAGCA	1143
QY	1159	GCCCCAGAGACTTGGAAATGGGTGCTAAATAATTAATAAGCTCATATGTAACAGGAACAA	1218
Db	1144	AGAAACAGCTTTGGAAAGAAAGTACAGACAGCTATTTTGGCGATAGAGCTCTGGCAGG	1203
QY	1219	CCAACAGCTATATATTTATATGATCTTTGCTGTCACTATTTTGTGTTGCCATCGAT	1278
Db	1204	AAGACCATATATGGAGTACAGCATCTCTCTGTACAAATATTTCTGGCATGTGATTCAT	1263
QY	1279	CGTTTGTGCAATTAGCTTTCAATCACTCCGGTACACCCGCTTACTGTATCGCTTC	1338
Db	1264	AGGACTTTGCTCGCGCTGTCTCACACGCGCCATTTGGCCCAACATTTCTGTACGATTC	1323
QY	1339	GACTGTGATTTGGAAATCTTATCAATCCCTATATGATATATGAGAGAGCGTGTGTT	1398
Db	1324	GATTTGCACTCG---AAGACTTCAATATATATGCGAATTTATACCTGTGGCGGCAAGGTG	1380

Qy	1399	AAGGTTTGATGCTGATGATTAACCTATTCTCTGGAATCAATTGGCCAAACGT	1458
Db	1381	CGCGGACACCTCTACCGGGGATGATCTGTCGATTGTTCTCAATCGCGCTGCCAAAAG	1440
Qy	1459	ATGCCCTAAGAANTCGCGTGAATACAAAACAATTGAAGCTATGCTGATATGATACAA	1518
Db	1441	CTGAAGCGCCGACAGCCGAGTTCACAGACCACTTAAGAGCTTTGGATCATGCTGTTAC	1500
Qy	1519	TTTCCACACCTGTAATCCTTATA-----GCAATGAATTTGAAGTATGCA	1566
Db	1501	TTTTCCATTTCGGGGGATCCCAACATCCGATGCTGCTCCGAGATGAGAAAGAACGCCG	1560
Qy	1567	AATTTTCCTCGGATCCCATTAAGAAATCCGATAGATACAGTGTGTAATTTAGT	1626
Db	1561	CGTGGCCGCTGCTGCCCATTTCCAGAGCAGATTAAGCTTCCAGCTTGAATATATCG	1620
Qy	1627	GATGAATTTGAATAATGATTTGATGCTCTGAAATGATTAAGATTTAAACAATGAGCTCATG	1686
Db	1621	CAGCATGTGATGTGATTTGATTTGCCGAGAACCCGAAAGCTGAGACTTTGGAGCTGCATC	1680
Qy	1687	TTTTGAAA	1693
Db	1681	TACGACA	1687
RESULT 11			
AB102066			
ID	AB102066	standard; cDNA; 6175 BP.	
XX	AC	AB102066;	
XX	AC	AB102066;	
XX	DT	26-MAR-2002 (first entry)	
XX	DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 680.	
XX	KM	Drosophila; developmental biology; cell signalling; insecticide;	
XX	KM	pharmaceutical; gene; ss.	
XX	OS	Drosophila melanogaster.	
XX	PN	WO200171042-A2.	
XX	PD	27-SEP-2001.	
XX	PE	23-MAR-2001; 2001WO-US09231.	
XX	PR	23-MAR-2000; 2000US-191637P.	
XX	PR	11-JUL-2000; 2000US-0614150.	
XX	PA	(PEKE) PE CORP NY.	
XX	PI	Venter JC, Adams M, Li PMD, Myers EW,	
XX	PI	WPI; 2001-656860/75.	
XX	DR	P-PSDB; ABB57963.	
XX	DR		
PT	PT	New isolated nucleic acid detection reagent for detecting 1000 or more	
PT	PT	genes from Drosophila and for elucidating cell signalling and cell-cell	
PT	PT	interactions -	
PS	PS	Claim 1; SEQ ID NO 680; 21pp + Sequence Listing; English.	
XX	XX		
XX	XX	The invention relates to an isolated nucleic acid detection reagent	
XX	XX	capable of detecting 1000 or more genes from Drosophila. The invention is	
XX	XX	useful in developmental biology and in elucidating cell signalling and	
XX	XX	cell-cell interactions in higher eukaryotes for the development of	
XX	XX	insecticides, therapeutics and pharmaceutical drugs. The invention	
XX	XX	discloses genomic DNA sequences (AB101840-AB116175-AB130511), expressed DNA	
XX	XX	sequences (AB101840-AB116175) and the encoded proteins	
XX	XX	(ABB57737-ABB72072).	
XX	XX	The sequence data for this patent did not form part of the printed	
XX	XX	specification, but was obtained in electronic format directly from WIPO	
XX	XX	at ftp.wipo.int/pub/published_pcl_sequences.	

QY 1190 TTAAGAGCTCATGTATACAGAGAAACACACAGATATTTATGATCTTCT 1249
 Db 1291 TCTACTTCAACACAGATGACAGATGATGAGATGTTGAGGCCCTGATATATTT 1340
 QY 1250 CTCACATCTATTTGTTGCCATGATGCTTTGTCATTAAGCTTCAATCACCT 1309
 Db 1341 CGCATGCGCATTTGGCAGATAGCATGCTTTATCTGCGCGCATCTTATGCCC 1400
 QY 1310 CCGGTACACCGCTCTACTTGTATGCTTGCAGCTTGCAGTGGAGATCTTATCCCT 1369
 Db 1401 CCAAAACGCGCCATCTATCTATGCTTTGACTGACTC---CCCGCATCTCAATCAT 1457
 QY 1370 ATCTATATGCTGATGAGCTGCTGTTAAGGCTGATGATGATGATGATGATGAT 1429
 Db 1458 TTCGCCGAGCTGCTGCGCGCATGCGATGCGGAGTACCGCATGCGATGATCAT 1517
 QY 1430 ATTTCTCTGATCAATGATGCGCAAGCTATGCTTAAGAAATGCGGATACAAACCA 1489
 Db 1518 ACCTGTTCTACACATCATATGCTTCCCAAACTGATTAAGTATGATGATGATGATGAT 1577
 QY 1490 TTGAACGATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1549
 Db 1578 TTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1637
 QY 1550 AAATTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1609
 Db 1638 AACGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1691
 QY 1610 AGTCTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1662
 Db 1692 AGTCTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1744

RESULT 14

ABL02103
 ID ABL02103 standard; cDNA; 1593 BP.
 AC ABL02103;
 XX 26-MAR-2002 (first entry)
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 791.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical; gene; ss.
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PF 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PA (PEKE) PE CORP NY.
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI: 2001-656860/75.
 DR P-PSDB: ABB58000.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX Claim 1; SEQ ID NO 791; 21pp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://ipo.int/pub/published_pct_sequences.

Sequence 1593 BP; 417 A; 394 C; 405 G; 377 T; 0 other;

Query Match 18.9%; Score 323.6; DB 23; Length 1593;
 Best local similarity 52.9%; Pred. No. 1,1e-78;
 Matches 831; Conservative 0; Mismatches 709; Indels 32; Gaps 5;

QY 111 TGAATATGCAAGTAAAGCGTTAAAGCTTTAACTGATGATGATGATGATGATGATGAT 170
 Db 6 TGACTGCGCTGCTGCGGAGTGAAGAAACAACTGCGGAGGAGGAGGAGGAGGAGGAGGAG 65
 QY 171 TTTGAGGATATACCGTACCGCCCAAGCCGAGTGGTGAAGTATTAAGCACCCCA 230
 Db 66 TTTGAGGAGATACCGCTTCCCAAGCCGAGTGGGAGATGCTTCAAGGCCCGCA 125
 QY 231 GCGAACCAACCGCTGAGTGGTGGGATGCTGCAATCAATCAATCAATCAATCAATCAAT 290
 Db 126 AGCAGTGAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 185
 QY 291 AGTGAATTTTAAAGGCGCAAGTGTGCTGAGAGATGCTTAACTAAAGTCTTA 350
 Db 186 GACACACATGTTTTCAGAAATAACGCGGCTCAGAGAGCTCCTTAATTAATGTTGA 245
 QY 351 TACGATATATCTAATCCCGCAATCAAGCTCCGTTTATGATATCAATCAATCAATCAAT 410
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 QY 711 CCATGCTGATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 770
 Db 606 CCACAAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 665
 QY 771 ACATGCTGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 830
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 QY 831 TGTGTTGAATTTCTTATGAAAGCCACAGATTTTAAATTAATTAATTAATTAATTAATTA 890
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 QY 951 ATATCAGACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1010

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:24:12 ; Search time 1663.49 Seconds
(without alignments)
16677.553 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6:	em_estpl:**
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9:	gb_estl:**
10:	gb_estl2:**
11:	gb_hlc:**
12:	gb_estl3:**
13:	gb_estl4:**
14:	gb_estl5:**
15:	em_estfun:**
16:	em_estom:**
17:	gb_gss:**
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20:	em_gss_pln:**
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26:	em_gss_pro:**
27:	em_gss_rod:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	315.2	18.4	778	9	AI062034 GH01076.5
2	282.4	16.5	649	9	AI388926 GH19977.5
3	266.8	15.6	688	9	AI403569 GH23036.5
4	258.2	15.1	671	9	AI517692 GH28740.5
5	256	14.9	569	13	BI609541 RH14337.5
6	251.6	14.7	674	13	BI628316 RH56682.5

7	251	14.7	676	13	BI635372
8	250	14.6	673	13	BI614181
9	248.6	14.5	660	13	BI639486
10	248.4	14.5	672	13	BI614443
11	248	14.5	670	13	BI233202
12	246.6	14.4	648	9	AI113763
13	246.6	14.4	648	9	AI403098
14	245	14.3	646	9	AI109901
15	245	14.3	646	9	AI293416
16	242.6	14.2	526	9	AI108080
17	241.4	14.1	516	9	AI108156
18	240.8	14.1	658	13	BI564586
19	240	14.0	656	13	BI619037
20	238.4	13.9	656	13	BI614821
21	238.2	13.9	669	13	BI588370
22	237.8	13.9	656	13	BI621302
23	234.8	13.7	628	9	AI109573
24	233	13.6	619	9	AI516869
25	232.6	13.6	638	13	BI564361
26	232.4	13.6	628	9	AI513346
27	232.2	13.6	630	9	AI403830
28	231.6	13.5	614	12	B6641228
29	231.6	13.5	647	13	BI575862
30	231.2	13.5	614	9	AI107729
31	231.2	13.5	614	9	AI134360
32	230.8	13.5	622	9	AI134524
33	229.6	13.4	633	13	BI370683
34	228.6	13.0	670	9	AI389766
35	221.4	12.9	614	13	BI617897
36	220.8	12.9	615	13	BI588504
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41	220.2	12.9	609	13	BI607309
42	220.2	12.9	609	13	BI622392
43	220.2	12.9	609	13	BI630054
44	220.2	12.9	611	13	BI572606
45	219.4	12.8	612	13	BI631806

ALIGNMENTS

RESULT 1
AI062034 778 bp mRNA EST 19-APR-2001
LOCUS GH01076.5
DEFINITION GH01076.5 Sprine GH Drosophila melanogaster head pot2 Drosophila melanogaster cDNA clone GH01076.5 Sprine similar to U51050:
Drosophila melanogaster alpha esterase (ae7) gene, partial cds,
mRNA sequence.

ACCESSION AI062034
VERSION AI062034.1 GI:3337873
KEYWORDS EST.
SOURCE Drosophila melanogaster
ORGANISM fruit fly.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 778)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G. M.
BDGP/HMT Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP

TITLE Lawrence Berkeley National Lab
JOURNAL One Cyclotron Rd, Berkeley, CA 94720, USA
COMMENT Fax: 510 486 6796
Email: <http://www.fruitfly.org/EST>, estfruitfly.berkeley.edu
Plate: 10 row: G column: 4
High quality sequence stop: 363.
Location/Qualifiers

FEATURES


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source
1. 778
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/clone="GH01076"
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/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/notes="Organ: head; Vector: pOT2; Site: 1; EcoRI: Site: 2;
XhoI: Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
BASE COUNT      182 a      196 c      220 g      180 t
ORIGIN
Query Match      18.4%; Score 315.2; DB 9; Length 778;
Best Local Similarity 66.1%; Pred. No. 3.3e-75;
Matches 455; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAAATGCAATTCATTAAT 60
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Db 91 ATGAATAAGAACCTCGGCTTTGTGAGCGCTTGCGGTGGCGCTCAAAACCATCGAGCAT 150
QY 61 AAGTTTAACTATCGTTTACTACCAATGAACGGTGTAGCTGAATGATATGCG 120
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Db 151 AAGTCCAGCAGTATCGCCAGTGCAGCAATGAACAGTTGTGCCGACAGAGTAAGGC 210
QY 121 AAGTGAAGGCGTTAAAGCTTAACTGTATGATGATTCCTACTACAGTTTGAAGGT 180
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Db 211 CAAGTGAAGGGATTCACACCGCTATCTCTACATGATGCGCTTACTTACGAGGCT 270
QY 181 ATACCGTACGCCCAACGCCAGTGGTGTAGCTGATTAAGACACCCAGCCAGCAACA 240
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Db 271 ATCCCGTACGCCCAACGCCAGTGGTGTAGCTGATTAAGACACCCAGCCAGCAACA 330
QY 241 CCTGGAATGATGCGGATTTGCAATCATTAAGATTAAGTCAAGTGAATTTT 300
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Db 331 CCTGGGAGCGATTCGCGACTGACGACGCAAGATTAAGCGCTCAGAGTTC 390
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Db 391 GCTTGTGATAGTGAAGGCTCCGAGGACTGCTCTATCTCAATGTGTACCAACAT 450
QY 361 CTAAATCCGGAACATTAAGTCCCGCTTGTATATACATGATGATGATTTATATC 420
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Db 511 GGGGAGGCGCAATCGGAATGATGCGCGGATTTACTTATGAAGAATGATGATGCTC 570
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Db 571 GTACAGCTACAGTACGACTTGGGCTTTGGATTTATGACTTAAAGTCCCGGCTA 630
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Db 631 AATGTACAGGAATGCTGCTCAAGGATCAGTGTGCTGCTCAAGTGAAGCAAGAC 690
QY 601 AATGTGCCCACTTTGTGTGCAATCCGATTAATTAACATCTTTGTGAAGTGGCGGT 660
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Db 691 AATGTGCTAGTTGCGGAGGATTCCAACTGCATCTTTTGTGAAGATGCTGGA 750
QY 661 GCTGCTCTACCCACTACATGATGTTAA 688
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Db 751 GGGCGCTTCCACTACTACATGATGCTTAA 778

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RESULT 2
A1388926      649 bp      mRNA      linear      EST 19-APR-2001
LOCUS      A1388926
DEFINITION  GH19977.5prlme GH Drosophila melanogaster head pot2 Drosophila
              melanogaster cDNA GH19977.5prlme similar to U51050:
              Drosophila melanogaster alpha esterase (ae7) gene, partial cds,

ACCESSION   mRNA sequence.
VERSION     A1388926
KEYWORDS    GI:4202937
SOURCE      EST.
ORGANISM   fruit fly.
            Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 649)
AUTHORS    Harvey,D., Broksstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
            BDGP/HMI Drosophila EST Project
            Unpublished (2001)
TITLE       JOURNAL
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: 199 row: G column: 5
            High quality sequence stop: 559.
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                pOT2. Plasmid cDNA library."
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Query Match      16.5%; Score 282.4; DB 9; Length 649;
Best Local Similarity 66.4%; Pred. No. 3e-66;
Matches 422; Conservative 0; Mismatches 211; Indels 3; Gaps 1;

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Db 4 ATGGGGAATGATATGCGCGGATTAATTAAGAAATGATTTGTCGACGATAC 63
QY 491 AATATCTTTGGAGCTCTATGTTTCTAAGTTTAATTCAGAAACCTTAATGTGCCG 550
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Db 64 AGTACCGACTTGGGCTTTGGATTTATGATCTTAAGTCCCGGAGCTAAATGTACAG 123
QY 551 GTATATGCGGCTTAAAGATCAAGTATGCGCTTGTGATTAATAATTAATGCGGCA 610
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QY 611 ACTTGTGCAATCCGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 670
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Db 184 GTTTCGGGGAGATCCCACTGCTCTGTTTGTGAAGATGCTGGAGGCGCTTCCA 243
QY 671 CCCCATCATGATTTAATGCAAGCAACAACTGCGGCTTTTCCATCTGTTGATTAAT 730
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 CTCATCATATGATCTAAGCATGATCAGACCAAGGCTCTTCAATCCGGATGCTCAG 303
QY 731 CGGATATGATTTGTTCATTTGCTAATACC---AATTCACATGCTGCTTACCT 787
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QY 788 TAGCCAAATTTGGCGGCTTAAGAGTGAAGTGAATTAAGATGTTTGAATTTCTTA 847
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QY 848 TGAAGCAAGCCAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 907
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QY	968	GGTGTTCACCCCAACATCTCTCGGAAATGGTAAACTGCTTGGGCTAATTCGATACCA	1027
DB	544	GGTGTATATCCACAGCCTCCAAAGAGATGATGACACCGCTCGAGTAACTCATTCGCCA	603
QY	1028	CTATGATGGGTACACTTCATATAGAGGGCTATATTTT	1063
DB	604	TGTTATAGAAACACTTCGTACGAGCGCTGCTGT	639
RESULT 3			
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DEFINITION	AI403569	688 bp	linear EST 19-APR-2001
ACCESSION	GH23036.5	prime GH	Drosophila melanogaster head port2 Drosophila
VERSION	melanogaster cDNA clone GH23036	5prime	similar to U51050;
KEYWORDS	Drosophila melanogaster	alpha esterase (aE7) gene, partial cds,	
SOURCE	RNA sequence.		
ORGANISM	AI403569		
REFERENCE	AI403569.1	GI:4246656	
AUTHORS	EST.		
TITLE	fruit fly.		
JOURNAL	Drosophila melanogaster		
COMMENT	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
	1 (bases 1 to 688)		
	Harvey D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.		
	BDGP/HMT Drosophila EST Project		
	Unpublished (2001)		
	Contact: stapleton, M.		
	BDGP		
	Location: Berkeley National Lab		
	One Cyclotron Rd, Berkeley, CA 94720, USA		
	Fax: 510 486 6798		
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu		
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Best Local Similarity	65.4%;	Pred. No. 5.7e-62;	
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QY	61	AAGTTTAACTATTCGTTTAACCTACCATGAAACGGGTGCTAGCTGAAACTAATATGCG	120
DB	151	AAAGTCACACATATTCGCCAGTCGACCAATGAAACAGTTGTCCGACACGAGATACGCG	210
QY	121	AAAGTGAAGGCGGTTAAACGTTAACTGATGTCAGATGATCTTACTACGATTTGAGGT	180
DB	211	CAAGTGAAGGCGGTTAAACGTTAACTGATGTCAGATGATCTTACTACGATTTGAGGT	270
QY	181	ATACGCTACGCCAACCGCACCTGCGGTGAGCTGAGATTTAAAGCAACCCAGCGACCAACA	240

DB	Accession	Version	Source	Organism	Title	Journal	Comment
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Qy	241	CCCTGGGATGCTGTGCGCATTTGTCATCATTAAGATCAAGTCAGTCATTTATTTT	300				
Db	331	CCCTGGGAGCAGTTTCGCGACCTACGACCCGGAAGATTAAGCCCTCAGTGCAGTTTC	390				
Qy	301	ATTAAGGCGCAAGTGTGTGCTCAGAGCATTTGTCTATACCTAATGTCTATACGAATAT	360				
Db	391	GCTTCGATTAAGTATAGAGGGCTCCAGGACCTCCTCTATCTCAATGTGTACCAACAAT	450				
Qy	361	CTAATCCCGAATCAAGTCCCTTTAGTATACATCAATGATGGTGTGTTTATATAC	420				
Db	451	GTGAAGCCCGCAAGGCTCCCGGCTTAAAGTTTGGATTCACGAGGAGGCTTCATATAC	510				
Qy	421	GGTGAATAATCATGCTGATTTATGTATGCTCTGATTTATTTATTAAGATGTGTTG	480				
Db	511	GGCGAGGCAATCGGGAATGATATGCGCGGATTAATATGAAAGATGTTGTTC	570				
Qy	481	ATTAACTAATCAATATTCGTTTGGAGCTCTAGGCTTTCTAATTTAAATTCAGAGACCTT	540				
Db	571	GTACAGATACAGTACGAGCTTGGGGCTTTGGGATTTATGATGCTTAAGTCCCGGAGCTA	630				
Qy	541	AATGTGCGCGGATATGCGCGCTTAAAGTCAAGTCATGATGCGCTTGGCTTGAATATAA	598				
Db	631	AATGTACCAAGAAATGCTGCTCAAGATCAAGTGTGCGCTCAAGTGGATCAAGA	688				
RESULT 4							
LOCUS	A1517692	671 bp	mRNA	linear	EST 19-APR-2001		
DEFINITION	GH28740.5prine GH Drosophila melanogaster head por2 Drosophila						
ACCESSION	A1517692.1	GI:4420792					
VERSION	A1517692.1	GI:4420792					
KEYWORDS	EST.						
SOURCE	fruit fly.						
ORGANISM	Drosophila melanogaster						
REFERENCE	Eukaryota: Metazoa; Arthropoda: Hexapoda; Insecta: Pterygota:						
AUTHORS	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;						
	Ephydroidea; Drosophilidae; Drosophila.						
	1 (bases 1 to 671)						
	Harvey,D., Brockstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,						
	Lewis,S. and Rubin,G.M.						
	BDGP/HMI Drosophila EST project						
	Unpublished (2001)						
	Contact: Stapleton, M.						
	BDGP						
	Lawrence Berkeley National lab						
	One Cyclotron Rd. Berkeley, CA 94720, USA						
	Fax: 510 486 6798						
	Email: http://www.fruitfly.org/EST , estfruitfly@berkeley.edu						
	Plate: 287 row: D column: 4						
	High quality sequence stop: 538.						
	Location/Qualifiers						
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	/organism="Drosophila melanogaster"						
	/db_xref="taxon:7227"						
	/clone="GH28740"						
	/clone_lib="GH Drosophila melanogaster head por2"						
	/sex="male and female"						
	/dev_stage="adult"						
	/lab_host="DHS - alpha"						
	/note="Organ: head; Vector: por2; Site_1: EcoRI; Site_2:						
	XhoI; sized fractionated cDNAs were directly ligated into						
	POT2. Plasmid cDNA library."						
	BASE COUNT	155 a	170 c	193 g	153 t		
	ORIGIN						
	Query Match	15.1%	Score 258.2	DB 9	Length 671		
	Best Local Similarity	65.6%	Pred.No. 1.3e-59				

KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 674)
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Chape, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Mungall, C. J., Nuno, J., Pacleb, J., Pargass, V., Park, S., Phouanevong, S., Wan, K., Yu, C., Lewis, S. E., Celnik, S. and Rubin, G. M.
TITLE BDGP/HMI RH Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: RH.566 row: G column: 10
High quality sequence stop: 558.
Location/Qualifiers
1..674
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH56682"
/clone_lib="RH Drosophila melanogaster normalized Head p1C-1"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tona"
/note="Organ: head; Vector: p1C1. Site.1: XhoI. Site.2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
BASE COUNT 153 a 170 c 195 g 155 t 1 others
ORIGIN
Query Match 14.7%; Score 251.6; DB 13; Length 674;
Best Local Similarity 65.4%; Pred. No. 8.2e-58;
Matches 368; Conservative 0; Mismatches 195; Indels 0; Gaps 0;
OY 1 ATGATTTCAACGCTAGTTGATGAGAAATTAATGAACATTAATGATGAAT 60
DB 111 ATGATTAAGAACCTCGGCTTGTGGAGCGCTTGGCGGCTCAAAACCATCGAGCAT 170
OY 61 AAGTTTAAACTATCGTTTAACTACCAATGAACGGTGTAGTGAACATAATATGCG 120
DB 111 AAGTCAGCACTATCGGCTGAGCAGCAATGAACAGTTGTGCGGACAGAGTACGCG 230
OY 121 AAGTGAAGGCGTTAAAGCTTAACTGTAGATGATGATCTCTACTACAGTTTGAAGGT 180
DB 231 CAAGTGAAGGCGTATCAAGCTCTATCTCTACGATGTGCGCTTACTTACGTTTCAAGGT 290
OY 161 ATACCGTACGCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGACCCCGAGGACACACA 240
DB 291 ATCCCGTACGCCACCTCCGCTGGGTGGGAGTGGCGGTTAAAGCCCGCCAGAGGCCCAT 350
OY 241 CCGTGAAGTGTGCGGATGTGTCATCATTAAGATTAATGATGATGATGATTTT 300
DB 351 CCGTGAAGGCGTGTGCGGCTGAGGAGCTGCTCTATCTCAATGTGATGACCAACAT 470
OY 301 ATACGGGCAAAAGTGTGCGTCAAGATTTGCTATACCTAAGTGTCTATACGATAAT 360
DB 411 GCTTCGATTAAGTGAAGGCTCCGAGGAGCTGCTCTATCTCAATGTGATGACCAACAT 470
OY 361 CTAAATCCCGAACTAAAGCTCCCTTTTATATACATACATAGTGTGTTTATATATC 420
DB 471 GTGAAGCCCGACAAAGCTGCGCGGTTATGTTGATTCACGAGGAGGCTTCAATATC 530
OY 421 GGTGAATATCATCGTATATGATGTCTCTATTAATTCATTAAGAGATGTGTTG 480

DB 531 GCGAGGCCAATCGGGAATGATGCGCCGAGTTACTTATGAAGACATTTGTTC 590
OY 461 ATTAACATACATATATGCTTTGGAGCTCTAGTTTCTTAAGTTAAATTCAGAACCTT 540
DB 591 GTACAGATACATATACGACTTGGGCTTNGGATTAATGATGATTAAGTCCCGAGCTA 650
OY 541 ATGTGCCCGGTATGCGGCGCT 563
DB 651 AATGTACAGGAATGCTGGCT 673
RESULT 7
LOCUS B1635372 676 bp mRNA linear EST 10-SEP-2001
DEFINITION SD16705.5prine SD Drosophila melanogaster Schneider L2 cell culture
port2 Drosophila melanogaster cDNA clone SD16705 5 similar to
alpha-Est7: FBan0001112 GO: [carboxyesterase (GO:0004091);
carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5; 05/18/2001
mRNA sequence.
ACCESSION B1635372
VERSION B1635372.1 GI:15537582
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 676)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G. M.
TITLE BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: SD.167 row: A column: 5
High quality sequence stop: 641.
Location/Qualifiers
1..676
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="SD16705"
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/lab_host="DH5-alpha"
/note="Vector: port2; Site.1: EcoRI; site.2: XhoI. Sized fractionated cDNAs were directly ligated into port2. Plasmid cDNA library."
BASE COUNT 155 a 173 c 194 g 154 t
ORIGIN
Query Match 14.7%; Score 251; DB 13; Length 676;
Best Local Similarity 65.4%; Pred. No. 1.2e-57;
Matches 368; Conservative 0; Mismatches 195; Indels 0; Gaps 0;
OY 1 ATGATTTCAACGCTAGTTGATGAGAAATTAATGAACATTAATGATGAAT 60
DB 114 ATGATTAAGAACCTCGGCTTGTGGAGCGCTTGGCGGCTCAAAACCATCGAGCAT 173
OY 61 AAGTTTAAACTATCGTTTAACTACCAATGAACGGTGTAGTGAACATAATATGCG 120
DB 174 AAGTCAGCACTATCGGCTGAGCAGCAATGAACAGTTGTGCGGACAGAGTACGCG 233
OY 121 AAGTGAAGGCGTTAAAGCTTAACTGTAGATGATGATCTCTACTACAGTTTGAAGGT 180
DB 234 CAAGTGAAGGCGTATCAAGCTCTATCTCTACGATGTGCGCTTACTTACGTTTCAAGGT 293
OY 181 ATACCGTACGCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGACCCCGAGGACACACA 240

Db 294 ATCCGTCAGCCACCCCTCCGGTGGGGAGTTGCGGTTTAAAGCCCTGAGAGGCCCAT 353
 QY 241 CCTGGGATGATGTGCGGATGTTGCAATCATTAAGATAGTCAGTCAAGTGTATTT 300
 Db 354 CCTGGGAGGAGTTCGCGACTGCGAGCCGAGGAGATAGGCCGTCAGGTGAGTTC 413
 QY 301 ATAAACGGCAAGTGTGTGCTCAGAGATGTTCTATACCTAGTGTCTATACGATAT 360
 Db 414 GTCTTCGATAGAGTACAGGCTCCGAGGAGCTCCTCTATCTCATGTGATACCAACAT 473
 QY 361 CTAAATCCGGAACCTAAAGCTCCGCTTTTACTATACATAGTGTGTGTTTATTC 420
 Db 474 GTACAGCCCAACAGCTCGCCGCTTGTGATTCACGAGAGAGCTTCATATTC 533
 QY 421 GGTGAATATCATCTGATATGATGCTGCTGATATTTCAATTAAGAGATGTGTTG 480
 Db 534 GCGGAGCCCAATCGGAGATGTGTGCGGATTTACTTTATGAAGATATGTTGTTC 593
 QY 481 ATTAACATACATATGCTTTGGAGCTAGTCTTCTAAGTTTAAATTCAGAACCTT 540
 Db 594 GTACGATACATACGACTTGGGGCTTTGGATTTATGATCTTAAGTCCCGAGCTA 653
 QY 541 AATGTGCCCGTAATGCCGCT 563
 Db 654 AATGTACAGGAATGCTGCT 676
 RESULT 8
 B1614181 673 bp mRNA linear EST 07-SEP-2001
 LOCUS B1614181
 DEFINITION RH43493.5prime RH Drosophila melanogaster normalized Head pLIC-1
 Drosophila melanogaster cDNA clone RH43493.5 similar to alpha-Est7:
 FBan0001112 GO: [carboxylesterase (GO:0004091)] carboxylesterase
 (GO:0004091) located on: 3R 84D5-84D5:: 08/18/2001, mRNA sequence.
 B1614181
 ACCESSION B1614181 GI:15509706
 VERSION EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 673)
 Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
 J., Chame, M., Chavez, C., Dorsett, V., Farfan, D., Fitse, E., George
 R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miera, S.,
 Mungall, C.J., Nunoo, J., Pacle, J., Paragas, V., Park, S.,
 Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celinker, S. and Rubin
 G.M.
 BDGP/HMI RH Drosophila EST Project
 UNPUBLISHED (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
 Plate: RH.434 row: H column: 9
 High quality sequence stop: 553.
 Location/Qualifiers
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 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="RH43493"
 /clone_1bp="RH Drosophila melanogaster normalized Head
 pLIC-1"
 /sex="male and female"
 /dev_stage="adult"
 /lab_host="DHS-alpha Tona"
 /note="Organ: head; Vector: pLIC1; Site:1; XhoI; Site:2;
 BamHI; Library was kindly generated by Piero Carninci at
 the RIKEN. The library was normalized and excised using
 Cre recombinase. Plasmid cDNA library."

BASE COUNT 153 a 169 c 195 g 155 t 1 others
 ORIGIN
 Query Match 14.6%; Score 250; DB 13; Length 673;
 Best Local Similarity 65.2%; Pred. No. 2,2e-57;
 Matches 367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
 QY 1 ATGAATTTCAACCTTGGTTGATGAGAAATTAATAGAGATTAATGATTCGAAT 60
 Db 111 ATGAATTAAGAACTCGGCTTTGTGAGCCCTTGCGGCTCAACATCGAGCAT 170
 QY 61 AAGTTTAAACATATGCTTTAACTACCATGAACGCTGTGCTGAACATGATGAC 120
 Db 171 AAATCCAGAGATATCCGAGTACCAATGAAGAGTGTGCGACACGAGATAGCC 230
 QY 121 AAATGAAGAGCGTTAAAGCTTTAACTGTGATGATGATCTTCACTCAAGTTGAGGT 180
 Db 221 CAAGTGAAGGATATCAAGCTCTATCTCTAGATGTGCTCACTCAAGCTCGAGGT 290
 QY 181 ATACGTCAGCCCAACGCCAGTGTGAGCTGAGATTTAAACGACCCGACGACACA 240
 Db 291 ATCCGTCAGCCCAACGCCCTCGGTGGGAGTGTGCGTTAAAGGCTCCAGAGGCCATT 350
 QY 241 CCTGGGATGATGTGCGGATGTTGCAATCATTAAGATAGTCAAGTGTGATTTT 300
 Db 351 CCTGGGAGGAGTGTGCGGACTGACAGCCAGCGGAAGATTAAGGCGCTCCAGGTGCA 410
 QY 301 ATACGCGCAAGAGTGTGCTCAGAGAGATTTCTATACCTAAGTGTCTATAGAAATAT 360
 Db 411 GTCTTCGATTAAGTGAAGGCTCCGAGGAGCTCCTCTATCTCAATGTGTACCAACAT 470
 QY 361 CTAAATCCGGAACCTAAAGCTCCGCTTTTAACTATACATACATAGTGTGTTTATATC 420
 Db 471 GTGAACCCCGAAGAGCTGCGCGGTTATGTTGATTCACGAGAGGCGCTTATATC 530
 QY 421 GGTGAATATCATCTGATATGATGCTGCTGATTTTCAATTAAGAGATGTGTTG 480
 Db 531 GCGGAGCCCAATCGGGAATGTATGCGCGGATTTCTTATGAAGAAGATGTTGTC 590
 QY 481 ATTAACATACATATGCTTTGGAGCTAGTCTTCTAAGTTTAAATTCAGAACCTT 540
 Db 591 GTACGATACATACGACTTGGGGCTTTGGATTTATGATCTTAAGTCCCGAGCTA 650
 QY 541 AATGTGCCCGTAATGCCGCT 563
 Db 651 AATGTACAGGAATGCTGCT 673
 RESULT 9
 B1639486 660 bp mRNA linear EST 10-SEP-2001
 LOCUS B1639486
 DEFINITION SD22067.5prime SD Drosophila melanogaster Schneider I2 cell culture
 POT2 Drosophila melanogaster cDNA clone SD22067.5 similar to
 alpha-Est7: FBan0001112 GO: [carboxylesterase (GO:0004091)]
 carboxylesterase (GO:0004091) located on: 3R 84D5-84D5:: 05/19/2001
 mRNA sequence.
 B1639486
 ACCESSION B1639486 GI:15541696
 VERSION EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 660)
 Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S. and Rubin, G.M.
 BDGP/HMI Drosophila EST Project
 UNPUBLISHED (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA

Db 471 GTGAAGCCGAGAGGCTCGCCGGTTATGTTGGATTTCACGAGAGGCTTCATTATC 530

QY 421 GGTAATAATCATCGTATGATATGATGCTGATTTATTTATTAAGATGCGTGG 480

Db 531 GCGAGAGCCCAATCGGAATGATATGCGCCGATTTACTTATGAAAGATGTTGTTTC 590

QY 481 ATTACATACATATGATGTTGGAGCTAGGTTTCTAAGTTTAATTCAGAGACCTT 540

Db 591 GTACAGTACAGTACGAGCTTGGCGTTTATGATGCTTAAGTCCCGGAGCTA 650

QY 541 AATGTCCCGGTAATGCCGCC 562

Db 651 AATGTACCAAGAAATGCTGCC 672

RESULT 11

Bi233202 670 bp mRNA linear EST 11-JUL-2001

LOCUS RE29491.5prlme RE Drosophila melanogaster normalized Embryo pFlc-1

DEFINITION Drosophila melanogaster cDNA clone RE29491 5 similar to alpha-EST7: FBan0001112 located on: 3R 84D5-84D5; 04/12/2001, mRNA sequence.

ACCESSION Bi233202

VERSION Bi233202.1 GI:14700784

KEYWORDS EST

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

AUTHORS Stapleton, M., Brokslein, P., Hong, L., Tyler, D., Bertman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouaneavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin, G. M.

TITLE BDGP/HMI RE Drosophila EST Project

JOURNAL Unpublished (2001)

COMMENT Contact: Stapleton, M.

BDGP Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Plate: RE 294 row: H column: 7

High quality sequence stop: 534.

FEATURES

source

1..670

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="RE29491"

/clone_lib="RE Drosophila melanogaster normalized Embryo pFlc-1"

/sex="male and female"

/dev_stage="0-24 hours mixed stage embryonic"

/lab_host="DHS-alpha Tona"

/note="Organ: embryo; Vector: pFlc1, Site_1: XhoI, Site_2: BamHI. Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

BASE COUNT 152 a 168 c 194 g 155 t 1 others

ORIGIN

Query Match 14.5%; Score 248; DB 13; Length 670;

Best Local Similarity 65.1%; Pred. No. 7.9e-57;

Matches 365; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 1 ATGATTTCAACGCTAGTTGATGAGAAATTAATGAACATTAATGCATTGAAT 60

Db 110 ATGATTAAGAACCTTCGCTTGTGGAGCGCTTGCGCGCTCAAAAACCTTCGAGCAT 169

QY 61 AAGTTTAACTATCGTTTAACTACCAATGAACGGTGTAGCTGAACATGATATGCC 120

Db 170 AAAGTCACAGATATGCCAGTCGACCAATGAACAGTTGTGCGGACAGGAGTACGCC 229

QY 121 AAAGTAAAGCGCTTAACGTTTAACGTGTAGATGATTCCTACTACGTTTAGGCT 180

Db 230 CAAGTAGGGGATACAGGCTATCTCTCTAGAGATGCCCTACTACGCTTCAGAGGT 289

QY 181 ATACCGTAGCCCAACCGCCAGTGGTGAAGTGAAGTGAAGCAACCCAGACCAACA 240

Db 290 ATCCGTACGCCACGCTCCGGTGGGAGTTGCGGTTTAAGCCCTCAGAGGCCATT 349

QY 241 CCCTGGATGTGTGCGCGATTTTGCAATCATTAAGATAGTCAGTCAAGTATT 300

Db 350 CCTGGGAGCGAGTTCCGACAGCCAGCCAGAGATGAAGCCGTCAGGTGAGTT 409

QY 301 ATAACGGCAAGTGTGTGCTCAGAGATGTCTATACCTAAGTGTATAGCAATAT 360

Db 410 GTCTTCGATTAAGGTAGAGGCTCCAGAGACTGCTCTATCTCAATGTACCAACAT 469

QY 361 CTAAATCCCGAAACTTAACGCTCCGTTTATGATATCATATCATGCTGTTTATTATC 420

Db 470 GTGAAGCCCGAACAAGGCTCGCCGGTTATGTTGATTCACGAGAGAGGCTTCATTATC 529

QY 421 GGTAATAATCATCGTATGATATGATGCTGCTGATTTATTTATTAAGATGCTGTTG 480

Db 530 GCGAGGCCAATCGGAATGATGCGCCGATTTACTTATGAAAGATGTTGTTCTC 589

QY 481 ATTACATACATATGCTTTGGAGCTAGGTTTCTTAAGTTTAATTCAGAACACTT 540

Db 590 GTACAGTACATACGACTTGGCGTTTGGAGTTTATGAGTCTTAAGTCCCGGAGCTA 649

QY 541 AATGTCCCGGTAATGCCGCC 561

Db 650 AATGTACCAAGAAATGCTGCC 670

RESULT 12

At113763 648 bp mRNA linear EST 19-APR-2001

LOCUS GH10213.5prlme GH Drosophila melanogaster head pot2 Drosophila

DEFINITION melanogaster cDNA clone GH10213 5prlme similar to u51050: Drosophila melanogaster alpha esterase (aef) gene, partial cds, mRNA sequence.

ACCESSION At113763

VERSION At113763.1 GI:3514566

KEYWORDS EST

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

AUTHORS Harvey, D., Brokslein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G. M.

TITLE BDGP/HMI Drosophila EST Project

JOURNAL Unpublished (2001)

COMMENT Contact: Stapleton, M.

BDGP Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Plate: 102 row: B column: 1

High quality sequence stop: 435.

FEATURES

source

1..648

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="GH10213"

/clone_lib="GH Drosophila melanogaster head pot2"

/sex="male and female"

/dev_stage="adult"

/lab_host="DHS - alpha"

/note="Organ: head; Vector: pot2; Site_1: EcoRI; Site_2:

VERSION A1109901.1 GI:3478225
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 646)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S., and Rubin, G.M.
TITLE BDGP/HHMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: 92 row: H column: 8
High quality sequence stop: 513.
Location/Qualifiers
1..646
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH09292"
/clone_1lb="GH Drosophila melanogaster head POT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: POT2; Site:1: EcoRI; Site:2:
XhoI; Sized fractionated cDNAs were directly ligated into
POT2. Plasmid cDNA library."
BASE COUNT 152 a 163 c 182 g 149 t
ORIGIN
Query Match 14.3%; Score 245; DB 9; Length 646;
Best Local Similarity 65.0%; Pred. No. 5.2e-56;
Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;
1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATAAGGAGTAAATGCAATGGAAT 60
89 ATGAATAGAACCTCGCTTTGTGTGGCGCTGCGTGGCGCTCAAAACATCGAGCAT 148
61 AAGTTTAACTATGCTTTAACTACCAATGAAGCGTGTAGCTGAACATGATATGCC 120
149 AAGTCCAGCAGTATGCCAGTCGACCAATGAACAGTTGTGCGGACACGAGATCGCG 208
121 AAGTGAAAGCGTTAAAGCTTTAACTGTGTACGATGATTTCTACTACAGTTTGAGGT 180
209 CAGGTAGGGGTATCAAGCGTCTATCTCTACGATGTCCTTACTTTCAGCTTCAGGGT 268
181 ATACCGTACCCCAACCGCGAGTGGGAGCTGAGATTAAAGCACCCGAGCAGACACA 240
269 ATCCGTCAGCCCGCTCGGTGGGAGGAGTTGCGTTAAAGCCCTCAGAGGCCCAT 328
241 CCCTGGATGTGTGCCGATTTGTCATCAATGAAGTAAAGTCACTGCAAGTGTATTT 300
329 CCGTGGGAGCGATTCGCGACTGACGACCCGAGAGGATGAGCCGCGCAGGTGCG 368
301 ATACGGGCAAGTGTGTGGCTGAGAGATTGTCTATACCTAAGTGTCTATACGAAT 360
389 GTCTTCGATGAAGTAGAGGCTCCGAGAGTCTCTATCTCATATGTGTACACCAAT 448
361 CTAAATCCCGAAGTAAAGCTCCGTTTAACTATACATACATGTTGTTTATATATC 420
449 GTGAAGCCCGAAGAGCTCGCCCGTTATGTTGATTCACGAGAGGCTTCATATATC 508
421 GGTGAATATCATGCTGATATGATGCTGATTTATTTCAATTAAGAGTGTGTTCG 480
509 GCGGAGCCCAATCGGGAATGATGGCCGATTAATTAAGAAAGATGTGTCTC 568
481 ATTACATCATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAATTCGAAGACCTT 540

DB 569 CTCAGATACAGTACGACTGGGGCTTTGGATTATAGCTTTAAGTCCCGCAGACTA 628
QY 541 AATGTCGGCGGTAATGC 557
DB 629 AATGTACCAAGAAATGC 645
RESULT 15
A1293416 646 bp mRNA linear EST 19-Apr-2001
LOCUS LP06524.5prime LP Drosophila melanogaster larval-early pupal POT2
DEFINITION Drosophila melanogaster cDNA clone LP06524 5prime similar to
US1050: Drosophila melanogaster alpha esterase (AE7) gene, partial
cds, mRNA sequence.
ACCESSION A1293416
VERSION A1293416.1 GI:3942823
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 646)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S., and Rubin, G.M.
TITLE BDGP/HHMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: 65 row: B column: 12
High quality sequence stop: 493.
Location/Qualifiers
1..646
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="LP06524"
/clone_1lb="LP Drosophila melanogaster larval-early pupal
POT2"
/sex="male and female"
/dev_stage="larvae-pupae"
/lab_host="DH5 - alpha"
/note="Organ: whole body; Vector: POT2; Site:1: EcoRI;
Site:2: XhoI; Sized fractionated cDNAs were directly
ligated into POT2. Plasmid cDNA library."
BASE COUNT 151 a 163 c 184 g 148 t
ORIGIN
Query Match 14.3%; Score 245; DB 9; Length 646;
Best Local Similarity 65.0%; Pred. No. 5.2e-56;
Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;
1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATAAGGAGTAAATGCAATGGAAT 60
89 ATGAATAGAACCTCGCTTTGTGTGGCGCTGCGTGGCGCTCAAAACATCGAGCAT 148
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209 CAGGTAGGGGTATCAAGCGTCTATCTCTACGATGTCCTTACTTTCAGCTTCAGGGT 268
181 ATACCGTACCCCAACCGCGAGTGGGAGCTGAGATTAAAGCACTTCAGAGCCACA 240
269 ATCCGTCAGCCCGCTCGGTGGGAGGAGTTGCGTTAAAGCCCTCAGAGGCCCAT 328
241 CCCTGGATGTGTGCCGATTTGTCATCAATGAAGTAAAGTATGATGCAAGTTGATTT 300

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GenCore version 5.1.4.p5 4578
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:41:37 ; Search time 40.5118 Seconds
(without alignments)
12967.505 Million cell updates/sec

Title: US-09-776-910-3

Perfect score: 1713
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1713	100.0	1713	US-09-068-960-3	Sequence 3, Appl
2	1711.4	99.9	1713	US-09-068-960-9	Sequence 9, Appl
3	1709.8	99.8	1713	US-09-068-960-1	Sequence 1, Appl
4	1706.6	99.6	1713	US-09-068-960-5	Sequence 5, Appl
5	1701.8	99.3	1713	US-08-669-524-1	Sequence 1, Appl
6	1701.8	99.3	1713	US-09-068-960-7	Sequence 7, Appl
7	1676.6	97.9	1713	US-08-669-524-2	Sequence 2, Appl
8	955	55.8	1713	US-09-068-960-14	Sequence 14, Appl
9	178	10.4	1584	US-08-747-221B-51	Sequence 52, Appl
10	178	10.4	1584	US-08-747-221B-52	Sequence 52, Appl
11	178	10.4	1584	US-09-005-051-51	Sequence 51, Appl
12	178	10.4	1584	US-09-005-051-52	Sequence 52, Appl
13	178	10.4	2007	US-08-747-221B-36	Sequence 36, Appl
14	178	10.4	2007	US-08-747-221B-38	Sequence 38, Appl
15	178	10.4	2007	US-09-005-051-36	Sequence 36, Appl
16	178	10.4	2007	US-09-005-051-38	Sequence 38, Appl
17	143.8	8.4	1590	US-08-747-221B-23	Sequence 23, Appl
18	143.8	8.4	1590	US-09-005-051-23	Sequence 23, Appl
19	143.8	8.4	1650	US-08-747-221B-21	Sequence 21, Appl
20	143.8	8.4	1650	US-08-747-221B-22	Sequence 22, Appl
21	143.8	8.4	1650	US-09-005-051-21	Sequence 21, Appl
22	143.8	8.4	1650	US-09-005-051-22	Sequence 22, Appl
23	143.8	8.4	1792	US-08-747-221B-18	Sequence 18, Appl
24	143.8	8.4	1792	US-08-747-221B-20	Sequence 20, Appl
25	143.8	8.4	1792	US-09-005-051-18	Sequence 18, Appl
26	143.8	8.4	1792	US-09-005-051-20	Sequence 20, Appl
27	140.2	8.2	1650	US-08-747-221B-60	Sequence 60, Appl

C	28	140.2	8.2	1650	3	US-08-747-221B-61	Sequence 61, Appl
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C	36	139.6	8.1	1515	3	US-08-747-221B-17	Sequence 17, Appl
C	37	139.6	8.1	1515	4	US-09-005-051-16	Sequence 16, Appl
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C	40	139.6	8.1	1982	3	US-08-747-221B-15	Sequence 15, Appl
C	41	139.6	8.1	1982	4	US-09-005-051-13	Sequence 13, Appl
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C	43	88.8	5.2	1694	3	US-09-136-421-11	Sequence 11, Appl
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C	45	88.8	5.2	2989	1	US-08-453-323-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-068-960-3
Sequence 3, Application US/09068960A
Patent No. 6235515

GENERAL INFORMATION:

APPLICANT: Commonwealth Scientific and Industrial Rarch. Org.

TITLE OF INVENTION: MALATHION CARBOXYESTERASE

FILE REFERENCE: Attorney Docket No. 6235515 50179-051

CURRENT APPLICATION NUMBER: US/09/068,960A

CURRENT FILING DATE: 1998-05-20

EARLIER APPLICATION NUMBER: PCT/AU96/00746

EARLIER FILING DATE: 1996-11-22

EARLIER APPLICATION NUMBER: AU 6751

EARLIER FILING DATE: 1995-11-23

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 3

LENGTH: 1713

TYPE: DNA

ORGANISM: Lucilia cuprina

US-09-068-960-3

Query Match

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	ATGATTTTCAACGTTAGTTGATGAGAAATTAAGAAATTAATGATGAAAT	60
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DB	61	AAAGTTTAACTATCTTTAACTACCAATGAACGGTGTGAGTGAACATGATATG	120
QY	121	AAAGTTTAACTATCTTTAACTACCAATGAACGGTGTGAGTGAACATGATATG	180
DB	121	AAAGTTTAACTATCTTTAACTACCAATGAACGGTGTGAGTGAACATGATATG	180
QY	181	ATACCGTACGCGCAACGCGGAGTGTGAGTGAATTAAGCAACCCAGGACACCA	240
DB	181	ATACCGTACGCGCAACGCGGAGTGTGAGTGAATTAAGCAACCCAGGACACCA	240
QY	241	CCCTGGATGCTGTGCGGATTTGCAATCAATGAATGAATGATGATGATTTT	300
DB	241	CCCTGGATGCTGTGCGGATTTGCAATCAATGAATGAATGATGATGATTTT	300
QY	301	ATAACGGGCAAGGTGTGCTGCTGAGAGGATTTGCTATACCTAAGTGTCTAATAT	360
DB	301	ATAACGGGCAAGGTGTGCTGCTGAGAGGATTTGCTATACCTAAGTGTCTAATAT	360


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DB 361 CTAATTCGCCAAGCTAAGCTCCGTTTGTAGTATACATGATGGTGGTTTATTATC 420
QY 421 GGTGAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 421 GGTGAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 481 ATTAACATACATATGCTTTGGGAGCTCTAGGTTTCTAGTTTAAATTCAGAGACT 540
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DB 721 ATACTATGCGGGTATGCTATTTGTCATTTGGCTAATACCAATGTCACATCGTGC 780
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DB 781 TTACCTTACCAATTTGGCGGCTATTAAGGCTGAGGATTAATGATGATGATTTGGA 840
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DB 841 TTCTCTATGAAGCCCAAGCCACAGGATTTATTAACCTTGAGGAAAAAGTTTAACTTA 900
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RESULT 2
US-09-068-960-9
; Sequence 9, Application US/09068960A
; Patent No. 623515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 623515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068, 960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-9

Query Match 99.9%; Score 1711.4; DB 4; Length 1713;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 841 TTCTTTAAGAACCAACACACAGATTTAATAAATCTGAGAAAGTTTAACTTA 900
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Db 901 GAAGAGGCTACAAATTAAGGTATGTTTCTTTGCTCCACTGTTGAGCCATACAGAC 960
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RESULT 3
US-09-068-960-1
; Sequence 1, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ. ID NOS: 43
; SOFTWARE: Patentln Ver. 2.0
; SEQ. ID NO. 1
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-1

Query Match 99.8%; Score 1709.8; DB 4; Length 1713;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1711; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1261 TTCTGGTCCCATGATGCTTGTGCAATTAAGTTCATACACTCCGCTGACACC 1320
Qy 1321 GTCTACTGATGCTGTCGATCTGATGGAAGATCTTATCAATCCCTATGATATG 1380
Db 1321 GTCTACTGATGCTGTCGATCTGATGGAAGATCTTATCAATCCCTATGATATG 1380
Qy 1381 CGTAGTGAAGTGTGTTAAGGTTAGTCACTGATGATTAACCTATTTCTTGG 1440
Db 1381 CGTAGTGAAGTGTGTTAAGGTTAGTCACTGATGATTAACCTATTTCTTGG 1440
Qy 1441 AATCAATGCGCAAGCTATGCTTAAAGATGCGTGAATACAAACATTTGAGCTAG 1500
Db 1441 AATCAATGCGCAAGCTATGCTTAAAGATGCGTGAATACAAACATTTGAGCTAG 1500
Qy 1501 ACTGCTATGATACAAATTTGGCAGCACTGATTAATCTTTATAGCAATGAAGCT 1560
Db 1501 ACTGCTATGATACAAATTTGGCAGCACTGATTAATCTTTATAGCAATGAAGCT 1560

Qy 1561 ATGGAATATGTTCTGGGATCCATTAAGAAATCCGATGAGTATACAGTGTGAT 1620
Db 1561 ATGGAATATGTTCTGGGATCCATTAAGAAATCCGATGAGTATACAGTGTGAT 1620
Qy 1621 ATTAGATGAATGAATGAATGATGATGCTGATTAAGTAAATGAATGAATGAG 1680
Db 1621 ATTAGATGAATGAATGAATGATGATGCTGATTAAGTAAATGAATGAATGAG 1680
Qy 1681 TCGATGTTGAAAAACATAGATTTATTTAG 1713
Db 1681 TCGATGTTGAAAAACATAGATTTATTTAG 1713

RESULT 4
US-09-068-960-5
; Sequence 5, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-5

Query Match 99.6%; Score 1706.6; DB 4; Length 1713;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAAGGAAATTAATGCAATGAAT 60
Db 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAAGGAAATTAATGCAATGAAT 60
Qy 61 AAGTTTAACTATGCTTAACTACCAATGAACGCTGAGTGAATGATGATGAT 120
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Db 121 AAAGTAAAGCGGTTAAACGTTAACTGTTGATGATGATGATGATGATGAT 180
Qy 181 ATACCTAGCCCAACCGCAGTGGTGAATGATGATGATGATGATGATGATGAT 240
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Qy 241 CCCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
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Qy 301 ATACGGGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db 301 ATACGGGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Qy 361 CTAATATCCGAATTAAGCTCCGTTTATGATATCAATCAATGATGATGATGAT 420
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Qy 421 GGTGAAATATCGTGAATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 421 GGTGAAATATCGTGAATGATGATGATGATGATGATGATGATGATGATGAT 480
Qy 481 ATTAACATACATATGTTGGAGCTAGGTTTCTAAGTTTAAATTCAGAAAGCT 540

QY 181 ATACCGTACGCCCAACCCGAGTGGGTGAGCTGAGATTTTAAAGCACCCAGGACCACACA 240
 Db 181 ATACCGTACGCCCAACCCGAGTGGGTGAGCTGAGATTTTAAAGCACCCAGGACCACACA 240
 QY 241 CCCTGGGATGGTGGCGGATTTGTCAGATCAATAAGATGAATGATGATGATTTT 300
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 QY 301 ATAAAGGCAAGTGTGGCTCAGAGATGTGTATACCTAAGTGTATACAGATATAT 360
 Db 301 ATAAAGGCAAGTGTGGCTCAGAGATGTGTATACCTAAGTGTATACAGATATAT 360
 QY 361 CTAAATCCCGAAAGCTAACGTCGGTTTATATACATACATACATGATGATTTATATC 420
 Db 361 CTAAATCCCGAAAGCTAACGTCGGTTTATATACATACATACATGATGATTTATATC 420
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 Db 421 GGTGAAATCATGATGATATGATGATGATGATGATGATGATGATGATGATGATG 480
 QY 481 ATTAACATACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
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 Db 601 AATGTCGGCGGTATGCGGCGCTTAAAGATCAAGTATGCGCTTGGATTTAAAT 660
 QY 661 GCTGCTCTACCCACTACATGATGATGATGATGATGATGATGATGATGATGATG 720
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 QY 721 ATACTATGTCGGGTATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 Db 721 ATACTATGTCGGGTATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 QY 781 TTACCTTTAGCCAAATTTGCGGCTATAGGATGATGATGATGATGATGATGATG 840
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QY 1261 TTTGCTTCCCATGATCGTTTGTTCATATACCTTACACACCTCGGTACACC 1320
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 QY 1441 AATCAATTTGCGCAACCTAATGCTAAGAAATGCGGTGAATACAAACATTTAAGCTATG 1500
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 QY 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
 Db 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
 QY 1561 ATGGAATAATGTTTCTGGGATCCAAATTAAGAATCCGATGAATATACAAGTGTGAAAT 1620
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 QY 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 Db 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 QY 1681 TCGATGTTGAAAACATAGATGATGATGATGATGATGATGATGATGATGATG 1740
 Db 1681 TCGATGTTGAAAACATAGATGATGATGATGATGATGATGATGATGATGATG 1740

RESULT 6
 US-09-068-960-7
 ? Sequence 7, Application US/09068960A
 ? Patent No. 6235515
 ? GENERAL INFORMATION:
 ? APPLICANT: Commonwealth Scientific and Industrial Rerch. Org.
 ? TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
 ? FILE REFERENCE: Attorney Docket No. 6235515 50179-051
 ? CURRENT APPLICATION NUMBER: PCT/AU96/00746
 ? EARLIER FILING DATE: 1998-05-20
 ? EARLIER FILING DATE: 1996-11-22
 ? EARLIER APPLICATION NUMBER: AU 6751
 ? NUMBER OF SEQ ID NOS: 43
 ? SOFTWARE: PatentIn Ver. 2.0
 ? SEQ ID NO 7
 ? LENGTH: 1713
 ? TYPE: DNA
 ? ORGANISM: Lucilia cuprina
 US-09-068-960-7

Query Match 99.3%; Score 1701.8; DB 4; Length 1713;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATCAATTTCAACGTTAGTTGATGAGAAATTTAAATGGAAGATTAATGATGAAAT 60
 Db 1 ATCAATTTCAACGTTAGTTGATGAGAAATTTAAATGGAAGATTAATGATGAAAT 60
 QY 61 AAGTTTAACTATCGTTTAACTACCAATGAACGCGTGTAGTGAACATGAATATGCG 120
 Db 61 AAGTTTAACTATCGTTTAACTACCAATGAACGCGTGTAGTGAACATGAATATGCG 120
 QY 121 AAGTGAAGAGCGTTAAACGTTTAACTGTGTACATGATGATGATGATGATGATG 180
 Db 121 AAGTGAAGAGCGTTTAAACGTTTAACTGTGTACATGATGATGATGATGATGATG 180
 QY 181 ATACCGTACGCCCAACCCGAGTGGGTGAGCTGAGATTTTAAAGCACCCAGGACCACACA 240

Db 181 ATACGCAACGCCCAACGCCGAGTGGTGAAGCTTAAAGCAACCCACGACCAACA 240
 Qy 241 CCCTGGATGGTGGCGGATGTTGCAATCATAAAGATAGAGTGCAGAGTATGATTT 300
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 Db 301 ATACGGGCAAAAGTGTGGCTCAGAGATGCTATACCTAAGTGTCTATACCAATAT 360
 Qy 361 CTAATCCCGCAAACTAAACGTCCTGTTTACATACATACATGCTGCTTTATATC 420
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 Db 661 GCTGCTCTACCACTACATGATGATTAACGCAACAACTCGGCTCTTCCATCGTGT 720
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 Db 721 ATACTAATGTCGGTAACTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
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 Db 841 TTCTTATGAAGCAAGCCACAGATTTTAAACTTGAGGAAAGTTTAACTGTA 900
 Qy 901 GAAGAGGCTACAAATTAAGTATGCTTCTTGGTCCACTGTTGAGCCATACAGAC 960
 Db 901 GAAGAGGCTACAAATTAAGTATGCTTCTTGGTCCACTGTTGAGCCATACAGAC 960
 Qy 961 GCTGATGTCCTTACCCAAATCCTCGGAAATGTTAAACTGCTTGGGTAATTCG 1020
 Db 961 GCTGATGTCCTTACCCAAATCCTCGGAAATGTTAAACTGCTTGGGTAATTCG 1020
 Qy 1021 ATACCCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 Db 1021 ATACCCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
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 Db 1081 CAAATGCTATGCTTGAAGAAATGGAACCTGTGTCAATTTTGTCAGAGTGAATG 1140
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 Db 1141 GCTGATGCTGAAGCACCAGCCAGAGACCTTGAATGGTGTCTTAAATTAAGGCT 1200
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 Db 1201 CATGTTACAGAGAAACCAACAGCTGATTAATTTTATGATGCTGCTCAATCAT 1260
 Qy 1261 TTCTGTTCCCATGATGCTTGTGCAATTAAGTTCATTCACACCTCGGTACACCC 1320
 Db 1261 TTCTGTTCCCATGATGCTTGTGCAATTAAGTTCATTCACACCTCGGTACACCC 1320

Qy 1321 GTCTACTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
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 Db 1381 CGTAGTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
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 Db 1441 AATCAATTTGGCCAAACGATGCTTAAAGATGCGGTGATACAAACATTTGAACG 1500
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 Db 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
 Qy 1561 ATGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
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 Db 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
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 Db 1681 TCGATGTTGAAACATAGAGATTTTATTTTATG 1713
 RESULT 7
 US-08-669-524-2
 : Sequence 2, Application US/08669524
 : Patent No. 5843758
 : GENERAL INFORMATION:
 : APPLICANT: RUSSELL, Robyn J.
 : APPLICANT: NEMCOMB, Richard D.
 : APPLICANT: ROBIN, Geoffrey C.
 : APPLICANT: BOYCE, Thomas M.
 : APPLICANT: CAMPBELL, Peter M.
 : APPLICANT: PARKER, Anthony G.
 : APPLICANT: OAKESHOT, John G.
 : APPLICANT: SMYTH, Kerrie A.
 : TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
 : NUMBER OF SEQUENCES: 22
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lowe Price Leblanc & Becker
 : STREET: 99 Canal Center Plaza, Suite 300
 : CITY: Alexandria
 : STATE: Virginia
 : COUNTRY: USA
 : ZIP: 22314
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/669,524
 : FILING DATE:
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Price, Robert L.
 : REGISTRATION NUMBER: 22,685
 : REFERENCE/DOCKET NUMBER: 1451-021
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 703-684-1111
 : TELEFAX: 703-684-1124
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1713 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single


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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-669-524-2

Query Match      97.9%  Score 1676.6;  DB 2;  Length 1713;
Best Local Similarity 98.0%  Pred. No. 0;
Matches 1679;  Conservative 0;  Mismatches 34;  Indels 0;  Gaps 0;

QY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAGACATTAATGATGAAAT 60
DB 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAGACATTAATGATGAAAT 60
QY 61 AAGTTTAAATATATGTTAACTACCAATGAACGGTGTAGCTGAATATGCTG 120
DB 61 AAGTTTAAATATATGTTAACTACCAATGAACGGTGTAGCTGAATATGCTG 120
QY 121 AAGAGTAAAGGGGTTAAAGCTTAACTGTGATGATGATTCCTACTACAGTTTGAGGGT 180
DB 121 AAGAGTAAAGGGGTTAAAGCTTAACTGTGATGATGATTCCTACTACAGTTTGAGGGT 180
QY 181 ATACGGTACGCCCAACCGCCAGTGGGTGAGATTTAAAGCACCAGCCAGCCACAGA 240
DB 181 ATACGGTACGCCCAACCGCCAGTGGGTGAGATTTAAAGCACCAGCCAGCCACAGA 240
QY 241 CCCTGGGATGATGTCGGCATTGTTGCATCATTAAGATATAGTCAGATGATTTT 300
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DB 301 ATACGGGCAAGATGTCGTGCTCAGAGATTTCTATACCTAAGTGTCTATACGATTAAT 360
QY 361 CTAAATCCCGAAACTAAACGTCCTGTTTAACTATACATACATGATGATGATTAATC 420
DB 361 CTAAATCCCGAAACTAAACGTCCTGTTTAACTATACATACATGATGATGATTAATC 420
QY 421 GGTGAAATCATGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
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QY 481 ATTAACATATCATATGCTTTGGAGCTTACGTTTCTAAGTTTAAATTCAGAAAGCTT 540
DB 481 ATTAACATATCATATGCTTTGGAGCTTACGTTTCTAAGTTTAAATTCAGAAAGCTT 540
QY 541 AATGTCGCCGTAATGCGGCTTAAAGATCAAGTCATGCGCTTGGATTAATAAAT 600
DB 541 AATGTCGCCGTAATGCGGCTTAAAGATCAAGTCATGCGCTTGGATTAATAAAT 600
QY 601 AATGTCGCCGTAATGCGGCTTAAAGATCAAGTCATGCGCTTGGATTAATAAAT 660
DB 601 AATGTCGCCGTAATGCGGCTTAAAGATCAAGTCATGCGCTTGGATTAATAAAT 660
QY 661 GCTGCTTACCCACTACATCATGATGATGATGATGATGATGATGATGATGATGATG 720
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QY 781 TTACACCTTACCCAAATTTGCGGCTTAAAGGATGATGATGATGATGATGATGATG 840
DB 781 TTACACCTTACCCAAATTTGCGGCTTAAAGGATGATGATGATGATGATGATGATG 840
QY 841 TTTCTTATGAAAGCCAGCCAGATTTTAAATTAATTAATTAATTAATTAATTAAT 900
DB 841 TTTCTTATGAAAGCCAGCCAGATTTTAAATTAATTAATTAATTAATTAATTAAT 900
QY 901 GAAGAGCCGTACAATTAAGTTCATGTTTCTTTGCTCCAGCTGTTGAGCCATATCAGACC 960
DB 901 GAAGAGCCGTACAATTAAGTTCATGTTTCTTTGCTCCAGCTGTTGAGCCATATCAGACC 960
QY 961 GCTGATTTGCTTACCCAAACATCTCGGGAATGTTAAATCTGCTTGGGGTAAATTCG 1020

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DB 961 GCTGATTTGCTTACCCAAACATCTCGGGAATGTTAAATNTGCTGGGGTAAATTCG 1020
QY 1021 ATACCCACTATGATGCGGTAAACACTTATCATATGAGGGCTATATTTTCTACTCAATCTTAAG 1080
DB 1021 ATACCCACTATGATGCGGTAAACACTTATCATATGAGGGCTATATTTTCTACTCAATCTTAAG 1080
QY 1081 CAAATGCTATGCTTTTAAAGAAATGGAACCTTGTCAATTTTGTGCCAAGTGAATG 1140
DB 1081 CAAATGCTATGCTTTTAAAGAAATGGAACCTTGTCAATTTTGTGCCAAGTGAATG 1140
QY 1141 GCTGATGCTGAAGCCAGCCGCCAGAGACCTTGAATATGGGCTTAAATTAATTAAGGCT 1200
DB 1141 GCTGATGCTGAAGCCAGCCGCCAGAGACCTTGAATATGGGCTTAAATTAATTAAGGCT 1200
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DB 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTCAGATCTAT 1260
QY 1261 TTCTGTTCCCATGCTGATGCTTGTGCAATTAAGTTTCAATCAGCTCCGCTACACCC 1320
DB 1261 TTCTGTTCCCATGCTGATGCTTGTGCAATTAAGTTTCAATCAGCTCCGCTACACCC 1320
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DB 1621 ATTAGGANGAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
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DB 1681 TCGATGTTGAAAAACATGAGATTTATTTAG 1713

RESULT 8
US-09-068-960-14
; Sequence 14, Application us/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068, 960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Musca domestica
US-09-068-960-14

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Query Match 55.8%; Score 955; DB 4; Length 1710;
 Best Local Similarity 73.3%; Pred. No. 3,4e-268;
 Matches 1222; Conservative 0; Mismatches 445; Indels 0; Gaps 0;

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 QY 104 CTGAATGCAATGAAATGAAAGCGTTTAACTTAACTTAACTTAACTTAACTTAACT 163
 DB 104 TCGATACGAAATGAGCAAAATTAAGGTTTAAAGGTAATGCAATGCAATGCAATGCA 163
 QY 164 ACTACAGTTTGAAGGTTTACCGTACCGCCCAACCGCGTGGTGGTGGTGGTGGTGGT 223
 DB 164 ACTACAGTTTGAAGGTTTACCGTACCGCCCAACCGCGTGGTGGTGGTGGTGGTGGT 223
 QY 224 CACCCACGAGCAACACCGTGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 283
 DB 224 CACCCACGAGCAACACCGTGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 283
 QY 284 CAGTCAAGTTGATTTTAAACGGGCAAGTGTGGCTCAGAGATTTGTCTATACCTPA 343
 DB 284 CAGTCAAGTTGATTTTAAACGGGCAAGTGTGGCTCAGAGATTTGTCTATACCTPA 343
 QY 344 GTGCTATACGAAATTAATCCGAAACGTAACGTCGGTTTGTATATACATACAG 403
 DB 344 ATGTATATACCAATGACTTGAACCCAGCAAAAGCGTCTGTTATGTTTACATCCAG 403
 QY 404 GTGCTATATATATATCGGTGAAATCATCGTATATGATGATGATGATGATGATGAT 463
 DB 404 GTGCTATATATATATCGGTGAAATCATCGTATATGATGATGATGATGATGATGAT 463
 QY 464 AAAAGATGTGTGTGATTAACATACATATCGTTGGAGCTTACGTTTCTTAAGTT 523
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 QY 584 TGCCTGATTAATAAATAATGCGCAACTTGTGTGCAATCCGATATATATACAGTCT 643
 DB 584 TGCCTGATTAATAAATAATGCGCAACTTGTGTGCAATCCGATATATATACAGTCT 643
 QY 644 TTGCTGAAAGTCCGCTGCTTACCCACTACATGATGTTAAACCAAACTCCG 703
 DB 644 TTGCTGAAAGTCCGCTGCTTACCCACTACATGATGTTAAACCAAACTCCG 703
 QY 704 GTCTTTCCATCGGTGATTAATGATGCGGTAATGATGATGATGATGATGATGATGAT 763
 DB 704 GTCTTTCCATCGGTGATTAATGATGCGGTAATGATGATGATGATGATGATGATGAT 763
 QY 764 AATGTCACATCGTGCCTTACCTTACCAAAATTTGGCCGCTATTAAGGTTGAAGTAATG 823
 DB 764 AATGTCACATCGTGCCTTACCTTACCAAAATTTGGCCGCTATTAAGGTTGAAGTAATG 823
 QY 824 ATAAGATGTTTGAATTTCTTATGAAGCCACAGCAAGTAAATAAAGCTTGAG 883
 DB 824 ATAAGATGTTTGAATTTCTTATGAAGCCACAGCAAGTAAATAAAGCTTGAG 883
 QY 884 AAAAAGATATCTGGAATTTCTTAATGAAGCAAACTTATGATTTGATCAAAAGAGAGC 883
 DB 884 AAAAAGATATCTGGAATTTCTTAATGAAGCAAACTTATGATTTGATCAAAAGAGAGC 883
 QY 884 CACAAGTTTGAACACCCCAAAAGATGCAAAATTAAGGTATGTTTCTTTTGGACCCAGC 943
 DB 884 CACAAGTTTGAACACCCCAAAAGATGCAAAATTAAGGTATGTTTCTTTTGGACCCAGC 943
 QY 944 TTGACCATATACAGCCGCTGATGTTGTTTACCCCAACATCTTCCGGAATGTTTAA 1003
 DB 944 TTGACCATATACAGCCGCTGATGTTGTTTACCCCAACATCTTCCGGAATGTTTAA 1003
 QY 1004 CTGCTGGGGAATTTGATACCACTATGATGGTAAACATTTCAATATGAGGTCTATTTT 1063
 DB 1004 CTGCTGGGGAATTTGATACCACTATGATGGTAAACATTTCAATATGAGGTCTATTTT 1063

QY 1064 TCACCTCAATCTTAAAGCAAAATGCCATGCTTGTAAAGCAATTTGGAACCTTGTCAAT 1123
 DB 1064 CCAATTAATTTGCCAAACAAATATCCGAGGTTGTAAAGATTTGGAATCTGTGTGANT 1123
 QY 1124 TTGTGCCAAGTGAATTTGCTGATGCTGAACGACCCGCCAGACCTTGGAAATGGGTG 1183
 DB 1124 ATGTGCTTGGGAGTTGGCTGACATGAACGACGAGTCCCGGAAACCTGGAGAGGGCTG 1183
 QY 1184 CTAAATTAAGGCTCATGTTACAGAGAAACCAACGCTATATTTTATGATC 1243
 DB 1184 CCATTTGAAAAAGGCCCATGATGATGGGAAACACTATCTGATATATTTTATGAGC 1243
 QY 1244 TTTGCTCACATCTATTTTCTGCTTCCCATGATCGTTTGTGCAATTAATGCTTCAATC 1303
 DB 1244 TTTGCTCCTATTTCTATTTTCTTCCCTTCCCATGATCGTTTGTGCAATTAATGCTTCA 1303
 QY 1304 ACACCTCGGTACACCCGCTTCACTTGTATCGCTTGGTGGTGGTGGTGGTGGTGGT 1363
 DB 1304 ACACAGCTGGCAGCTCCATTTATTTGTAATGCTTGGATTTGATTTCCGAAGAAATTA 1363
 QY 1364 ATCCCTATCTATTTATGCTGATGACGATGCTGTTAAGGTTTATGCTATGCTATGANT 1423
 DB 1364 ACCCTATCTGATTTATGCTGATGACGATGCTGTTAAGGTTTATGCTATGCTATGANT 1423
 QY 1424 TAACCTATTTCTTGTGATCATGATGCGCAACGTAATGCTTAAAGATGCGTGAATCA 1483
 DB 1424 TAACCTATTTCTTGTGATCATGATGCGCAACGTAATGCTTAAAGATGCGTGAATCA 1483
 QY 1484 AAACATTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
 DB 1484 AAACATTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
 QY 1544 GCAATGAATTTGAAGTATGCAAAATTTCTTCTGGGATTCATTAAGAAATCCGATGAG 1603
 DB 1544 GCAATGAATTTGAAGTATGCAAAATTTCTTCTGGGATTCATTAAGAAATCCGATGAG 1603
 QY 1604 TATACAGGTTTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
 DB 1604 TATACAGGTTTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
 QY 1664 AGATTAAACATGAGTGCATGTTTGAAGAAACATGAGATTTATTT 1710
 DB 1664 AAATTAAACATGAGTGCATGTTTGAAGAAACATGAGATTTATTT 1710

RESULT 9
 US-08-747-221B-51
 : Sequence 51, Application US/08747221B
 : Patent No. 6063610
 : GENERAL INFORMATION:
 : APPLICANT: Silver, Gary W.
 : APPLICANT: Wisniewski, Nancy
 : TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
 : TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 : NUMBER OF SEQUENCES: 66
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Carol Talkington Verser, Ph.D.
 : ADDRESSEE: Heska Corporation
 : STREET: 1825 Sharp Point Drive
 : CITY: Fort Collins
 : STATE: Colorado
 : COUNTRY: USA
 : ZIP: 80525
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: Windows 95
 : SOFTWARE: Wordperfect for Windows, Version 7.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/747,221B
 : FILING DATE: No. 6063610e1, 1996
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:

Query Match	10.4%	Score 1/6;	DS 2;	Confer: 22
Best Local Similarity	56.1%	Pred. No. 4.9e-42;		
Matches 359; Conservative		0; Mismatches 275;	Indels 6;	Gaps 1.

RESULT 10
US-08-747-221B-52/C
; Sequence 52, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
;

Query Match	10.4%;	Score 178;	DB 3;	Length 1584;
Best Local Similarity	56.1%;	Pred. No. 4,9e-42;		
Matches 359; Conservative	0;	Mismatches 275;	Indels 6;	Gaps 1

[illegible]

TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-005-051-52

Query Match 10.4%; Score 178; DB 4; Length 1584;
Best Local Similarity 56.1%; Pred. No. 4.9e-42;
Matches 359; Conservative 0; Mismatches 275; Indels 6; Gaps 1;

QY 116 ATGCAAGAGGAGGCGGTTAAAGCTTTAACTGTGTCAGATGATCTCTACTACAGTTTG 175
DB 1556 AAGGTACTTTAAAGAGAGAGCAATTTAGTAAAAAGAAATGCTTCCATAGTTATT 1497
QY 176 AGGGTATACCGTACGCCCAACCGCCAGTGGTGAAGCTTAAAGCAACCCAGCGAC 235
DB 1496 CTGGAATTCATATGCCAAACCTCTGTAGTGTAGTATTAAGCCACCTCAACCTG 1437
QY 236 CAACACCCCTGGATGCTGCTCCGATTTGTCATCATTAAGATAAGTCACTGCAAGTTG 295
DB 1436 CAGAACCTTGGTCAGGTTCTTGTATGCTAAGTAAAGAGGAAATAGTTAGATCAGTAC 1377
QY 296 ATTTTAAACGGGCAAGTGTGCTCAGAGGATGCTATATCTAAGTCTTATACGA 355
DB 1376 ATTTTATTTAAATAATTTAAAGTAGGGCTGAAGATTGTTATACCTCAATGCTATGATC 1317
QY 356 ATATCTAAATCCCGAACTAAACGTCCTTTTAACTATACATACATGCTGCTGTTTAA 415
DB 1316 CAATAACATCAGAGAAATCACTCTTCAGTATGATGATGATGATGAGAGGCTTCT 1257
QY 416 TTATCGGTAAATCATCGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 475
DB 1256 TCTATGGATCTGGAATATGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1197
QY 476 TGTGATTAACATCAATATCGTTTGGAGCTCTAGTTTCTTAACTTAAATTCGAAG 535
DB 1196 TTTCTGTTACTTCAATTTATGATATGATGCTGCTGCTGCTGCTGCTGCTGCTG 1137
QY 536 ACCTTAATGCGCCGCTATGCGCGCTTAAAGATCAAGTCACTGCGCTGCTGCTGCTG 595
DB 1136 AA-----GCGCTGGCAATGTTGTTTATGATGATGATGATGATGATGATGATG 1083
QY 596 AAAATTAATGCGCACTTGTGCGCATCCGATATATTTACAGTCTTGTGGAAGTG 655
DB 1082 AAACAAATTTGATGATCTTGTGCTGATGACCCCAACAAATGATGATTTTGGAGATCAG 1023
QY 656 CCGGTGCTGCTCTACCACTACATGATGTTAAACGAAACCTGCGGCTCTTTCATC 715
DB 1022 CAGGTGCTGCAAGTGTTCATTTATGATGATGATGATGATGATGATGATGATG 963
QY 716 GTGCTTACTAATGCGGTAATGCTATTTGCCATGCG 755
DB 962 AAGCATCTCACAAGTGAAGTCTTTAATCCTTGGGC 923

RESULT 13
US-08-747-221B-36
Sequence 36, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS: Molecules, Proteins and Uses Thereof
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeka Corporation

STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610e1 December 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 11..1594
US-08-747-221B-36

Query Match 10.4%; Score 178; DB 3; Length 2007;
Best Local Similarity 56.1%; Pred. No. 5.5e-42;
Matches 359; Conservative 0; Mismatches 275; Indels 6; Gaps 1;

QY 116 ATGCAAGAGGAGGCGGTTAAAGCTTTAACTGTGTCAGATGATCTCTACTACAGTTTG 175
DB 39 AAGGTACTTTAAAGAGAGAGCAATTTAGTAAAAAGAAATGCTTCCATAGTTATT 98
QY 176 AGGGTATACCGTACGCCCAACCGCCAGTGGTGAAGCTTAAAGCAACCCAGCGAC 235
DB 99 CTGGAATTCATATGCCAAACCTCTGTAGTGTAGTATTAAGCCACCTCAACCTG 158
QY 236 CAACACCCCTGGATGCTGCTCCGATTTGTCATCATTAAGTCAAGTCAAGTTG 295
DB 159 CAGAACCTTGGTCAGGTTGCTTGTGATGCTAGTAAAGAGGAAATGCTGATCAGTAC 218
QY 296 ATTTTAAACGGGCAAGTGTGCTCAGAGATTTGCTATACCTAAGTGTCTATACGA 355
DB 219 ATTTTATTTAAATAATTTAAAGTAGGGCTGAAGATTGTTTATACCTCAATGCTATG 278
QY 356 ATATCTAATCCCGAACTAAACGTCCTTTTATGATATCAATGATGCTGCTGCTGTTTA 415
DB 279 CAATAACATCAGAGAAATCACTCTTCAGTATGATGATGATGATGATGATGATG 338
QY 416 TTATCGTAAATATCATGCTGATATGATGCTGCTGATATTTCTTAAAGAGATGCG 475
DB 339 TCATGGATCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATG 398
QY 476 TGTGATTAACATCAATATGCTTTGGAGAGCTTAAAGTCTTAAATTCAGAG 535
DB 399 TTTCTGTTACTTCAATATATGATGATGATGATGATGATGATGATGATGATGATG 458
QY 536 ACCTTAATGCGCCGCTATGCGCGCTTAAAGATCAAGTCACTGCGCTTGCCTGATTA 595
DB 459 AA-----GCGCTGGCAATGTTGTTTATGATGATGATGATGATGATGATGATG 512
QY 596 AAAATTAATGCGCACTTGTGCTGCAATCCGATATATTTACAGTCTTGTGGAAGTG 655
DB 513 AAACAAATTTGATGATCTTGTGCTGATGACCCCAACAAATGCTATTTTGGAGATCAG 572

NAME/KEY: CDS
LOCATION: 11..1594
US-09-005-051-36

Query Match 10 4%; Score 178; DB 4; Length 2007;
Best Local Similarity 56.1%; Pred. No. 5,5e-42;
Matches 359; Conservative 0; Mismatches 275; Indels 6; Gaps 1;

```
QY 116 ATGGCAAGTGAAGCGCTTAAACGTTTAACTGTACAGATGATCTTACTACAGTTTG 175
DB 39 AAGCTACTTAAAGAGAAAAGCAATTAAGAAAAAGAAATGTGTCATAGTATT 98
QY 176 AGGGTATACCGTACGCCCAACCGCCAGTGGAGCTGAGATTAAAGCACCAGCGAC 235
DB 99 CTGAATTCATATGCCAAACCTCGTAGGATCTTAAGATTAAAGCACCAGCGAC 158
QY 236 CAACACCCCTGGAGTGGTCCGCAATGTCATTAAGATAAGTCAAGTTG 295
DB 159 CAGAACCTTGTCAGGTCTTCTAGTAAAGAGAAATAGTTAGATCAGTAC 218
QY 296 ATTTTATACGGCAAGTGTGGCTCAGAGATGTCATACCTAAGTCTATACGA 355
DB 219 ATTTTATTAATAAATTAAGTAGAGGCTGAGATGTTTATACCTCAATGCTATGTC 278
QY 356 ATATCTTAATCCGAAACTAAAGTCCGTTTAACTATACATACATGTTGTTTA 415
DB 279 CAAAACATCAGAAATCACTTCTCAGTAATGATGATACATGGAGAGCTTCT 338
QY 416 TTATCGTGAATAATCATGATATGATATGATGATATTTTCAATTAAGAGATG 475
DB 339 TCATGGGATCTGAAATAGTATGATGATGATGATGATGATGATGATGATGATG 398
QY 476 TGTGATTAACATACATATGCTTTGGAGCTTAGTTTCTAAGTTTAAATTCAGAG 535
DB 399 TTCTGTTACTTCAATATGATAGTGTGTTGGATTTTGAACCTGGGAATGAG 458
QY 536 ACCTTAATGTGCGCGTATGCGGCTTAAAGATCAAGTCATGCGCTTGGTGA 595
DB 459 AA-----GCGCTGCAATGTTGTTGATGACCAAGCTTAATAATGGTAA 512
QY 596 AAAATTAATGCGCAACTTGGTGGCAATCCGATATATTAAGTCTTTGGTGAAG 655
DB 513 AAAACAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 572
QY 656 CCGTCTGCTCTTACCCCTACATGATGATGATGATGATGATGATGATGATG 715
DB 573 CAGGTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 632
QY 716 GTGATATACATATGCTGATGATGATGATGATGATGATGATGATGATGATG 755
DB 633 AAGGATCTCAAAAGTGAAGTCTTAAATCCTTGGGC 672
```

Search completed: April 11, 2003, 08:51:16
Job time : 46.5118 secs

Db 731 AATCCTAAAGTGTACTCTCTTGGAGAAAGTGCAGAGACGCTTC 777

```

RESULT 4
US-09-880-107-2271
% Sequence 2271, Application US/09880107
% Patent No. US20020142981A1
% GENERAL INFORMATION:
% APPLICANT: Horne, Darci T.
% APPLICANT: Vockley, Joseph G.
% APPLICANT: Scherf, Uwe
% APPLICANT: Gene Logic, Inc.
% TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
% FILE REFERENCE: 44921-5028-WO
% CURRENT APPLICATION NUMBER: US/09/880,107
% CURRENT FILING DATE: 2001-06-14
% PRIOR APPLICATION NUMBER: US 60/211,379
% PRIOR FILING DATE: 2000-06-14
% PRIOR APPLICATION NUMBER: US 60/237,054
% PRIOR FILING DATE: 2000-10-02
% NUMBER OF SEQ ID NOS: 3950
% SOFTWARE: PatentIn Ver. 2.1
% SEQ ID NO 2271
% LENGTH: 2381
% TYPE: DNA
% ORGANISM: Homo sapiens
% FEATURE:
% OTHER INFORMATION: Genbank Accession No. US20020142981A1 MI6474
US-09-880-107-2271

```

	Query Match	3.6%	Score 62.2;	DB 10;	Length 2381;
	Best Local Similarity	54.8%;	Pred. NO. 6e-06;		
	Matches 190;	Conservative 0;	Mismatches 148;	Indels 9;	Gaps 3.
DQ	325 GAGCATTTGCTATACCTTAAAGTCGTATACGAATAATCAATCCCGAACAATAAGCTGCC	384			
DQ	427 GAAGACGTATTATATCTAAATGTATGATGATCCAGCACCTTAACC---AAAAATGGCACT	483			
OY	385 GTTTTAGTATACATACATAGTGCTGGTTTTTATATCGTGAAAATCATCGTATATGAT	444			
DQ	484 GTATTGATATGATTTATGCTGCTGGTTTTTCMAACTGACATCATCTTTACATGTTAT	543			
OY	445 GGCTCTGTTTATTTTCATTAANAAGA---TGGGCTGTGATTAACATACATATCGTTTG	501			
DQ	544 GATGGCAAGTTTCTGGCTCGCGGTTGAAGAAGTATTATGTAGTGTCAATGAACATATAGGGTG	603			
OY	502 GGAGCTCAGGTTTTTCTAAGTTTAAATTCAGACAGCTTAATGTCGCCGATATACCGGC	561			
DQ	604 GGTCGCCATGAGATTCCTTAGCTTT---GGCAGAGAAATCCTGAGGCTTCAGAGAACATGSGT	660			
OY	562 CTTAAAGATCAAGTCATGACCTTGCTTGATTAATAAATAATTTGCGCCAATTTGGTGGC	621			
DQ	661 TTATTGTATCAACAGTGGCTCTTCAGTGGGCTCAAAAAAAAAATAATAGCAGCCCTTTGGTGA	720			
OY	622 AATCCGATATATATACAGTCTTTGGTGAAGATGCGCGCTGCGCTC	668			
DQ	721 AATCCTAAAGTGTACCTCTTTTGGAGAAATAATGAGAGGACGCTTC	767			

```

RESULT 5
US-09-748-739A-3
: Sequence 3, Application US/09748739A
: Patent No. US20020119489A1
: GENERAL INFORMATION:
:
: APPLICANT: Lockridge, Oksana
:
: TITLE OF INVENTION: Butyrylcholinesterase Variants and
: FILE REFERENCE: P-IX 4143
: CURRENT APPLICATION NUMBER: US/09/748,739A
: CURRENT FILING DATE: 2000-12-06
: NUMBER OF SEQ ID NOS: 31

```

```

: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 3
: LENGTH: 2416
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Human Butyrylcholinesterase variant
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (214)...(1935)
: US-09-748-739A-3

```

	Query Match	3.68;	Score 62.2;	DB 10;	Length 2416;
	Best Local Similarity	54.88;	Pred. No. 6e-06;		
	Matches 190;	Conservative	0;	Mismatches 148;	Indels 9;
					Gaps
QY	325	GAGCATTCGTCTATACCTTACGTAGTCTGTCTATPACGAATATCTAAATCCCGAAACTAAACGTCCC	384		
DB	481	GAAGACTGTCTTATATCTAAATGTATGTACATCCACACCTTAACC---AAAAAATGCCACT	537		
QY	385	GTTTACGATATACATACATACATGGTGGTGGTTTATTTATCGGTGAAATCATCGTGAATGTAT	444		
DB	538	GTATTTGAATATGGAATTTATGTGGTGGTTCCTAAACTGGAAATCATCTTTACATCAATTTAT	597		
QY	445	GGTCCTGATTTATTTTCATTTAAAAAGA---TGTGGTGTGATTAATACATACATATTCGTTTG	501		
DB	598	GATGGACAGTTTCTGGCTCGGGGTGAAAGACTTTTGTAGTGTCAATGAACCTATATAGGGTG	655		
QY	502	GGAGCTCTAGGTTTTCTTAAAGTTTAAATTCACAGAACCTTATATGACCCGGTAAATCCGGC	561		
DB	658	GGTGCCCTAGGATTTCTTAGCTT---GCCAGGAATCTGTAGGCTCCAGGGAAACATGGGT	714		
QY	562	CTTAAGATCAAGTCATGCGCTTGCCTTGCGATTGAATTAATAATATTCGCCACACTTTGGTGGC	622		
DB	715	TTATTTGTATCAACAGTTGGCTCTTCACGTGGCTTCAAAAAAATATATAGCAGCTTTGGTGGGA	774		
QY	622	AATCCCGATATATTTACAGTCTTTGGTGAATCCCGGTGCTGCTC	668		
DB	775	AATCTTAAGATGTATACCTCTTTTGGAGAAAGTACAGAGACAGCTTC	821		

```

RESULT 6
US-09-748-739A-5
Sequence 5, Application US/09/48739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockheed, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2416
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
NAME/KEY: CDS
LOCATION: (214)...(1935)
US-09-748-739A-5

```

	Query Match	3.6%	Score 62.2	DB 10	Length 2416
	Best Local Similarity	54.8%	Pred. No. 6e-06		
	Matches 190	Conservative 0	Mismatches 148	Indels 9	Gaps 3
OY	325	GAGCATGTCTTAACCTAGTGTCTATACGAATAACTTAATCCGGAACCTAACGTC	384		
db	481	GAAAGCTCTTATTAATCTTAATAGTATGATTCGAGCACTTAAC---AAAAATCCACT	537		


```

Db      775  AATCTTAAAAAGTAACTCTTTTGAGCAAGACTGCAGSAGCAGCTTC 821

RESULT 8
US-09-748-739A-16
/ Sequence 16, Application US/09748739A
/ Patent No. US20020119489A1
/ GENERAL INFORMATION:
/ APPLICANT: Lockridge, Oksana
/ TITLE OF INVENTION: Butyrylcholinesterase Variants and
/ TITLE OR INVENTION: Methods of Use
/ FILE REFERENCE: P-IX 4143
/ CURRENT APPLICATION NUMBER: US/09/748,739A
/ CURRENT FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16
/ LENGTH: 2416
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-748-739A-16

```

Query Match	3.6%	Score 62.2;	DB 10;	Length 2416;
Best Local Similarity	54.8%	Pred. NO. 6e-06;		
No. Mismatches	148;	Indels 9;	Gaps 3	

RESULT 9
 US-09-893-519A-112
 : Sequence 112, Application US/09893519A
 : Publication No. US20030027243A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: ANADIS PHARMACEUTICALS, INC.
 :
 : APPLICANT: THOMPSON, Craig
 :
 : APPLICANT: MOORE, Jeffrey
 :
 : APPLICANT: BUURMAN, Ed T.
 :
 : APPLICANT: BRADLEY, John
 :
 : APPLICANT: DESILVA, Thimara
 :
 : APPLICANT: HARRIS, Sandra
 :
 : APPLICANT: KOMARNITSKY, Svetlana
 :
 : APPLICANT: MENDILLO, Marc
 :
 : APPLICANT: MOORE, Daniel
 :
 : APPLICANT: MCCOY, Melissa
 :
 : APPLICANT: SANDERSON, Karen
 :
 : APPLICANT: HAO, Tariq
 :
 : APPLICANT: ZHU, Shuhao
 :
 : APPLICANT: LONG, Fan
 :
 : APPLICANT: DAVIDOV, Eugene


```

RESULT: 10
US-09-974-300-1107
; Sequence 1107, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085 500-US
; CURRENT APPLICATION NUMBER: US/09/974, 3000
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680, 598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279, 526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO: 1107
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-1107

```

	Query Match	Similarity	3.4%	Score	57.6:	DB	Length	2508;
	Best Local	Similarity	54.2%;	Pred.	9.7e-05			
	Matches	117;	Conservative	0;	Mismatches	99;	Indels	0;
							Gaps	0
OY	530	CAGAAACCTTAATGTGCCCCGGTAAATGCCGCCTTAAAGATCAAGTCATGGCCTTGCTT	589					
		" " " " " "	" " " " " "					
Db	671	CCGGGAGCCAGCGCTGCAGAAAGCAACTAATGAGGCTCCTGGACCAGATCCAGGCCCTCGCT	730					
OY	590	GGATTAAAAATAATTTGGCCCACTTTGGTGGCAATCCCAGATATATATACAGTCTTGGTG	649					
		" " " " " "	" " " " " "					
Db	731	GGCTCAGTGAAGAACATCGCCACTTTGGGGGGGAGCCCCAGAGCATCACCATCTTTGGTT	790					
OY	650	AAAGTGC CGGTCTGCTGCTTACCCACTACATGATGTTTAAACGACAACCTCGCGTCTTT	709					
		" " " " " "	" " " " " "					
Db	791	CGGGGCGAAGGGGCTCTCTCGTCACAOCTTCTATCTCTCCACCATTTGAGAAAGSGCTGT	850					
OY	710	TCCATCGTGCTTACTAATATGTGGGTAATGCTATTT	745					
		" " " " " "	" " " " " "					
Db	851	TCCAGAAGGCCATCGCCAGAGTGGACCGCATTT	886					

RESULT 12
US-09-934-323-1


```
Sequence 1, Application US/09934323
Patent No. US20020150910A1
GENERAL INFORMATION:
APPLICANT: Curtiss, Rory A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
FILE REFERENCE: 10448-081001
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4667
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (420)...(2924)
US-09-934-323-1
```

```
Query Match 3.4%: Score 57.6; DB 10; Length 4667;
Best Local Similarity 54.2%; Pred. No. 0.00014;
Matches 117; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
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QY 590 GGATTAATAATGTCGCCCACTTTGGTGCAATCCGATATTAACAGCTTTGGTG 649
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US-09-954-531-1038
Sequence 1038, Application US/09954531
Patent No. US20020165180A1
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GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
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FILE REFERENCE: 689290-77
CURRENT FILING DATE: 2002-05-02
PRIOR FILING DATE: 2000-09-18
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PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-20
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PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
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PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
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PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
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PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
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NUMBER OF SEQ ID NOS: 1392
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1038
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LENGTH: 2191
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-531-1038
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Query Match 3.3%: Score 56.8; DB 9; Length 2191;
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Best Local Similarity 53.2%; Pred. No. 0.00015;
Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;
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RESULT 14
US-09-880-107-3854
Sequence 3854, Application US/09880107
Patent No. US20020142981A1
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GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
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FILE REFERENCE: 44921-5028-MO
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
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PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-10-02
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PRIOR FILING DATE: 2000-10-02
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NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Homo sapiens
OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y09616
US-09-880-107-3854
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Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;
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GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:59:47 ; Search time 2944.03 Seconds

(Without alignments)
16933.650 Million cell updates/sec

Title: US-09-776-910-5

Perfect score: 1713

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries

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6: gb_ov: *
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32: em_rod: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1708.2	99.7	1713	6	ARI53442
3	1706.6	99.6	1713	6	ARI53438
4	1706.6	99.6	1713	6	ARI53439
5	1698.6	99.2	1713	6	ARI53437
6	1698.6	99.2	1713	6	ARI53441
7	1698.6	99.2	2240	3	LCU56636
8	1673.4	97.7	1713	6	AR062838
9	982.4	57.3	2160	3	AF133341
10	961	56.1	2175	3	AF139082
11	951.8	55.6	1710	6	ARI53445
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ALIGNMENTS

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ACCESSION  ARI53440
VERSION    ARI53440.1 GI:15120972
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1713)
AUTHORS   Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
          Robin,G.Charlesde,Quetteville., Claudianos,C., Smyth,K.A.,
          Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
TITLE     Malathion carboxylesterase

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JOURNAL Patent: US 6235515-A 5 22-MAY-2001;
 FEATURES Location/Qualifiers
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 BASE COUNT 516 a 305 c 369 g 523 t
 ORIGIN

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 Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 VERSION AR153442.1 GI:15120974
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 ORGANISM
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 UNCLASSIFIED.
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 AUTHORS Russell,R.,Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
 Robin,G.Charlesde,Quetleville., Claudianos,C., Smyth,K.A.,
 Boyce,T.Mark., Oakeshot,J.Graham. and Brownlie,J.Colin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 6235515-A 9 22-MAY-2001;
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BASE COUNT 515 a 305 c 370 g 523 t
ORIGIN

Query Match 99.7%, Score 1708.2; DB 6; Length 1713;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1710; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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ACCESSION ARI53438
VERSION ARI53438.1 GI:15120970
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
TITLE Journal.
FEATURES
source Location/Qualifiers
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BASE COUNT 515 a 304 c 370 g 524 t
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Query Match 99.6%; Score 1706.6; DB 6; Length 1713;
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 Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 QY 61 AAGTTTAACTAATGTTAACTAATGAAAGCGTGTAGTGAATGATATGTC 120
 61 AAGTTTAACTAATGTTAACTAATGAAAGCGTGTAGTGAATGATATGTC 120
 DB 61 AAGTTTAACTAATGTTAACTAATGAAAGCGTGTAGTGAATGATATGTC 120
 QY 121 AAAGTGAAGCGCTTAAAGCTTAACTGTCGATGATGATGATGATGATGAT 180
 121 AAAGTGAAGCGCTTAAAGCTTAACTGTCGATGATGATGATGATGATGAT 180
 DB 121 AAAGTGAAGCGCTTAAAGCTTAACTGTCGATGATGATGATGATGATGAT 180
 QY 181 ATACCGTACGCGCCAGTGGGTGAGTGAATTAAGCACCACGACGACCA 240
 181 ATACCGTACGCGCCAGTGGGTGAGTGAATTAAGCACCACGACGACCA 240
 DB 181 ATACCGTACGCGCCAGTGGGTGAGTGAATTAAGCACCACGACGACCA 240
 QY 241 CCCTGGATGGTGTGCTGATGTTGCAATCATTAAGATAGTCAGTGAATTT 300
 241 CCCTGGATGGTGTGCTGATGTTGCAATCATTAAGATAGTCAGTGAATTT 300
 DB 241 CCCTGGATGGTGTGCTGATGTTGCAATCATTAAGATAGTCAGTGAATTT 300
 QY 301 ATACGGGCGCAAGTGTGCTGATGATGATGATGATGATGATGATGAT 360
 301 ATACGGGCGCAAGTGTGCTGATGATGATGATGATGATGATGATGAT 360
 DB 301 ATACGGGCGCAAGTGTGCTGATGATGATGATGATGATGATGATGAT 360
 QY 361 CTAAATCCGCAAGTGTGCTGATGATGATGATGATGATGATGATGAT 420
 361 CTAAATCCGCAAGTGTGCTGATGATGATGATGATGATGATGATGAT 420
 DB 361 CTAAATCCGCAAGTGTGCTGATGATGATGATGATGATGATGATGAT 420
 QY 421 GGTGAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 421 GGTGAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 421 GGTGAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 481 ATTAACATCAATATGATGATGATGATGATGATGATGATGATGATGAT 540
 481 ATTAACATCAATATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 481 ATTAACATCAATATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 541 AATGCGCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 541 AATGCGCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 541 AATGCGCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 601 AATGCGCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 601 AATGCGCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 601 AATGCGCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 661 GCTGCTTACGCAATGATGATGATGATGATGATGATGATGATGATGAT 720
 661 GCTGCTTACGCAATGATGATGATGATGATGATGATGATGATGATGAT 720
 DB 661 GCTGCTTACGCAATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 721 ATACTAATGCGGATGATGATGATGATGATGATGATGATGATGATGAT 780
 721 ATACTAATGCGGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 721 ATACTAATGCGGATGATGATGATGATGATGATGATGATGATGATGAT 780
 QY 781 TTACCTTAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 840
 781 TTACCTTAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 781 TTACCTTAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 840
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 841 TTTCTTATGAAGCCAGCAGATGATGATGATGATGATGATGATGATGAT 900
 DB 841 TTTCTTATGAAGCCAGCAGATGATGATGATGATGATGATGATGATGAT 900
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 901 GAAGAGCGTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 DB 901 GAAGAGCGTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 QY 961 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 961 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 DB 961 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020

QY 1021 ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 1021 ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 DB 1021 ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 QY 1081 CAATGCGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 1081 CAATGCGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 DB 1081 CAATGCGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 QY 1141 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 1141 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 DB 1141 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
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 1201 CATGTTACAGGAGAAACACCAACAGCTGATGATGATGATGATGATGAT 1260
 DB 1201 CATGTTACAGGAGAAACACCAACAGCTGATGATGATGATGATGATGAT 1260
 QY 1261 TTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 1261 TTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 DB 1261 TTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
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 1321 GTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 DB 1321 GTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 QY 1381 GTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 1381 GTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 DB 1381 GTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1441 AATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 1441 AATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 DB 1441 AATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 QY 1501 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 1501 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 DB 1501 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 QY 1561 ATGGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 1561 ATGGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 DB 1561 ATGGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 QY 1621 ATAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 1621 ATAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 DB 1621 ATAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 QY 1681 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 1681 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 DB 1681 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740

RESULT 4
 ARI53439 1713 bp DNA linear PAT 08-AUG-2001
 LOCUS ARI53439
 DEFINITION Sequence 3 from patent US 6235515.
 ACCESSION ARI53439
 VERSION ARI53439.1 GI:15120971
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1713)
 Russell, R., Joyce, R., Newcomb, R., David, P., Malcolm, J.,
 Roblin, G., Charles, D., Quetleville, C., Claudianos, C., Smyth, K., A.,
 Boyce, T., Mark, J., Oakeshott, J., Graham, J., and Brownlie, J., Collin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 6235515-A 3 22-MAY-2001;
 FEATURES
 source 1. 1713
 /organism="unknown"
 BASE COUNT 515 a 306 c 370 g 522 t
 ORIGIN
 Query Match 99.6%; Score 1706.6; DB 6; Length 1713;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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OY 1 ATGATTTTCACGCTAGTTGATGAGAAATTAATAATGAGATTAATGCTTGAAT 60
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Db 1 ATGATTTTCACGCTAGTTGATGAGAAATTAATAATGAGATTAATGCTTGAAT 60
OY 61 AAGTTTTAACTATCGTTTAACTACCAATGAAACGCTGCTGTAACATGATGCG 120
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Db 61 AAGTTTTAACTATCGTTTAACTACCAATGAAACGCTGCTGTAACATGATGCG 120
OY 121 AAGTGAAGGCGTTAAACGTTAACTGTAGATGATGATCTTCTACTAGTTTGA 180
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Db 121 AAGTGAAGGCGTTAAACGTTAACTGTAGATGATGATGATCTTCTACTAGTTTGA 180
OY 181 ATACGCTAGCCCAACCCGCAATGGGTGAGCTGAGATTTAAAGCACCAGGACCA 240
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Db 181 ATACGCTAGCCCAACCCGCAATGGGTGAGCTGAGATTTAAAGCACCAGGACCA 240
OY 241 CCCCTGGATGCTGCTGATGTTGCAATCATTAAGATTAAGTCAGTCAGTTGAT 300
   |||||
Db 241 CCCCTGGATGCTGCTGATGTTGCAATCATTAAGATTAAGTCAGTCAGTTGAT 300
OY 301 ATACGCGCAAAAGTGTGCTCAGAGATGCTATACCTAAGTGTCTAATGAAAT 360
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Db 301 ATACGCGCAAAAGTGTGCTCAGAGATGCTATACCTAAGTGTCTAATGAAAT 360
OY 361 CTAAATCCGAACTAAACGTCGCTTATGATACATACATGAGTGTGTTATATC 420
   |||||
Db 361 CTAAATCCGAACTAAACGTCGCTTATGATACATACATGAGTGTGTTATATC 420
OY 421 GGTGAAATCATCATGATATGATGCTGCTGATTTTTCATTAAGAAAGATGCT 480
   |||||
Db 421 GGTGAAATCATCATGATATGATGCTGCTGATTTTTCATTAAGAAAGATGCT 480
OY 481 ATTAACATATCATATGCTTTGGAGCTAGTGTCTTCTAAGTTTAAATTCAGA 540
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Db 481 ATTAACATATCATATGCTTTGGAGCTAGTGTCTTCTAAGTTTAAATTCAGA 540
OY 541 AATGCGCCGATATGCGGCTTAAAGATCAAGTCATGCGCTTCATGATTTAAAT 600
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Db 541 AATGCGCCGATATGCGGCTTAAAGATCAAGTCATGCGCTTCATGATTTAAAT 600
OY 601 AATTGCGCAACTTTGGTGGCAATCCGATTAATATTACAGTCTTGGTGAAGT 660
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Db 601 AATTGCGCAACTTTGGTGGCAATCCGATTAATATTACAGTCTTGGTGAAGT 660
OY 661 GCTGCTCTACCCACTATGATGCTATTTGCTCATTTGCTAATACCAATGCA 720
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Db 661 GCTGCTCTACCCACTATGATGCTATTTGCTCATTTGCTAATACCAATGCA 720
OY 721 ATACTAATGTGGGTAATGCTATTTGCTCATTTGCTAATACCAATGCAATG 780
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Db 721 ATACTAATGTGGGTAATGCTATTTGCTCATTTGCTAATACCAATGCAATG 780
OY 781 TTCACCTTAGCCAAATGCGCGCTATAAGGCTGAGAAATATGATPAAGATCT 840
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Db 781 TTCACCTTAGCCAAATGCGCGCTATAAGGCTGAGAAATATGATPAAGATCT 840
OY 841 TTTCTTAAGAAGCCAGCCAGATTTAGTAAACTTTGAGGAAAGTTTAACTCT 900
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Db 841 TTTCTTAAGAAGCCAGCCAGATTTAGTAAACTTTGAGGAAAGTTTAACTCT 900
OY 901 GAAGAGCTACAAATTAAGTCAATGCTTTGCTTGTCCACAGTGTGAGCATAT 960
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Db 901 GAAGAGCTACAAATTAAGTCAATGCTTTGCTTGTCCACAGTGTGAGCATAT 960
OY 961 GCTGATTTGCTTACCCAAACATCTCGGAAATGTTTAAACTCTTGCGGTAT 1020
   |||||
Db 961 GCTGATTTGCTTACCCAAACATCTCGGAAATGTTTAAACTCTTGCGGTAT 1020
OY 1021 ATACCCACTATGATGGTATACACTTCAATATGAGGCTATATTTTCACTT 1080
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Db 1021 ATACCCACTATGATGGTATACACTTCAATATGAGGCTATATTTTCACTT 1080
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OY 1081 CAATGCCCTATGCTTGTATAGAAATTTGCAATTTTGTGCAAGTGAAT 1140
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Db 1081 CAATGCCCTATGCTTGTATAGAAATTTGCAATTTTGTGCAAGTGAAT 1140
OY 1141 GCTGATGCTGAACGCGACGCCCAAGACCTTGAAGTGGTCTTAAATTTAAAG 1200
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Db 1141 GCTGATGCTGAACGCGACGCCCAAGACCTTGAAGTGGTCTTAAATTTAAAG 1200
OY 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTTATGATCTTGTCTCATCT 1260
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Db 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTTATGATCTTGTCTCATCT 1260
OY 1261 TTTCTGTTCCCATCATCTGTTGTTGCAATACGTTTCAATCACACCTCCG 1320
   |||||
Db 1261 TTTCTGTTCCCATCATCTGTTGTTGCAATACGTTTCAATCACACCTCCG 1320
OY 1321 GCTACTGTATGCTGCTGACCTTCAATTCGAAAGATCTTATCAATCCAT 1380
   |||||
Db 1321 GCTACTGTATGCTGCTGACCTTCAATTCGAAAGATCTTATCAATCCAT 1380
OY 1381 GGTAGTGAAGCTGTGTTAAGGCTTACTATGCTGATGAATTAACCTATTC 1440
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Db 1381 GGTAGTGAAGCTGTGTTAAGGCTTACTATGCTGATGAATTAACCTATTC 1440
OY 1441 AATCAATGGCCCAACGATGCTAAAGATGCGGTAATACAAACATTTGAC 1500
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Db 1441 AATCAATGGCCCAACGATGCTAAAGATGCGGTAATACAAACATTTGAC 1500
OY 1501 ACTGTAATATGATATCAATTTGCCACACTGTATTCCTTATAGCAATTA 1560
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Db 1501 ACTGTAATATGATATCAATTTGCCACACTGTATTCCTTATAGCAATTA 1560
OY 1561 ATGAAATGTTTCTGCGGATCCAAATTAAGAAATCCGATGAAGTATCA 1620
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Db 1561 ATGAAATGTTTCTGCGGATCCAAATTAAGAAATCCGATGAAGTATCA 1620
OY 1621 ATTAGATGATTTGAATGAATGATGATGCTGAAATGATTAAGTAAAC 1680
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Db 1621 ATTAGATGATTTGAATGAATGATGATGCTGAAATGATTAAGTAAAC 1680
OY 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
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Db 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
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RESULT 5
AR062837 1713 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 1 from patent US 5843758.
ACCESSION AR062837
VERSION AR062837.1 GI:5990528
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.,Joyce., Newcomb,R.David., Robin,G.,Charlesde,Quetleville.,
Boyce,T.Mark., Campbell,P.,Malcolm., Parker,A.Gerard.,
Oakesholt,J.,Graham, and Smyth,K.-A.
TITLE Enzyme based bioremediation
JOURNAL Patent: US 5843758-A 1 01-DEC-1998;
FEATURES
source 1..1713
BASE COUNT 516 a 305 c 370 g 522 t
ORIGIN
Query Match 99.2%; Score 1698.6; DB 6; Length 1713;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1 ATGATTTTCACGCTAGTTGATGAGAAATTAATAATGAGATTAATGCTTGAAT 60

Db	1	ATGAAATTTCAACGTTAGTTTATGATGAGAAATTTAAATGGAAGATTTAAATGATGAAAT	60
Qy	61	AAATTTTAAACCTATCGTTTAACTACCAATGAAACGGGTGAGCTGAACACTGAATATAGGC	120
Db	61	AAATTTTAAACCTATCGTTTAACTACCAATGAAACGGGTGAGCTGAACACTGAATATAGGC	120
Qy	121	AAAGTGAAGAGCGCTTAAACGTTTAACTGCTGACGTGACGTGATTCCTACTACAGTTTGAAGGT	180
Db	121	AAAGTGAAGAGCGCTTAAACGTTTAACTGCTGACGTGACGTGATTCCTACTACAGTTTGAAGGT	180
Qy	181	ATACGCTACGCCCAACCGCCACAGTGGGTAGCTGAGATTTAAAGCACCCACGACCAACA	240
Db	181	ATACGCTACGCCCAACCGCCACAGTGGGTAGCTGAGATTTAAAGCACCCACGACCAACA	240
Qy	241	CCCTGGAGATGCTGCTGCGTGATTTGTTGCAATCATTAAGAATAGTCGTCGACAGTTGATTTT	300
Db	241	CCCTGGAGATGCTGCTGCGTGATTTGTTGCAATCATTAAGAATAGTCGTCGACAGTTGATTTT	300
Qy	301	ATPACGGGCAAGTGTGTGGCTCAGAGATTTGCTATACCTCAAGTGTATACGAATAT	360
Db	301	ATPACGGGCAAGTGTGTGGCTCAGAGATTTGCTATACCTCAAGTGTATACGAATAT	360
Qy	361	CTAAATCCCGAAACCTAAAGTCGCCGTTTATATACATACATGCTGTGTTTATATAC	420
Db	361	CTAAATCCCGAAACCTAAAGTCGCCGTTTATATACATACATGCTGTGTTTATATAC	420
Qy	421	GGTGAATATCATTCGTATATGATATGCTGCTGATTTATTTATTAAGAGATGTGCTGTG	480
Db	421	GGTGAATATCATTCGTATATGATATGCTGCTGATTTATTTATTAAGAGATGTGCTGTG	480
Qy	481	ATTACATATCAATATGTTTGGAGCTTAGGTTTCTAAGTTTAAATTCAGACACTT	540
Db	481	ATTACATATCAATATGTTTGGAGCTTAGGTTTCTAAGTTTAAATTCAGACACTT	540
Qy	541	AATGTGCCCGGTATATGCGCGCTTAAAGATCAAGTCATGCGCTGATTTGAATTAAT	600
Db	541	AATGTGCCCGGTATATGCGCGCTTAAAGATCAAGTCATGCGCTGATTTGAATTAAT	600
Qy	601	AATGGCCCAACTTGTGTGGCAATCCCGATTAATTTACATCTTTGTGTGAAGTCCGGT	660
Db	601	AATGGCCCAACTTGTGTGGCAATCCCGATTAATTTACATCTTTGTGTGAAGTCCGGT	660
Qy	661	GCTGCTCTACCCACTACATGATGTTTAACCGAACAACCTGCGGCTTTCCATCGGGT	720
Db	661	GCTGCTCTACCCACTACATGATGTTTAACCGAACAACCTGCGGCTTTCCATCGGGT	720
Qy	721	ATACTATGTCGGGTATGCTATTTGTCCATTTGGCTAATCCCAATGTCACATCGTGC	780
Db	721	ATACTATGTCGGGTATGCTATTTGTCCATTTGGCTAATCCCAATGTCACATCGTGC	780
Qy	781	TTACCTTTAGCCAAATTTGGCCGCTATTAAGGGTGAAGAAATATGATTAAGATGTTTTGGA	840
Db	781	TTACCTTTAGCCAAATTTGGCCGCTATTAAGGGTGAAGAAATATGATTAAGATGTTTTGGA	840
Qy	841	TTTCTTATGAAGCAAGCCACAGATTTTATTAACCTGAGGAAAAAGTTTAACTCTA	900
Db	841	TTTCTTATGAAGCAAGCCACAGATTTTATTAACCTGAGGAAAAAGTTTAACTCTA	900
Qy	901	GAAGAGCTACAAATTAAGTATGTTTCCTTTGTGCCACTGTTGAGCCATACACAC	960
Db	901	GAAGAGCTACAAATTAAGTATGTTTCCTTTGTGCCACTGTTGAGCCATACACAC	960
Qy	961	GCTGATTTGTCTTATACCAAACTTCCTGGGAATGTTAAACGCTGGGGTAATTCG	1020
Db	961	GCTGATTTGTCTTATACCAAACTTCCTGGGAATGTTAAACGCTGGGGTAATTCG	1020
Qy	1021	ATACCCACTATGATGGGTAAACACTTCAATAGGGTCTATTTTTCACCTCAATCTTAAG	1080
Db	1021	ATACCCACTATGATGGGTAAACACTTCAATAGGGTCTATTTTTCACCTCAATCTTAAG	1080
Qy	1081	CAAAATGCTATGCTTGTTAAGGAATGGAACTTGTGCATTTTGTGCCAAGGAATG	1140
Db	1081	CAAAATGCTATGCTTGTTAAGGAATGGAACTTGTGCATTTTGTGCCAAGGAATG	1140

[illegible]

OY	61	AAAGTTTAAACTATCGTTTA	ACTACCAATGAACGGTGTG	TACGTAACCACTGATATGGC	120
Db	61	AAAGTTTAAACTATCGTTTA	ACTACCAATGAACGGTGTG	TACGTAACCACTGATATGGC	120
OY	121	AAAGTGAAGAGCGGTTAAACG	TTTAACGTGTACGATGATCTCT	CACTACAGTTTGAGGGT	180
Db	121	AAAGTGAAGAGCGGTTAAACG	TTTAACGTGTACGATGATCTCT	CACTACAGTTTGAGGGT	180
OY	181	ATACCGTAGCGCCCAACCGC	AGTGGGTGAGCTGAGATTTT	AAAGACCCACGACGACACA	240
Db	181	ATACCGTAGCGCCCAACCGC	AGTGGGTGAGCTGAGATTTT	AAAGACCCACGACGACACA	240
OY	241	CCCGGGATGGTGTGCGCTG	ATTGTTCACATCAATAAGAT	TAACAGTGCAGTTGATTTT	300
Db	241	CCCGGGATGGTGTGCGCTG	ATTGTTCACATCAATAAGAT	TAACAGTGCAGTTGATTTT	300
OY	301	ATAACGGGCAAAAGTGTGCT	AGACGATGTCATTAAGTCTAT	ACGATATAT	360
Db	301	ATAACGGGCAAAAGTGTGCT	AGACGATGTCATTAAGTCTAT	ACGATATAT	360
OY	361	CTAAATCCCGAAACTAAAGC	TGCTCCGTTTAGTATACAT	ACATGAGTGTTTATATTC	420
Db	361	CTAAATCCCGAAACTAAAGC	TGCTCCGTTTAGTATACAT	ACATGAGTGTTTATATTC	420
OY	421	GGTGAATAATCATCGTATAT	GTATGTCCTGATATTTATTA	TAATAAAGAGATGTGTG	480
Db	421	GGTGAATAATCATCGTATAT	GTATGTCCTGATATTTATTA	TAATAAAGAGATGTGTG	480
OY	481	ATTAAACATACAAATTCAT	CTTTTGGAGGCTAGTATG	TTTCTAAGTTTAAATTCAGAAACCTT	540
Db	481	ATTAAACATACAAATTCAT	CTTTTGGAGGCTAGTATG	TTTCTAAGTTTAAATTCAGAAACCTT	540
OY	541	AATGTGCCCGGTAAATGCC	CGGCTTTAAAGATCAAGTC	ATGAGCTTGATTTTAAAT	600
Db	541	AATGTGCCCGGTAAATGCC	CGGCTTTAAAGATCAAGTC	ATGAGCTTGATTTTAAAT	600
OY	601	AATTGGCGCAACTTTGGTGG	CAATCCCGATATATTTAC	AGTCTTTGGTGAAGTCCGGT	660
Db	601	AATTGGCGCAACTTTGGTGG	CAATCCCGATATATTTAC	AGTCTTTGGTGAAGTCCGGT	660
OY	661	GCTGCCCTACCCACTCATAT	GATGTTAAACGAAACAC	TCGGGCTTTTCCATGCTGGT	720
Db	661	GCTGCCCTACCCACTCATAT	GATGTTAAACGATGTTAA	ACGAACTCGGGCTTTTCCATGCTGGT	720
OY	721	ATACTAATGTCGGGTAAATG	CTATTTGTCCATTGGCTAAT	ACCAATGTCACATCGTCC	780
Db	721	ATACTAATGTCGGGTAAATG	CTATTTGTCCATTGGCTAAT	ACCAATGTCACATCGTCC	780
OY	781	TTTCACCTTAGCCAAATTTG	CGCGGCTATTAAGGGT	GAGATATATGATPAGAGTGT	840
Db	781	TTTCACCTTAGCCAAATTTG	CGCGGCTATTAAGGGT	GAGATATATGATPAGAGTGT	840
OY	841	TTTCTTTATGAAGGCAAGC	CAACGAGATTTATTAAC	CTTGAGCAAAAAGTTTAACTCTA	900
Db	841	TTTCTTTATGAAGGCAAGC	CAACGAGATTTATTAAC	CTTGAGCAAAAAGTTTAACTCTA	900
OY	901	GAAAGAGGTACAAATTAAG	TATGTCATGTTTCCGTCAC	CACTGTGAGCATATAGAC	960
Db	901	GAAAGAGGTACAAATTAAG	TATGTCATGTTTCCGTCAC	CACTGTGAGCATATAGAC	960
OY	961	GCTGATTTGTCTTACCAACA	ACATCTCGGGAAATGTT	TAACACTGCTTGGGTAATTCG	1020
Db	961	GCTGATTTGTCTTACCAACA	ACATCTCGGGAAATGTT	TAACACTGCTTGGGTAATTCG	1020
OY	1021	ATACCCACTATGATGGGTAT	CACTCTCATATGAGGGTCT	ATTTTCACTTCAATTTCTTAAG	1080
Db	1021	ATACCCACTATGATGGGTAT	CACTCTCATATGAGGGTCT	ATTTTCACTTCAATTTCTTAAG	1080
OY	1081	CAAAATGCTATGCTTTGTA	GAAATTGGAACCTGTGCT	CAATTTTGTGGCAAGTAAATG	1140
Db	1081	CAAAATGCTATGCTTTGTA	GAAATTGGAACCTGTGCT	CAATTTTGTGGCAAGTAAATG	1140
OY	1141	GCTGATGCTGAAGCACCGC	CCGACGAGACCTTGGAAT	GGTGCTAAATTTAAAGGCT	1200

Dd	1141	GCTGATGCTGAACGGACCGCCCCAGAGACTTTGGAAAATGGGTGCTAAATTAAAAAGGCT	1200
Oy	1201	CATGTTACAGGAGAACAACCAACACAGCTGATTAATTTATGATACCTTTCACATCAT	1260
Dd	1201	CATGTTACAGGAGAACAACCAACAGCTGATTAATTTATGATCCTTTCACATCAT	1260
Oy	1261	TTCGTGTTCCCGCATCGTTTGTTGGCAATTTACGTTTCAATCACACCTCGGGTACACC	1320
Dd	1261	TTCGTGTTCCCGCATCGTTTGTTGGCAATTTACGTTTCAATCACACCTCGGGTACACC	1320
Oy	1321	GCTACCTGTAACGCTTGACCTTGATTCGGAAGATCTTATCAATCCCTATCGTATATG	1380
Dd	1321	GCTACCTGTAACGCTTGACCTTGATTCGGAAGATCTTATCAATCCCTATCGTATATG	1380
Oy	1381	CGTAGTGCACGCTGTTAAGGGTTATAGTCATGCTGATGAATTAACCTATTTCTTCGG	1440
Dd	1381	CGTAGTGCACGCTGTTAAGGGTTATAGTCATGCTGATGAATTAACCTATTTCTTCGG	1440
Oy	1441	AATCAATTGGCCCAAACGTAATGCCATAAAGATCGGTGAATACAAAACAATTGAACGTATG	1500
Dd	1441	AATCAATTGGCCCAAACGTAATGCCATAAAGATCGGTGAATACAAAACAATTGAACGTATG	1500
Oy	1501	ACTGTTATATGATATCAATTTTCCACCACTGGTATCCTTATAGCAATGAATGAAGT	1560
Dd	1501	ACTGTTATATGATATCAATTTTCCACCACTGGTATCCTTATAGCAATGAATGAAGT	1560
Oy	1561	ATGGAANAATGTTTTCCCGGATATCAATTTAAGAATCCGATGAAGTATACAGTGTGTAAT	1620
Dd	1561	ATGGAANAATGTTTTCCCGGATATCAATTTAAGAATCCGATGAAGTATACAGTGTGTAAT	1620
Oy	1621	ATTAGTATGATGAATTAAGAAATGATTTGATGCTCCGTAATGATTAAGATTAACCAATGGAG	1680
Dd	1621	ATTAGTATGATGAATTAAGAAATGATTTGATGCTCCGTAATGATTAAGATTAACCAATGGAG	1680
Oy	1681	TTCGATGTTTGAANAACATAGAGATTTATTTTNG	1713
Dd	1681	TTCGATGTTTGAANAACATAGAGATTTATTTTNG	1713
RESULT 7			
LOCUS	LCU56636	2240 bp	mRNA linear INV 10-JAN-2002
DEFINITION	Lucilia cuprina alpha esterase (lceae) mRNA, implicated in organophosphate resistance, complete cds.		
ACCESSION	U56636		
VERSION	U56636.1	GI:1336079	
KEYWORDS			
SOURCE	Lucilia cuprina.		
ORGANISM	Lucilia cuprina		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Lucilia.		
AUTHORS	Newcomb,R.D., East,P.D., Russell,R.J. and Oakeshott,J.G.		
TITLE	Isolation of alpha cluster esterase genes associated with organophosphate resistance in Lucilia cuprina		
JOURNAL	Insect Mol. Biol. 5 (3), 211-216 (1996)		
MEDLINE	96392952		
PUBMED	8799740		
REFERENCE	2 (bases 1 to 2240)		
AUTHORS	Newcomb,R.D., Campbell,P.M., Russell,R.J. and Oakeshott,J.G.		
TITLE	cDNA cloning, baculovirus-expression and kinetic properties of the esterase, E3, involved in organophosphorus resistance in Lucilia cuprina		
JOURNAL	Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)		
MEDLINE	97215578		
PUBMED	9061925		
REFERENCE	3 (bases 1 to 2240)		
AUTHORS	Newcomb,R.D., Campbell,P.M., Ollis,D.L., Cheah,E., Russell,R.J. and Oakeshott,J.G.		
TITLE	A single amino acid substitution converts a carboxylesterase to an organophosphorus hydrolase and confers insecticide resistance on a		

blowfly
Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997)
MEDLINE
97352821
PUBMED
9207114
REFERENCE
4 (bases 1 to 2240)
Campbell, P.M., Newcomb, R.D., Russell, R.J. and Oakeshott, J.G.
Two different amino acid substitutions in the *ali-esterase*, *E3*,
confer alternative types of organophosphorus insecticide resistance
in the sheep blowfly
JOURNAL
Unpublished
5 (bases 1 to 2240)
Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
Direct Submission
Submitted (24-APR-1996) Richard D. Newcomb, Molecular Genetics,
HortResearch, Private Bag 92 169, Auckland, New Zealand
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ACCESSION AR062838
VERSION AR062838.1 GI:5990529
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1713)
Russell,R.Joyce., Newcomb,R.David., Robin,G.Charlesde,Quetreville.,
Boyce,T.Mark., Campbell,P.Malcolm., Parker,A.Gerrard.,
Oakeshott,J.Graham. and Smyth,K.A.
TITLE Enzyme based bioremediation
JOURNAL Patent: US 5843758-A 2 01-DEC-1998;
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BASE COUNT 506 a 299 c 363 g 515 t 30 others
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REFERENCE	1 (bases 1 to 1710)		
AUTHORS	Russell,R.Joyce., Newcomb,R.David., Campelli,P.Malcolm., Robin,G.Charlesde,Queterville., Claudianos,C., Smyth,K.-A., Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Collin.		
TITLE	Malathion carboxylesterase		
JOURNAL	Patent: US 6235515-A 14 22-MAY-2001:		
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 ACCESSION AY051473
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 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster.
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 1 (bases 1 to 2017)
 Stapleton, M., Brokslein, P., Hong, L., Aghayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunoo, J., Pacle, J., Paragas, V., Park, S., Phouenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
 Direct Submission
 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA
 Sequence submitted by: Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Berkeley, CA 94720
 This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our web site (<http://fruitfly.berkeley.edu>) or send email to cdna@fruitfly.berkeley.edu.
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FEATURES
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ACCESSION	AY121675
VERSION	AY121675.1
KEYWORDS	Full-CDNA.
SOURCE	Fruit fly.
ORGANISM	Drosophila melanogaster

REFERENCE AUTHORS

Stapleton, M., Brockstein, P., Hong, L., Abghayani, A., Carlson, J., Champagne, M., Chavez, C., Dorsett, V., Dresnek, D., Fafian, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G., Miranda, A., Mungall, C. J., Nuno, J., Patel, J., Perages, V., Park, S., Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M., and Celisner, S.

TITLE Direct Submission
JOURNAL Submitted (13-JUN-2002) Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
COMMENT Sequence submitted by:

DECLASSIFIED ON 01/20/2001

This clones was sequenced as part of a high-throughput process to sequence clones from *Drosophila* Gene collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (<http://ffniffity.berkeley.edu>) or send email to cdosgen@ffniffity.berkeley.edu.

FEATURES
Source

Восстановитель/хуа тителс

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TYDRELLY" £33 ~ £50 ~ £51 +

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ORIGIN

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ACCESSION U51050
VERSION U51050.1 GI:1272313
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            1 (bases 1 to 2820)
            Roblin,C., Medveczky,K.M., Russell,R.J. and Oaksbott,J.G.
            Duplication and Divergence of the genes of the alpha-esterase
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            J. Mol. Evol. (1996) In press
            2 (bases 1 to 2820)
            Roblin,C.
            Direct Submission
            Submitted (11-MAR-1996) Charles Roblin, Biotechnology, CSIRO div.
            Entomology, Clunies Ross Street, Canberra, ACT 2601, Australia
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 QY 1463 CTAAAGATTCGCTGATTAATTAACCAATTTGAAGCTATGATGATGATGATGATGATGAT 1522
 Db 2570 GCAAGGAAGTGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2629
 QY 1523 CCACCACTGTGATATCTTATGCAATGAATTAAGGATGATGATGATGATGATGATGATGAT 1582
 Db 2630 CTGCAACGGGTATCTCTACACGAGAGATCAACGGTATGATGATGATGATGATGATGAT 2689

QY 1583 CAATTAAGAAATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1642
 Db 2690 CAGTTGCAATTCGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2749
 QY 1643 TTGATGCTGCTGAATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1702
 Db 2750 TGTATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2809
 QY 1703 ATTTATTTT 1711
 Db 2810 ATTTATTTT 2818

RESULT 15

AC015272/c 57335 bp DNA linear HTG 16-NOV-1999
 LOCUS Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered

DEFINITION

pieces.

ACCESSION

AC015272

VERSION

AC015272.1 GI:6436063

KEYWORDS

HTG; HTGS; PHASE2.

SOURCE

Drosophila melanogaster.

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 57335)

AUTHORS

Adams, M. and Venter, J.C.

TITLE

Direct Submission

JOURNAL

Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA

COMMENT

This sequence was identified as CDM:10213452 by the submitter. For further information on this sequence e-mail to fly@celera.com.

NOTE

* NOTE: This is a 'working draft' sequence.

NOTE

* This sequence will be replaced

NOTE

* by the finished sequence as soon as it is available and

NOTE

* the accession number will be preserved.

FEATURES

location/Qualifiers

source

1..57335

BASE COUNT

17106 a 11816 c 11532 g 16881 t

ORIGIN

1..57335

Query Match

Best Local Similarity 54.5%; Pred. No. 2.6e-72;

Matches 1051; Conservative

0; Mismatches 615; Indels 263; Gaps 5;

QY 46 AATGCAATGAATTAAGTTTAACTATGCTTTAACTACCAATGAAGAGTGTAGCT 105
 Db 36481 AATGCAATGAATTAAGTTTAACTATGCTTTAACTACCAATGAAGAGTGTAGCT 36422
 QY 106 GAACTGATATGAGCAAGTGAAGAGCGTTTAACTGTTAACTGTTGATGATGATGATGAT 165
 Db 36421 GAACTGATATGAGCAAGTGAAGAGCGTTTAACTGTTTAACTGTTGATGATGATGAT 36362
 QY 166 TACAGTTTGAAGGATATACCGTACCGCCCAACGCTGAGTGTGATGATGATGATGAT 225
 Db 36361 TACAGTTTGAAGGATATACCGTACCGCCCAACGCTGAGTGTGATGATGATGATGAT 36302
 QY 226 CCCGAGCGCAACCAACCGGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 285
 Db 36301 CCCGAGCGCGATTCCTCGGAGGAGTGTGATGATGATGATGATGATGATGATGATGAT 36242
 QY 286 GTCAAGTGTATTTAATACGCGCAAGTGTGCTCAGAGATGTTCTATACCTAAGT 345
 Db 36241 GTCAAGTGTATTTAATACGCGCAAGTGTGCTCAGAGATGTTCTATACCTAAGT 36182
 QY 346 GTCTATACGAATTAAT----- 360
 Db 36181 GTCTATACGAATTAAT----- 36122

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:58:21 ; Search time 246.905 Seconds

(Without alignments)
15624.094 Million cell updates/sec

Title: US-09-776-910-5

Perfect score: 1713

Sequence: 1 atgaattcaacgttagttt.....aacatagagattatttttag 1713

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1698.6	99.2	1713	16	AA091561
2	1698.6	99.2	1713	18	AA168596
3	1677.8	97.9	1713	16	AA091566
4	1674.6	97.8	1713	16	AA091564
5	1674.6	97.8	1713	16	AA091565
6	1673	97.7	1713	16	AA081563
7	1671.4	97.6	1713	16	AA091562
8	951.8	55.6	1710	18	AA168597
9	677.2	39.5	2001	23	AB102067

10	378.6	22.1	1704	23	AB102081	Drosophila melanog
11	369	21.5	6175	23	AB102066	Drosophila melanog
12	366.6	21.4	1665	23	AB102099	Drosophila melanog
13	362.2	21.1	1792	23	AB104689	Drosophila melanog
14	325.2	19.0	1593	23	AB102103	Drosophila melanog
15	321.4	18.8	1863	23	AB101859	Drosophila melanog
16	309.8	18.1	1791	23	AB103337	Drosophila melanog
17	309.4	18.1	1878	23	AB101947	Drosophila melanog
18	304.2	17.8	1719	23	AB102101	Drosophila melanog
19	298.8	17.4	3856	23	AB101332	Drosophila melanog
20	298.8	17.4	67279	23	AB107668	Drosophila melanog
21	271.6	15.9	1809	24	ABA90480	Drosophila cell cy
22	236.6	13.8	4320	23	AB102102	Drosophila melanog
23	230.2	13.4	4242	23	AB102102	Drosophila melanog
24	228	13.3	1727	23	AB101943	Drosophila melanog
25	220.8	12.9	5008	23	AB102080	Drosophila melanog
26	199.2	11.6	1987	19	AAV40762	C. felis esterase,
27	199.2	11.6	4294	23	AB102098	Drosophila melanog
28	197.2	11.5	4294	23	AB102100	Drosophila melanog
29	197.2	11.5	2613	23	AB101906	Drosophila melanog
30	193.2	11.3	1626	23	AB101945	Drosophila melanog
31	192.8	11.3	5132	23	AB101858	Drosophila melanog
32	190.2	11.1	1590	19	AAV40764	C. felis esterase,
33	189	11.0	1590	19	AAV40765	C. felis esterase,
34	189	11.0	1540	19	AAV40756	C. felis esterase,
35	181.2	10.6	1584	19	AAV40757	C. felis esterase,
36	181.2	10.6	2007	19	AAV40754	C. felis esterase,
37	181.2	10.6	2007	19	AAV40755	C. felis esterase,
38	181.2	10.6	2007	22	AAV40754	Ctenocephalides fe
39	181.2	10.6	2007	22	AAV40754	Drosophila melanog
40	166	9.7	4288	23	AB101942	Drosophila melanog
41	162	9.5	1783	23	AB102029	Drosophila melanog
42	152.8	8.9	4283	23	AB101946	Drosophila melanog
43	143.8	8.4	1488	19	AAV40767	C. felis esterase
44	143.8	8.4	1590	19	AAV40763	C. felis esterase,
45	143.8	8.4	1590	22	AAV40763	Ctenocephalides fe

ALIGNMENTS

RESULT 1	AA091561	standard; CDNA: 1713 BP.
ID	AA091561	
XX	AA091561	
AC	22-DEC-1995	(first entry)
XX		
DT		
XX		
DE		OP-sensitive esterase E3 LC743 clone.
XX		
KW		Esterase; E3, bioremediation; organophosphate; carbamate;
KW		Insecticide; pesticide; water decontamination; meat decontamination;
KW		ss.
XX		
OS		Lucilia cuprina.
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..1713
FT		/*tag= a
XX		
PN	W09519440-A1.	
XX		
FD	20-JUL-1995.	
XX		
PF	13-JAN-1995;	95WO-AU00016.
XX		
PR	13-JAN-1994;	94AU-0003347.
XX		
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
XX		
PI	Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;	
PI	Parker AG, Robin GC, Russell RJ, Smyth K;	


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XX WPI: 1995-263870/34.
DR P-BSDb; AAR78142.
XX pure E3 esterase from Lucilia cuprina and related DNA - used to
PT eliminate residues of organo-phosphate and carbamate pesticides from
PT water, meat etc.
XX
XX Claim 5; page 12-17; 38pp; English.
XX
XX cDNA from organophosphate (OP)-sensitive L. cuprina pupa cDNA
XX library was amplified using cluster-specific esterase primers.
CC Isolated clone Lc743, a probable full-length cDNA, was expressed
CC using a baculovirus vector in insect cells and shown to encode
CC an OP-susceptible E3 esterase, useful in bioremediation.
XX
XX Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other:
SQ
Query Match 99.2%; Score 1698.6; DB 16; Length 1713;
Best local Similarity 99.5%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGAAATTTCAACCTTGTGATGAGAAATTAATGGAAGTTAAATGCAATGGAAT 60
DB 1 ATGAAATTTCAACCTTGTGATGAGAAATTAATGGAAGTTAAATGCAATGGAAT 60
QY 61 AAGTTTAACTATGCTTTAACTACCAATGAACGGTGTAGCTGAACATGATGGC 120
DB 61 AAGTTTAACTATGCTTTAACTACCAATGAACGGTGTAGCTGAACATGATGGC 120
QY 121 AAGTGAAGCGGTAAACGTTTAACGTGTAGATGATTCCTACTACAGTTTGAAGGT 180
DB 121 AAGTGAAGCGGTAAACGTTTAACTGTGTAGATGATTCCTACTACAGTTTGAAGGT 180
QY 181 ATACCGTAGCGCCACCGCCAGTGGGTAGCTGAGATTTAAAGCACCAGCCAGCAACA 240
DB 181 ATACCGTAGCGCCACCGCCAGTGGGTAGCTGAGATTTAAAGCACCAGCCAGCAACA 240
QY 241 CCCGTGGAGTGTGCTGATTTGCAATCATTAAGTAAAGTCAAGTGAATTTT 300
DB 241 CCCGTGGAGTGTGCTGATTTGCAATCATTAAGTAAAGTCAAGTGAATTTT 300
QY 301 ATAAAGGCAAGTGTGGCTCAGAGATGCTATACCTAAGTGTCTATACCAATAT 360
DB 301 ATAAAGGCAAGTGTGGCTCAGAGATGCTATACCTAAGTGTCTATACCAATAT 360
QY 361 CTAAATCCCGAAGCTAAACGTCCTGTTTAAATACATACATGCTGCTTATATC 420
DB 361 CTAAATCCCGAAGCTAAACGTCCTGTTTAAATACATACATGCTGCTTATATC 420
QY 421 GGTGAATATCATCGTATATGATGCTGATTTTCAATTAAGATGATGCTGTG 480
DB 421 GGTGAATATCATCGTATATGATGCTGATTTTCAATTAAGATGATGCTGTG 480
QY 481 ATTAACATACATATCGTTTGGAGCTCTAGCTTTTCTAAGTTTAAATTCGAAGACCTT 540
DB 481 ATTAACATACATATCGTTTGGAGCTCTAGCTTTTCTAAGTTTAAATTCGAAGACCTT 540
QY 541 AATGTGCCCGGTAAATGCGGCTTAAAGATCAAGTACGCTTGCATTTGAATTAAT 600
DB 541 AATGTGCCCGGTAAATGCGGCTTAAAGATCAAGTACGCTTGCATTTGAATTAAT 600
QY 601 AATGTGCCCGGTAAATGCGGCTTAAAGATCAAGTACGCTTGCATTTGAATTAAT 660
DB 601 AATGTGCCCGGTAAATGCGGCTTAAAGATCAAGTACGCTTGCATTTGAATTAAT 660
QY 661 GGTGCTCTACCACTACATGATGTTAAACGAAACCTCGGCTTTTCCATGCTGT 720
DB 661 GGTGCTCTACCACTACATGATGTTAAACGAAACCTCGGCTTTTCCATGCTGT 720
QY 721 ATACTATATGTGGGTAAATGCTATTTGTGATGCTAATACCAATGTCATGCTGCC 780
DB 721 ATACTATATGTGGGTAAATGCTATTTGTGATGCTAATACCAATGTCATGCTGCC 780

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QY 781 TTCACCTTACCAATTTGGCCGCTATTAAGGGTGAAGATATGATTAAGATGTTTGGAA 840
DB 781 TTCACCTTACCAATTTGGCCGCTATTAAGGGTGAAGATATGATTAAGATGTTTGGAA 840
QY 841 TTCTCTATGAAGCCAAAGCCAGAGATTTAGTAATTAACCTTGAGAAAAAAGTTTAACTCTA 900
DB 841 TTCTCTATGAAGCCAAAGCCAGAGATTTAGTAATTAACCTTGAGAAAAAAGTTTAACTCTA 900
QY 901 GAAGAGCTTACAAATTAAGTATGCTTCCCTTTGGTCCCACTGTGAGCCATATCAGACC 960
DB 901 GAAGAGCTTACAAATTAAGTATGCTTCCCTTTGGTCCCACTGTGAGCCATATCAGACC 960
QY 961 GCTATTTGTCTTACCAACCAACATCTCGGAAATGGTTAAACCTGCTGGGTAATTTG 1020
DB 961 GCTATTTGTCTTACCAACCAACATCTCGGAAATGGTTAAACCTGCTGGGTAATTTG 1020
QY 1021 ATACCACTATGATGGGTAACTTCAATATGAGGCTATTTTCACTTCAATTTTAAAG 1080
DB 1021 ATACCACTATGATGGGTAACTTCAATATGAGGCTATTTTCACTTCAATTTTAAAG 1080
QY 1081 CAAATGCTATGCTTTTAAAGATTTGAATTTGAATTTTGAATTTTGTGCAATTTTGTGCAAGTGAATTTG 1140
DB 1081 CAAATGCTATGCTTTTAAAGATTTGAATTTGAATTTTGAATTTTGTGCAATTTTGTGCAAGTGAATTTG 1140
QY 1141 GCTGATGCTGAACGACCGCCAGAGACCTTGAATTTGGTGTAAATTTAAATTAAGGCT 1200
DB 1141 GCTGATGCTGAACGACCGCCAGAGACCTTGAATTTGGTGTAAATTTAAATTAAGGCT 1200
QY 1201 CATGTTACAGGAAAGAACCAACAGCTATTAATTTTATGATTTTGTGCTGCTACATCTAT 1260
DB 1201 CATGTTACAGGAAAGAACCAACAGCTATTAATTTTATGATTTTGTGCTGCTACATCTAT 1260
QY 1261 TTCTGTTTCCCAATGCTTTTGTGAATTTGATTTTCAATCAGCTCGGTACACCC 1320
DB 1261 TTCTGTTTCCCAATGCTTTTGTGAATTTGATTTTCAATCAGCTCGGTACACCC 1320
QY 1321 GTCTACTTGTATGCTGCTGATTTGCAATTTGCAATTTTCAATTTTCAATTTTCAATTTT 1380
DB 1321 GTCTACTTGTATGCTGCTGATTTGCAATTTGCAATTTTCAATTTTCAATTTTCAATTTT 1380
QY 1381 CGTAGTGAAGTGTGCTTAAAGGCTGTAGTATGCTGATTTTCAATTTTCAATTTTCAATTTT 1440
DB 1381 CGTAGTGAAGTGTGCTTAAAGGCTGTAGTATGCTGATTTTCAATTTTCAATTTTCAATTTT 1440
QY 1441 AATCAATTTGCAACGATATGCTTAAAGATTCGCTGATTTCAATTTTCAATTTTCAATTTT 1500
DB 1441 AATCAATTTGCAACGATATGCTTAAAGATTCGCTGATTTCAATTTTCAATTTTCAATTTT 1500
QY 1501 ACTGATATGATGATTAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTT 1560
DB 1501 ACTGATATGATGATTAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTT 1560
QY 1561 ATGGAATATGTTTCTGGAATTCATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
DB 1561 ATGGAATATGTTTCTGGAATTCATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
QY 1621 ATTAGATATGATTAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTT 1680
DB 1621 ATTAGATATGATTAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTT 1680
QY 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
DB 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713

```

RESULT 2

AAT68596 standard; DNA: 1713 BP.

AAT68596;

08-AUG-1997 (first entry)

XX	Lc-alpha-E7 malathion susceptible esterase clone Lc743.
XX	Malathion carboxylesterase; organophosphate; insecticide;
KW	pesticide; remediation; bioremediation; decontamination; esterase;
XV	ss.
XX	
OS	Lucilia cuprinla.
XX	
FH	Key
FT	primer_bind
FT	/tag- a
FT	/note-"Lc743 5' primer"
FT	1686..1713
FT	/tag- b
FT	/note-"Lc743 3' primer"
FT	752
FT	mutation
FT	/tag- c
FT	/note-"base 752 is T in resistant clones
FT	(TTP to Leu mutation)"
FT	1344
FT	/tag- d
FT	/note-"base 1344 is C in resistant clones
FT	(silent mutation)"
FT	1362
FT	/tag- e
FT	/note-"base 1362 is C in resistant clones
FT	(silent mutation)"
FT	1599
FT	/tag- f
FT	/note-"base 1599 is T in resistant clones
FT	(silent mutation)"
FT	1629
FT	/tag- g
FT	/note-"base 1629 is T in resistant clones
FT	(silent mutation)"
PX	
PN	WO9719176-A1.
XX	
PD	29-MAY-1997.
XX	
PF	22-NOV-1996; 96MO-AU00746.
XX	
PR	23-NOV-1995; 95AU-0006751.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PI	Boyce T, Brownlie JC, Campbell PM, Claudianos C;
PI	Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
XX	WPI: 1997-298113/27.
DR	P-PSDB; AAW17765.
PT	DNA encoding enzyme that degrades organophosphate pesticides -
PP	useful for decontamination of soil, water, food etc
XX	
PS	Claim 4; Fig 1; 52pp; English.
CC	DNA molecule Lc743 (AAT68596) codes for an esterase (AAW17765) from
CC	a malathion susceptible strain of Lucilia cuprina. Comparison
CC	with a consensus sequence from derived from clones of the
CC	Lc-alpha-E7 resistant allele (see also AAW17768) indicated only one
CC	replacement site difference, a TTP to Leu substitution at amino
CC	acid position 251 (nucleotide position 752). This mutation is an
CC	excellent candidate for the malathion resistance mutation. The
CC	resistant enzyme acts as a malathion carboxylesterase and can be
CC	formulated for use in degrading environmental carboxylester or
CC	dimerhyl general organophosphates.
XX	
SQ	Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;
Query Match	99.2%; Score 1698.6; DB 18; Length 1713;
Best Local Similarity	99.5%; Pred. No. 0;

	Matches	1704:	Conservative	0:	Mismatches	9:	Indels	0:	Gaps	0:
QY	1	ATGAATTTCCACGGTAGTTGATGAGAAATTTAAAAATGGAAGATTAAATGCATTGAAAT	60							
Db	1	ATGAATTTCCACGGTAGTTGATGAGAAATTTAAAAATGGAAGATTAAATGCATTGAAAT	60							
QY	61	AAGTTTTTAACTATCGTTTAACTACCAATGAAAGGCTGTGCTGAAACTCAATATGGC	120							
Db	61	AAGTTTTTAACTATCGTTTAACTACCAATGAAAGGCTGTGCTGAAACTCAATATGGC	120							
QY	121	AAAGTGAAGAGCGGCTTAAACGTTTAACTGTCGTACGATGATTCCTACTACGTTTTGAGGT	180							
Db	121	AAAGTGAAGAGCGGCTTAAACGTTTAACTGTCGTACGATGATTCCTACTACGTTTTGAGGT	180							
QY	181	ATACCGTACGCCCAACCGCCAGTGGGTGAGTGAAGATTTAAAGCAACCCAGGACCAACA	240							
Db	181	ATACCGTACGCCCAACCGCCAGTGGGTGAGTGAAGATTTAAAGCAACCCAGGACCAACA	240							
QY	241	CCCTGGGATGTGTGCGTGATTTGGCAATCAATAAGATAACTCAGTGCAGTTGATTTT	300							
Db	241	CCCTGGGATGTGTGCGTGATTTGGCAATCAATAAGATAACTCAGTGCAGTTGATTTT	300							
QY	301	ATACAGGGGAAAGTGTGTGGCTCAGAGGATTTCTATACCTAAGTGTCTATACGAATAT	360							
Db	301	ATACAGGGGAAAGTGTGTGGCTCAGAGGATTTCTATACCTAAGTGTCTATACGAATAT	360							
QY	361	CTAAATCCCGAAACTAAACGTCGCCGTTTATGATACATACATGATGGTGGTTTATATC	420							
Db	361	CTAAATCCCGAAACTAAACGTCGCCGTTTATGATACATACATGATGGTGGTTTATATC	420							
QY	421	GGTGAATATCATCGTATATATGATGTCTGATTTATTTATTAAGAGATGTGTGTG	480							
Db	421	GGTGAATATCATCGTATATATGATGTCTGATTTATTTATTAAGAGATGTGTGTG	480							
QY	481	ATTAACATACAAATATCGTTTGGAGCTCAGGTTTCTAAGTTTAAATCAGAGACCTT	540							
Db	481	ATTAACATACAAATATCGTTTGGAGCTCAGGTTTCTAAGTTTAAATCAGAGACCTT	540							
QY	541	AATGTGCCCGGTAAATGCCGCTTAAAGATCAAGTCATGACCTGTGCATTGGATTAAAT	600							
Db	541	AATGTGCCCGGTAAATGCCGCTTAAAGATCAAGTCATGACCTGTGCATTGGATTAAAT	600							
QY	601	AATTTGGGCAACTTGTGTGGCAATCCCGATAATATTACAGTCTTTGGTAAAGTCCCGT	660							
Db	601	AATTTGGGCAACTTGTGTGGCAATCCCGATAATATTACAGTCTTTGGTAAAGTCCCGT	660							
QY	661	GCTGCCCTACCCACTACATGATGATTTAACGGAACAACTGGGCTTTTCCATCGTGT	720							
Db	661	GCTGCCCTACCCACTACATGATGATTTAACGGAACAACTGGGCTTTTCCATCGTGT	720							
QY	721	ATACTAATGTGCGGTAAATCTATTGTTGCCATTGGGCTAAATACCACATGTCACATGTCG	780							
Db	721	ATACTAATGTGCGGTAAATCTATTGTTGCCATTGGGCTAAATACCACATGTCACATGTCG	780							
QY	781	TTTACCTTAGCCAAATTTGGCCGGCTATAAGGCTGAGAAATATGATATAGGATGTTTGGAA	840							
Db	781	TTTACCTTAGCCAAATTTGGCCGGCTATAAGGCTGAGAAATATGATATAGGATGTTTGGAA	840							
QY	841	TTTTCTATGAAGCAAGCACAGGATTTAGTAAAACTTGAGAAAAAATTTTAACTCTA	900							
Db	841	TTTTCTATGAAGCAAGCACAGGATTTAGTAAAACTTGAGAAAAAATTTTAACTCTA	900							
QY	901	GAGAGCGTACAAATTAAGTTCATGTTTCTTTGGTCCAGCTGTGAGCATATCAGACC	960							
Db	901	GAGAGCGTACAAATTAAGTTCATGTTTCTTTGGTCCAGCTGTGAGCATATCAGACC	960							
QY	961	GCTGATTTGTCTACCCAAACATCCTCGGGAATGTTTAAACTGCTTGGGTAATTGC	1020							
Db	961	GCTGATTTGTCTACCCAAACATCCTCGGGAATGTTTAAACTGCTTGGGTAATTGC	1020							
QY	1021	ATACCCACTATATGGGTACACTTTCATATGAGGCTATTTTTTCACTTCAATTTCTTAAG	1080							
Db	1021	ATACCCACTATATGGGTACACTTTCATATGAGGCTATTTTTTCACTTCAATTTCTTAAG	1080							


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QY 1081 CAATGCTATGCTTGTATGAGAAATGAAACCTGTGTCATTTTGTGCCAAGTAATG 1140
DB 1081 CAATGCTATGCTTGTATGAGAAATGAAACCTGTGTCATTTTGTGCCAAGTAATG 1140
QY 1141 GCTGATGCTGAACGACGCGCCGACAGACCTTGGAAATGGGTCTTAAATTTAAAGCT 1200
DB 1141 GCTGATGCTGAACGACGCGCCGACAGACCTTGGAAATGGGTCTTAAATTTAAAGCT 1200
QY 1201 CAGTGTACAGGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTCACAATCAT 1260
DB 1201 CAGTGTACAGGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTCACAATCAT 1260
QY 1261 TTCTGATGCTCCCATGATGCTTTTGTGCAATTAACCTTCCGTTACACCC 1320
DB 1261 TTCTGATGCTCCCATGATGCTTTTGTGCAATTAACCTTCCGTTACACCC 1320
QY 1321 GTCTACTTGTATGCTGCTTGCAGCTTGTGATTCGGAAGATCTTAATCCCTATCGTATTA 1380
DB 1321 GTCTACTTGTATGCTGCTTGCAGCTTGTGATTCGGAAGATCTTAATCCCTATCGTATTA 1380
QY 1381 CGTAGTGAGAGTGGTGTAAAGGGGTGTAGTGTATGCTGATGATTAACCTATTTCTCTGG 1440
DB 1381 CGTAGTGAGAGTGGTGTAAAGGGGTGTAGTGTATGCTGATGATTAACCTATTTCTCTGG 1440
QY 1441 AATCAATTTGGCCAAACGATATGCTTAAAGAAATCGCGTGAATACAAACAAATTCGATATG 1500
DB 1441 AATCAATTTGGCCAAACGATATGCTTAAAGAAATCGCGTGAATACAAACAAATTCGATATG 1500
QY 1501 ACTGATATGATGATACAAATTTGCCACACGCTGAATCTTATAGCAATGAATTTGAAGGT 1560
DB 1501 ACTGATATGATGATACAAATTTGCCACACGCTGAATCTTATAGCAATGAATTTGAAGGT 1560
QY 1561 ATGGAATATGTTCTCTGGATCAATTAAGAATCCGATGAATACAAAGTGTGTAAT 1620
DB 1561 ATGGAATATGTTCTCTGGATCAATTAAGAATCCGATGAATACAAAGTGTGTAAT 1620
QY 1621 ATTATGATGATGATGAAATATGATGATGCTGAAATGATTAAGATTAACAATGGAG 1680
DB 1621 ATTATGATGATGATGAAATATGATGATGCTGAAATGATTAAGATTAACAATGGAG 1680
QY 1681 TCGATGTTGAAACATAGATGATTTATTTAG 1713
DB 1681 TCGATGTTGAAACATAGATGATTTATTTAG 1713

RESULT 3
AA091566
ID AA091566 standard; cDNA; 1713 BP.
XX
AC AA091566;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103con.
XX
KM Esterase; E3; bioremediation; organophosphate; carbamate;
KW insecticide; pesticide; water decontamination; meat decontamination;
KW ss.
XX
OS Lucilia cuprina.
XX
FH Key 1.1713 Location/Qualifiers
FT CDS /tag= a
XX
XX WO9519440-A1.
XX
XX 20-JUL-1995.
XX
XX 13-JAN-1995. 95WO-AU00016.
XX
XX 13-JAN-1994. 94AU-0003347.
PR

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XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX
XX WPI: 1995-263870/34.
XX
XX
XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX eliminate residues of organo:phosphate and carbamate pesticides from
XX water, meat etc.
XX
PS Example 4: Page 12-17; 38pp; English.
XX
CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC Op-susceptible esterase E3 of L. cuprina) from a diazinon
CC resistant strain, Llandillo 103. 4 isolated clones were
CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
CC esterases; a consensus sequence is given in AA091566.
XX
SQ Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;

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Query Match 97.9%; Score 1677.8; DB 16; Length 1713;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1691; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY 1 ATGAATTTCAAGCTTATGATGAGAAATTAATGGAATTAATGCAATTAATGCAATTAAT 60
DB 1 ATGAATTTCAAGCTTATGATGAGAAATTAATGGAATTAATGCAATTAATGCAATTAAT 60
QY 61 AAGTTTAACTATGCTTTAACTCAATGAACGGTGTAGTGAACCTGAATTAATGCG 120
DB 61 AAGTTTAACTATGCTTTAACTCAATGAACGGTGTAGTGAACCTGAATTAATGCG 120
QY 121 AAGTGAAGGGCGTTAAAGCTTAACTGTGTAGATGATTCCTACTACAGTTTGGAGGT 180
DB 121 AAGTGAAGGGCGTTAAAGCTTAACTGTGTAGATGATTCCTACTACAGTTTGGAGGT 180
QY 181 ATACGCTAGCCCAACCGCCAGTGGGTGAGCTGATTAATGAACGCCAGCAGACCAACA 240
DB 181 ATACGCTAGCCCAACCGCCAGTGGGTGAGCTGATTAATGAACGCCAGCAGACCAACA 240
QY 241 CCCTGGAGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 300
DB 241 CCCTGGAGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 300
QY 301 ATACGCGCAAGTGTGTGCTCAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
DB 301 ATACGCGCAAGTGTGTGCTCAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
QY 361 CTAAATCCCAACTAAGCTGCTGTTTATGATACATCATGATGCTGATTTATATC 420
DB 361 CTAAATCCCAACTAAGCTGCTGTTTATGATACATCATGATGCTGATTTATATC 420
QY 421 GGTGAATATCATGCTGATGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCT 480
DB 421 GGTGAATATCATGCTGATGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCT 480
QY 481 ATTAACATACATATGCTTTGGAGCTGTAGCTTCTAGTTAATTCAGAACGCTT 540
DB 481 ATTAACATACATATGCTTTGGAGCTGTAGCTTCTAGTTAATTCAGAACGCTT 540
QY 541 AATGTCGCGGTATGCGCGCTTAAGATCAAGTCAAGTCCCTGCAATGATTAATAAT 600
DB 541 AATGTCGCGGTATGCGCGCTTAAGATCAAGTCAAGTCCCTGCAATGATTAATAAT 600
QY 601 AATGCGCCCACTTTGGTGGCAATCCGATTAATTTACATCTTTGGTGAAGTGGCGGT 660
DB 601 AATGCGCCCACTTTGGTGGCAATCCGATTAATTTACATCTTTGGTGAAGTGGCGGT 660
QY 661 GCTGCTTACCCACTATGATGATGATTAACGCAACAACTGCGGTCTTTCCATCGTGT 720
DB 661 GCTGCTTACCCACTATGATGATGATTAACGCAACAACTGCGGTCTTTCCATCGTGT 720

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QY 721 ATACTAATGTGGGTAATGCTATTTGTCATTTGCTAAATACCAATGCAACATGCTGCC 780
DB 721 ATACTAATGTGGGTAATGCTATTTGTCATTTGCTAAATACCAATGCAACATGCTGCC 780
QY 781 TTACCTTACCAATTTGGCCGGCTATAAGGCTGAGAAATAGTAAGATTTTGGAA 840
DB 781 TTACCTTACCAATTTGGCTATAGGCTGAGAAATAGTAAGATTTTGGAG 840
QY 841 TTTCTTAAAGAACCAAGCCAGAGATTTAGTAAACCTTGAGAAAAGTTTAACTCA 900
DB 841 TTTCTTAAAGAACCAAGCCAGAGATTTAGTAAACCTTGAGAAAAGTTTAACTCA 900
QY 901 GAAGAGCCGTAACAATTAAGTCAATTTGCTTTGCTCCACATGAGGATATGAGACC 960
DB 901 GAAGAGCCGTAACAATTAAGTCAATTTGCTTTGCTCCACATGAGGATATGAGACC 960
QY 961 GCTGATTTGTCTTACCAACATCCTCGGGAATGGTTAAACCTGTTGGGGTAATTCG 1020
DB 961 GCTGATTTGTCTTACCAACATCCTCGGGAATGGTTAAACCTGTTGGGGTAATTCG 1020
QY 1021 ATACCCACATATGAGGTGATACACTTATATGAGGCTATTTTTCACCTTCAATTCAG 1080
DB 1021 ATACCCACATATGAGGTGATACACTTATATGAGGCTATTTTTCACCTTCAATTCAG 1080
QY 1081 CAAATGCTATGCTTTTAAAGAAATGGAACCTGTGCAATTTTGTGCCAGTGAATG 1140
DB 1081 CAAATGCTATGCTTTTAAAGAAATGGAACCTGTGCAATTTTGTGCCAGTGAATG 1140
QY 1141 GCTGATGCTGAACGCACGCCGCCAGAGACCTTGGAATGGTGTCTAAATTTAAAAAGGCT 1200
DB 1141 GCTGATGCTGAACGCACGCCGCCAGAGACCTTGGAATGGTGTCTAAATTTAAAAAGGCT 1200
QY 1201 CATGTTACGAGGAAACACCAACAGCTGATTAATTTATGATCTTTGCTCAGATCTAT 1260
DB 1201 CATGTTACGAGGAAACACCAACAGCTGATTAATTTATGATCTTTGCTCAGATCTAT 1260
QY 1261 TTCTGCTCCCATGCTGTTGTTGCAATTAACGTTTCAATCACACCTCCGGTACAGCC 1320
DB 1261 TTCTGCTCCCATGCTGTTGTTGCAATTAACGTTTCAATCACACCTCCGGTACAGCC 1320
QY 1321 GTCTACTTATGCTGCTTGCACCTTCGATTCGATGGAAGATCTTATCAATCCCTATGATATG 1380
DB 1321 GTCTACTTATGCTGCTTGCACCTTCGATTCGATGGAAGATCTTATCAATCCCTATGATATG 1380
QY 1381 CGTAGTGAAGCTGTGTTAAGGCTGTATGCTATGCTGATGAATTAACCTATTTCTCTGG 1440
DB 1381 CGTAGTGAAGCTGTGTTAAGGCTGTATGCTATGCTGATGAATTAACCTATTTCTCTGG 1440
QY 1441 AATCAATTTGGCCAAACGTTATGCTTAAAGAAATGCGGATGATACAAAACATTTGAAGCTATG 1500
DB 1441 AATCAATTTGGCCAAACGTTATGCTTAAAGAAATGCGGATGATACAAAACATTTGAAGCTATG 1500
QY 1501 ACTGTATATGATACAAATTTGCAACCACTGTAATCCTTATAGCAATGAAATTTGAAGT 1560
DB 1501 ACTGTATATGATACAAATTTGCAACCACTGTAATCCTTATAGCAATGAAATTTGAAGT 1560
QY 1561 ATGGAATATGTTTCTGGGATCCAAATTAAGAAATCCGATGAAGATATACAAGTGTGTAAT 1620
DB 1561 ATGGAATATGTTTCTGGGATCCAAATTAAGAAATCCGATGAAGATATACAAGTGTGTAAT 1620
QY 1621 ATTAGATGAATTAAGAAATGATGATGCTGGAATGGAATGGAATTAAGCAATGGGAG 1680
DB 1621 ATTAGATGAATTAAGAAATGATGATGCTGGAATGGAATGGAATTAAGCAATGGGAG 1680
QY 1681 TCGATGTTGAATAACATAGAGATTTATTAG 1713
DB 1681 TCGATGTTGAATAACATAGAGATTTATTAG 1713

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RESULT 4
AA091564
ID AA091564 standard; cDNA: 1713 BP.

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XX AC AA091564;
XX DT 22-DEC-1995 (first entry)
XX DE OP-resistant esterase Lc7LI03c allele.
XX KW Esterase; E3; bioremediation; organophosphate; carbamate;
XX KM Insecticide; pesticide; water decontamination; meat decontamination;
XX OS Lucilia cuprina.
XX FT Key Location/Qualifiers
XX CDS 1..1713
XX FT /*tag= a
XX PN W09519440-A1.
XX PD 20-JUL-1995.
XX PF 13-JAN-1995; 95WO-AU00016.
XX PR 13-JAN-1994; 94AU-0003347.
XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX DR WPI; 1995-263870/34.
XX PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX PT eliminate residues of organo:phosphate and carbamate pesticides from
XX PS water, meat etc.
XX SS Example 4; Page 12-17; 38pp: English.
XX CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
XX CC resistant strain, Llandillo 103. 4 isolated clones were
XX CC sequenced (Lc7LI03 A-D, AA091562-65) that encoded diazinon-resistant
XX CC esterases. The esterases, or cells expressing them, are used
XX CC in bioremediation.
XX SQ Sequence 1713 BP; 512 A; 308 C; 368 G; 525 T; 0 other;
XX
XX Query Match 97.8%; Score 1674.6; DB 16; Length 1713;
XX Best Local Similarity 98.6%; Pred. No. 0;
XX Matches 1689; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 ATGAATTTCAAGCTAGTTGATGAGAAATTAATGAAGATTAATGCAATGAAAT 60
DB 1 ATGAATTTCAAGCTAGTTGATGAGAAATTAATGAAGATTAATGCAATGAAAT 60
QY 61 AAGTTTTTAACATGCTTAACTTACCAATGAACGCTGTACTGAACCTGAATATGCG 120
DB 61 AAGTTTTTAACATGCTTAACTTACCAATGAACGCTGTACTGAACCTGAATATGCG 120
QY 121 AAAGTAAAGGCGTTAAAGTTAACTGTGTAAGATGATTCCTACTACAGTTTGAAGGT 180
DB 121 AAAGTAAAGGCGTTAAAGTTAACTGTGTAAGATGATTCCTACTACAGTTTGAAGGT 180
QY 181 ATACCGTACGCCCAACCGCAGTGGTGAAGCTGAGATTTAAAGCACCCAGCAGCAACA 240
DB 181 ATACCGTACGCCCAACCGCAGTGGTGAAGCTGAGATTTAAAGCACCCAGCAGCAACA 240
QY 241 CCTGGGATGCTGTGGCTGATTTCTTCATCAATGAAGATTAAGTGAAGTGAATTTT 300
DB 241 CCTGGGATGCTGTGGCTGATTTCTTCATCAATGAAGATTAAGTGAAGTGAATTTT 300
QY 301 ATAAAGGCAAGATGTGTGCTAGAGATTTGCTTACTTAAGTGTCTATAGCAATTAAT 360
DB 301 ATAAAGGCAAGATGTGTGCTAGAGATTTGCTTACTTAAGTGTCTATAGCAATTAAT 360

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Db 301 ATTACAGCAAGTGTGTGCTCAGAGATTGCTATACCTAAGCGCTATAGCAATAT 360
 QY 361 CTAAATCCGAACCTAACCTCCGTTTGTATACATACATGCTGCTTTTATATAC 420
 Db 361 CTAAATCCGAACCTAACCTCCGTTTGTATACATACATGCTGCTTTTATATAC 420
 QY 421 GGTGAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 Db 421 GGTGAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 QY 481 ATTAACATACATATGCTTTGGAGCTCTAGGTTTCTAAGTTAAATAGAGACCT 540
 Db 481 ATTAACATACATATGCTTTGGAGCTCTAGGTTTCTAAGTTAAATAGAGACCT 540
 QY 541 AATGTCGCGGATAGCGGCTTAAAGATCAAGTCACTGCGCTGATGATGATGAT 600
 Db 541 AATGTCGCGGATAGCGGCTTAAAGATCAAGTCACTGCGCTGATGATGATGAT 600
 QY 601 AATGTCGCGGATAGCGGCTTAAAGATCAAGTCACTGCGCTGATGATGATGAT 660
 Db 601 AATGTCGCGGATAGCGGCTTAAAGATCAAGTCACTGCGCTGATGATGATGAT 660
 QY 661 GCTGCTCTACCACTACATGATGATGATGATGATGATGATGATGATGATGAT 720
 Db 661 GCTGCTCTACCACTACATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 721 ATACTAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 780
 Db 721 ATACTAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 780
 QY 781 TTACCTTTAGCCAAATTTGGCGGCTATAGGGTGAGAAATATGATGATGATG 840
 Db 781 TTACCTTTAGCCAAATTTGGCGGCTATAGGGTGAGAAATATGATGATGATG 840
 QY 841 TTTCTTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 900
 Db 841 TTTCTTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 900
 QY 901 GAAGAGCGTCAATTAAGTATGCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCT 960
 Db 901 GAAGAGCGTCAATTAAGTATGCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 961 GCTGATGCTGCTTACCCAAACATCTCGGGAATGCTTAAACATGCTTAAAC 1020
 Db 961 GCTGATGCTGCTTACCCAAACATCTCGGGAATGCTTAAACATGCTTAAAC 1020
 QY 1021 ATACCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 Db 1021 ATACCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 QY 1081 CAATGCTATGCTTTTGAAGAAATGGAACCTTGTGCTCAATTTTGTGCCAAGTGA 1140
 Db 1081 CAATGCTATGCTTTTGAAGAAATGGAACCTTGTGCTCAATTTTGTGCCAAGTGA 1140
 QY 1141 GCTGATGCTGACGACCGCCCGCAGAGACCTTGGAAATGGTGTAAATTTAAAGGCT 1200
 Db 1141 GCTGATGCTGACGACCGCCCGCAGAGACCTTGGAAATGGTGTAAATTTAAAGGCT 1200
 QY 1201 CATGTTACAGAGAAACCAACCAAGCTGATTAATTTATGATCTTTGCTGCACATGAT 1260
 Db 1201 CATGTTACAGAGAAACCAACCAAGCTGATTAATTTATGATCTTTGCTGCACATGAT 1260
 QY 1261 TTTGCTTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 Db 1261 TTTGCTTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 QY 1321 GTCATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 Db 1321 GTCATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 QY 1381 CGTAGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 Db 1381 CGTAGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440

QY 1441 ATCAATGSCCAACGATGCTTAAAGAAATCCGCTGAATACAAACAATGAACTATG 1500
 Db 1441 ATCAATGSCCAACGATGCTTAAAGAAATCCGCTGAATACAAACAATGAACTATG 1500
 QY 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
 Db 1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
 QY 1561 ATGGAATAATGCTTCCGGAATGCAATTAAGAAATCCGATGATGATGATGATG 1620
 Db 1561 ATGGAATAATGCTTCCGGAATGCAATTAAGAAATCCGATGATGATGATGATG 1620
 QY 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 Db 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 QY 1681 TCGATGTTGAAAAACATAGAGATTTTATG 1713
 Db 1681 TCGATGTTGAAAAACATAGAGATTTTATG 1713

RESULT 5
 AA091565
 ID AA091565 standard; cDNA; 1713 BP.

XX AA091565;
 XX 22-DEC-1995 (first entry)

DE OP-resistant esterase Lc7L103D allele.
 XX Esterase; E3; bioremediation; organophosphate; carbamate;
 KM Insecticide; pesticide; water decontamination; meat decontamination;
 KW ss.

OS *Lucilia cuprina*.

XX Key Location/Qualifiers

XX FT CDS 1..1713

XX FT W09519440-A1.

XX PD 20-JUL-1995.

XX PE 13-JAN-1995; 95MO-AU00016.

XX PR 13-JAN-1994; 94AU-0003347.

XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;

XX PI Parker AG, Robin GC, Russell RJ, Smyth K;

XX DR WPI; 1995-263870/34.

XX PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to

XX PT eliminate residues of organo:phosphate and carbamate pesticides from

XX PT water, meat etc.

XX PS Example 4; Page 12-17; 38pp; English.

XX CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding

XX CC Op-susceptible esterase E3 of *L. cuprina*) from a diazinon

XX CC resistant strain, llandillo 103. 4 isolated clones were

XX CC sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant

XX CC esterases. The esterases, or cells expressing them, are used

XX CC in bioremediation.

XX SQ Sequence 1713 BP; 513 A; 307 C; 369 G; 524 T; 0 other;

Query Match 97.8%; Score 1674.6; DB 16; Length 1713;

Best Local Similarity 98.6%; Pred. No.: 0;
Matches 1689; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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QY 1 ATGATTTCAACGTTAGTTGATGAGAAATTTAAATGGAATTAATGCAATTTAAAT
Db 1 ATGATTTCAACGTTAGTTGATGAGAAATTTAAATGGAATTAATGCAATTTAAAT
QY 61 AAGTTTTAACTATCGTTTAACTACCAATGAAACGGTGTAGCTGAAGCAATGATGCG
Db 61 AAGTTTTAACTATCGTTTAACTACCAATGAAACGGTGTAGCTGAAGCAATGATGCG
QY 121 AAAGTGAAGCGTTTAAAGCTTTAACTGTACGATGATTCCTACTACAGTTTGGAGGT
Db 121 AAAGTGAAGCGTTTAAAGCTTTAACTGTACGATGATTCCTACTACAGTTTGGAGGT
QY 181 ATACCGTAGCGCCAAACCCGAGTGTGAGCTGAGATTTAAAGCCACCGACCAACA
Db 181 ATACCGTAGCGCCAAACCCGAGTGTGAGCTGAGATTTAAAGCCACCGACCAACA
QY 241 CCTGGAGTGTGTCGCTGATTTGTCAATCATAAAGATTAAGTCAAGTGTGATTTT
Db 241 CCTGGAGTGTGTCGCTGATTTGTCAATCATAAAGATTAAGTCAAGTGTGATTTT
QY 301 ATAAAGGCAAGTGTGTGCTCAGAGGATTTCTATACCTAAGTGTCTATACGAATAT
Db 301 ATAAAGGCAAGTGTGTGCTCAGAGGATTTCTATACCTAAGTGTCTATACGAATAT
QY 361 CTAAATCCCGAACTAAACGTCCTTTTACTATACATACATGCTGTGTTTATATATC
Db 361 CTAAATCCCGAACTAAACGTCCTTTTACTATACATACATGCTGTGTTTATATATC
QY 421 GGTGAATATCATGCTGATGATGATGCTGATTTTCAATTAAGATGCTGTG
Db 421 GGTGAATATCATGCTGATGATGATGCTGATTTTCAATTAAGATGCTGTG
QY 481 ATTAACATACATATATGTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT
Db 481 ATTAACATACATATATGTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT
QY 541 AATGAGCCCGGTAATGTCGGGCTTAAAGATCAAGCATGCGCTGCAATGATTAATAAT
Db 541 AATGAGCCCGGTAATGTCGGGCTTAAAGATCAAGCATGCGCTGCAATGATTAATAAT
QY 601 AATTGCGCACTTGTGTGGCAATCCGATATATTACAGTCTTGTGGAAGTCCGGT
Db 601 AATTGCGCACTTGTGTGGCAATCCGATATATTACAGTCTTGTGGAAGTCCGGT
QY 661 GCTGCTCTACCCACATACATGATGTTAACGAAACCTCGCGGTCTTTCCATCGTGT
Db 661 GCTGCTCTACCCACATACATGATGTTAACGAAACCTCGCGGTCTTTCCATCGTGT
QY 721 ATACTAATGTGGGTAATGCTATTTGTCCATTTGGCTAATACCAATGTCACATGCTGCC
Db 721 ATACTAATGTGGGTAATGCTATTTGTCCATTTGGCTAATACCAATGTCACATGCTGCC
QY 781 TTCACCTTAGCCAAATTTGGCGGCTATAAGGTTGAATGATGATGATGATTTTGA
Db 781 TTCACCTTAGCCAAATTTGGCGGCTATAAGGTTGAATGATGATGATGATTTTGA
QY 841 TTTCTTATGAAGCCAAACGACAGATTTAGTAAACTTGAAGAAAAGTTTAACTCTA
Db 841 TTTCTTATGAAGCCAAACGACAGATTTAGTAAACTTGAAGAAAAGTTTAACTCTA
QY 901 GAAGAGCTACAAATTAAGTATGTTTCTTTGCTCCACTGTTGACCATATACAGACC
Db 901 GAAGAGCTACAAATTAAGTATGTTTCTTTGCTCCACTGTTGACCATATACAGACC
QY 961 GCTGATTTGTCTTACCAACATCTGCGGAAATGTTAAACATGCTTGGGTAATTCG
Db 961 GCTGATTTGTCTTACCAACATCTGCGGAAATGTTAAACATGCTTGGGTAATTCG
QY 1021 ATACCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Db 1021 ATACCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG

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Db 1021 ATACCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
QY 1081 CAAATGCTTATGCTTGTATGAGAAATTTGCAATTTTGTGCAATTTTGTGCAAGTAAATG
Db 1081 CAAATGCTTATGCTTGTATGAGAAATTTGCAATTTTGTGCAATTTTGTGCAAGTAAATG
QY 1141 GCTGATGCTGAAGCGACCGCCCAAGAGACCTTGAAGTGGTGTCTTAAATTTAAAGGCT
Db 1141 GCTGATGCTGAAGCGACCGCCCAAGAGACCTTGAAGTGGTGTCTTAAATTTAAAGGCT
QY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATCTTGTCTCATCATAT
Db 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTTATGATCTTGTCTCATCATAT
QY 1261 TTTCTGTTTCCCATGATGCTTGTGCAATTTACGTTTCAATCACACCTCCGCTACACCC
Db 1261 TTTCTGTTTCCCATGATGCTTGTGCAATTTACGTTTCAATCACACCTCCGCTACACCC
QY 1321 GTCCTACTGATGCTGCTGACTTGCATTCGGAAGATCTATCATGCCATGCTATATG
Db 1321 GTCCTACTGATGCTGCTGACTTGCATTCGGAAGATCTTATTAATCCTATGCTATATG
QY 1381 GCTAGTGACGCTGTGTTAAGGCTGTATGCTATGCTGATGATTAACCTATTTCTTCTG
Db 1381 GCTAGTGACGCTGTGTTAAGGCTGTATGCTATGCTGATGATTAACCTATTTCTTCTG
QY 1441 AATCAATTTGGCCAAACGATGCTTAAAGATGCGCTGAATACAAACAAATTAAGCTATG
Db 1441 AATCAATTTGGCCAAACGATGCTTAAAGATGCGCTGAATACAAACAAATTAAGCTATG
QY 1501 ACTGATATGATGATCAATTTTCCACACCTGCTATGCTTATGAAATGAAATTAAGT
Db 1501 ACTGATATGATGATCAATTTTCCACACCTGCTATGCTTATGAAATGAAATTAAGT
QY 1561 ATGAAAAATGTTTCTGCGATCCAAATTAAGAAATCCGATGAAGTATACAGTGTGTAAT
Db 1561 ATGAAAAATGTTTCTGCGATCCAAATTAAGAAATCCGATGAAGTATACAGTGTGTAAT
QY 1621 ATTAGTGAATGATTAAGAAATGATGATGCTGGAAGTGAAGTATTAACATGCGAG
Db 1621 ATTAGTGAATGATTAAGAAATGATGATGCTGGAAGTGAAGTATTAACATGCGAG
QY 1681 TCATGTTTGAAGAAACATAGAGATTTATTTAG 1713
Db 1681 TCATGTTTGAAGAAACATAGAGATTTATTTAG 1713

RESULT 6
AA091563
ID AA091563 standard; cDNA; 1713 BP.
XX
AC AA091563;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103B allele.
XX
KW Esterase; E3: bioremediation; organophosphate; carbamate;
KW Insecticide; pesticide; water decontamination; meat decontamination;
KW ss.
XX
OS Lucilia cuprina.
XX
FH Key Location/Qualifiers
FT 1..1713
FT CDS /*tag= a
XX
PN W09519440-A1.
XX
PD 20-JUL-1995.
XX
PF 13-JAN-1995; 95WO-AU00016.
XX

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AA091562
ID AA091562 standard; cDNA: 1713 BP.
XX
AC AA091562;
XX
DT 22-DEC-1995 (first entry)
XX
DE Op-resistant esterase Lc7L103a allele.
XX
XX Esterase; E3: bioremediation; organophosphate; carbamate;
KW Insecticide; pesticide; water decontamination; meat decontamination;
ss.
XX
OS Lucilia cuprina.
XX
FH Key Location/Qualifiers
FT CDS 1..1713
FT /*tag= a
XX
PN M09519440-A1.
XX
PD 20-JUL-1995.
XX
PF 13-JAN-1995; 95WO-AU00016.
XX
PR 13-JAN-1994; 94AU-0003347.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX
XX WPI: 1995-263870/34.
XX
XX Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
XX eliminate residues of organo:phosphate and carbamate pesticides from
XX water, meat etc.
XX
XX Example 4: Page 12-17; 38pp; English.
XX
XX Rf-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX Op-susceptible esterase E3 of *L. cuprina*) from a diazinon
XX resistant strain, Llandillo 103. 4 Isolated clones were
XX sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
XX esterases. The esterases, or cells expressing them, are used
XX in bioremediation.
XX
XX Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other:
XX
XX Query Match 97.6%; Score 1671.4; DB 16; Length 1713;
XX Best Local Similarity 98.5%; Pred. No. 0;
XX Matches 1687; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 301 ATACGGGCAAGTGTGGCTCAGAGATGCTATACCTAGTCTATACGATAAT 360
DB 301 ATTACAGGCAAGTGTGGCTCAGAGATGCTATACCTAGTCTATACGATAAT 360
QY 361 CTAAATCCCGAACTAAACGTCCTTTAGTATACATCATGTGTGTTTATATC 420
DB 361 CTAAATCCCGAACTAAACGTCCTTTAGTATACATCATGTGTGTTTATATC 420
QY 421 GGTGAATATCATGTATATATGTATGTATATTTTCAATTAAGAGATGTGTG 480
DB 421 GGTGAATATCATGTATATATGTATGTATATTTTCAATTAAGAGATGTGTG 480
QY 481 ATTACATATACATATCTTTGGAGCTCTAGTCTTTCTAAGTTTAAATTCACAGACCTT 540
DB 481 ATTACATATACATATCTTTGGAGCTCTAGTCTTTCTAAGTTTAAATTCACAGACCTT 540
QY 541 AATGTGCGGTAATGCGGCTTAAAGATCAAGTCATGCGCTTCATGATGATTAATAAT 600
DB 541 AATGTGCGGTAATGCGGCTTAAAGATCAAGTCATGCGCTTCATGATGATTAATAAT 600
QY 601 AATGTGCGGTAATGCGGCTTAAAGATCAAGTCATGCGCTTCATGATGATTAATAAT 660
DB 601 AATGTGCGGTAATGCGGCTTAAAGATCAAGTCATGCGCTTCATGATGATTAATAAT 660
QY 661 GCTGCTCTACCCACTACATATATATATATATATATATATATATATATATATAT 720
DB 661 GCTGCTCTACCCACTACATATATATATATATATATATATATATATATATATAT 720
QY 721 ATACTAATGTCGGTATATGCTATTTGCTATGCTATATATATATATATATATATAT 780
DB 721 ATACTAATGTCGGTATATGCTATTTGCTATGCTATATATATATATATATATATAT 780
QY 781 TTACACCTTATACCAATTTGGCGGCTATTAAGGTGAGATATATATATATATATAT 840
DB 781 TTACACCTTATACCAATTTGGCGGCTATTAAGGTGAGATATATATATATATATAT 840
QY 841 TTCTTTATGAAGCCAGACAGATTTAGTAAACTTGAGAGAAAGTTTAACTCTA 900
DB 841 TTCTTTATGAAGCCAGACAGATTTAGTAAACTTGAGAGAAAGTTTAACTCTA 900
QY 901 GAAGAGCGTAAATTAAGTCAATGTTTCTTTGCTCCACTGTGAGCCATATCAGACC 960
DB 901 GAAGAGCGTAAATTAAGTCAATGTTTCTTTGCTCCACTGTGAGCCATATCAGACC 960
QY 961 GCTGATGTGTCTTACCAACATCTCTGGGAAATGTTAAACATGCTTGGGTAATTCG 1020
DB 961 GCTGATGTGTCTTACCAACATCTCTGGGAAATGTTAAACATGCTTGGGTAATTCG 1020
QY 1021 ATACCACATATATGAGTATATATATATATATATATATATATATATATATATAT 1080
DB 1021 ATACCACATATATGAGTATATATATATATATATATATATATATATATATATAT 1080
QY 1081 CAAATGCTTATGTTTAAAGAAATGGAACCTTGTCATATTTGTGCAAGTGAATG 1140
DB 1081 CAAATGCTTATGTTTAAAGAAATGGAACCTTGTCATATTTGTGCAAGTGAATG 1140
QY 1141 GCTGATGTGTCTTACCAACATCTCTGGGAAATGTTAAACATGCTTGGGTAATTCG 1200
DB 1141 GCTGATGTGTCTTACCAACATCTCTGGGAAATGTTAAACATGCTTGGGTAATTCG 1200
QY 1201 CATGTATACAGAGAAACACCAACAGCTGATATATATATATATATATATATATAT 1260
DB 1201 CATGTATACAGAGAAACACCAACAGCTGATATATATATATATATATATATATAT 1260
QY 1261 TTCTGTTCCCATGATGCTTTGTTGAATTAAGTTTCAATCAGCTCGGTACACC 1320
DB 1261 TTCTGTTCCCATGATGCTTTGTTGAATTAAGTTTCAATCAGCTCGGTACACC 1320
QY 1321 GCTGATGTGTCTTACCAACATCTCTGGGAAATGTTAAACATGCTTGGGTAATTCG 1380
DB 1321 GCTGATGTGTCTTACCAACATCTCTGGGAAATGTTAAACATGCTTGGGTAATTCG 1380
QY 1381 CTAAGTGAAGTGTGTGTTAAGGCTGTATGTCATGATGATTAACCTATTTCTTGG 1440


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OY 1004 CTGCTGGGTAATTCGATACCATATATGAGTAACTTACATTCATATGAGGCTATTTT 1063
DB 1004 GGCCTGGGAAATTCGATACCATATGATAGGCAATACCTCTACGAAAGTTGCTTT 1063
OY 1064 TCACCTCAATTCCTTAAGCAATGCTTATGCTTGAAGAAATGGAACCTGTGTCAAT 1123
DB 1064 CCAATCAATTCCTTAAGCAATGCTTGAAGAAATGGAACCTGTGTGTCAAT 1123
OY 1124 TTGTCCCAAGTATGCTGATGCTGAACGACGCCCGGAGACCTTTGCAATGCGTG 1183
DB 1124 ATGTGCTTGGAGATGCTGACAGTGAACGACGACGCGGAAACCTGAGAGGCTG 1183
OY 1184 CTAATATTAAGCAATGCTTACGAGAAACCAACCAACCTATATTTATTTATGATC 1243
DB 1184 CCATTGTGAAAGCAATGCTTACGAGAAACCAACCAACCTATATTTATTTATGAGAC 1243
OY 1244 TTGTGCTCAATTCCTTAAGCAATGCTTGAAGAAATGGAACCTGTGTGTCAAT 1303
DB 1244 TTGTGCTCAATTCCTTAAGCAATGCTTGAAGAAATGGAACCTGTGTGTCAAT 1303
OY 1304 ACACCTCGGTAATTCGATACCATATGATAGGCAATACCTTATGATGATGAT 1363
DB 1304 ACACGCTGGCAATTCGATACCATATGATAGGCAATACCTTATGATGATGAT 1363
OY 1364 ATCCCTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGAT 1423
DB 1364 ACCCTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGAT 1423
OY 1424 TAACCTATTCCTTGAATCAATTCGCAATTCGCAATTCGCAATTCGCAATTCAT 1483
DB 1424 TAACCTATTCCTTGAATCAATTCGCAATTCGCAATTCGCAATTCGCAATTCAT 1483
OY 1484 AAACATTAAGCAATTCGATACCATATGATAGGCAATACCTTATGATGATGAT 1543
DB 1484 AAACATTAAGCAATTCGATACCATATGATAGGCAATACCTTATGATGATGAT 1543
OY 1544 GCAATGAATTCGATACCATATGATAGGCAATACCTTATGATGATGATGAT 1603
DB 1544 GCAATGAATTCGATACCATATGATAGGCAATACCTTATGATGATGATGAT 1603
OY 1604 TATACAGTTCCTTGAATCAATTCGCAATTCGCAATTCGCAATTCGCAATTCAT 1663
DB 1604 TATACAGTTCCTTGAATCAATTCGCAATTCGCAATTCGCAATTCGCAATTCAT 1663
OY 1664 AGATTAACCAATGCTTATGATAGGCAATACCTTATGATGATGATGAT 1710
DB 1664 AGATTAACCAATGCTTATGATAGGCAATACCTTATGATGATGATGAT 1710

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RESULT 9
ABLO2067
ID ABLO2067 standard: cDNA: 2001 BP.
XX
AC ABLO2067;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 683.
XX
KM Drosophila: developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.

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XX (PEKE ) PE CORP NY.
PA Venter JC, Adams M, Li PWD, Myers EW;
PI WPI: 2001-656860/75.
XX P-PSDB: ABB57964.
DR New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
PT Claim 1: SEQ ID NO 683; 21bp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
XX sequences (AB101840-AB16175) and the encoded proteins
XX (ABB57737-ABB72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 2001 BP: 502 A: 488 C: 521 G: 490 T: 0 other:
XX
XX Query Match 39.5%; Score 677.2; DB 23; Length 2001;
XX Best Local Similarity 62.6%; Pred. No. 3.8e-175;
XX Matches 1073; Conservative 0; Mismatches 638; Indels 3; Gaps 1;
XX
OY 1 ATGAATTCACAGCTTATGATGAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 60
DB 95 ATGAATTAAGAACCTGCTGCTTGTGAGCGCTTGTGAGCGCTTGTGAGCGCTTGTGAGCGCT 154
OY 61 AAGTTTAACTATGCTTAACTATGCTTAACTATGCTTAACTATGCTTAACTATGCTTAACTATGCT 120
DB 155 AAGTCCAGCAATATGCTTAACTATGCTTAACTATGCTTAACTATGCTTAACTATGCTTAACTATGCT 214
OY 121 AAGTCCAGCAATATGCTTAACTATGCTTAACTATGCTTAACTATGCTTAACTATGCTTAACTATGCT 180
DB 215 CAAGTGAAGGATATCAAGGATATCAAGGATATCAAGGATATCAAGGATATCAAGGATATCAAGGAT 274
OY 181 ATACGCTAGCGCCCAAGGATATCAAGGATATCAAGGATATCAAGGATATCAAGGATATCAAGGAT 240
DB 275 ATCCCGTAGCGCCCAAGGATATCAAGGATATCAAGGATATCAAGGATATCAAGGATATCAAGGAT 334
OY 241 CCTGGAGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 300
DB 335 CCTGGAGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 394
OY 301 ATACGCGCAAGGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 360
DB 395 GCTTCGATTAAGTATGAGGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 454
OY 361 CTAATATCCGAACTTAAGGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 420
DB 455 GTGAAGCCCGCAAGGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 514
OY 421 GGTGAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 515 GGTGAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 574
OY 481 ATTAACATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 575 GTACAGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 634
OY 541 AATGTCGCCGTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 635 AATGTCGCCGTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 694
OY 601 AATGTCGCCGTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

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Db 695 AATTGGCGTAGTTTCGGCGAGATCCCACTGCATCTTTTGGAGAGTGCATGA 754
 Qy 661 GCTGCTTACCCACTACATGATGTTAACCAGAACTGGCGTCTTTCCATCGTGT 720
 Db 755 GGGCCCTCCACTACATGATGTTAACCAGAACTGGCGTCTTTCCATCGTGT 814
 Qy 721 ATACTAATGCGGTATGCTATTTGTCATGCGC--TAAATCCCAATGTCAACATCGT 777
 Db 815 ATCTTGACAGTGGCGATGCTATTTGCTTGGGCTTACAGCGCCATATACCCTAAT 874
 Qy 778 GCTTCACCTTACCAATTTGGCGGCTATTAAGGATGAGAAATGATTAAGATGTTTG 837
 Db 875 CCTACAGATAGCAAGCTGTTGGCTACAGGCGAGACAAGCAAGATGTCGTG 934
 Qy 838 GAATTTCTTATGAAGCAAGCCACAGATTTAGTAAACTTGAAGAAAGTTTAACT 897
 Db 935 GAGTTCTTGCAAGCAAGGCAAGGATCTTATCGCGTGAAGAAATGTCGACA 994
 Qy 898 CTAGAAGAGCGTACAAATTAAGTATGTTCTTTGGTCCACTGTTGAGCCATATCAG 957
 Db 995 CTGAGAGAACGCAATGAACGATATGTTTGGCTTGGCCATCCCGAAGCATCTCC 1054
 Qy 958 ACCGCTGATGTTGCTTACCAAAACATCTGGGAAATGTTAAACTGCTGGGTAAT 1017
 Db 1055 ACCGCCGAATGTGATATCCAAAGCTCCAAAGAGATGATGAAGACCCGCTGAGTAC 1114
 Qy 1018 TCGATCCCACTATGATGGTACACTTCAATATGAGGCTATTTTTCACCTCAATCTT 1077
 Db 1115 TCCATCCCACTGTTTATAGAAACACTTCTAGAGGCGCTGCTGGGTTCCAGAGTA 1174
 Qy 1078 AAGCAAAATGCTATGCTTGTAAAGAAATGTAATTTATGATCTTCTCTCACATC 1137
 Db 1175 AAGCTTATGCGCAGGTGCTGACAGCACTGATGCTGACACCTTCAATTCCTCAAGAA 1234
 Qy 1138 TTGGCTGATGCTGACAGCCGCCAGACCTGGAATGGGTGCTAATAATTAAGA 1197
 Db 1235 TTGCTGGCCAGGAGCCCAATGAAGAAATGATGCTGAGAGTGCAGATTCGAT 1294
 Qy 1198 GCTCATGTTACAGAGAAACCAACACAGTATATTTATGATCTTCTCTCACATC 1257
 Db 1295 GTTATGCGCAGGTGCTGACAGCACTGATGCTGACACCTTCAATTCCTCAAGAA 1354
 Qy 1258 TATTTGCTGTTCCCATGATCCTTTGTCGAATTCAGTTCAATCACCCTCCGTA 1317
 Db 1355 TACTTCTGTTCCGCGCTGAGAGGCTGCTATCCGACACGCGTGGGCTGAGCT 1414
 Qy 1318 CCGCTCATGTTATGCTTGCATGCTGATTCGAGATTCGAGATTCATCCATATCTAT 1377
 Db 1415 CCACTATATTTCTATGATGATGCTGATTCGAGATTCGAGATTCATCCATATCTAT 1474
 Qy 1378 ATGCTAGTGAAGCTGCTGTTAAGGCTGTTAGTCAATCTGATGAATTAACCTATCTTC 1437
 Db 1475 ATGCGTTGGAGCGGCTGCAAGGGGTCAGCATGCGCATGTTGAGTCAACAAATTC 1534
 Qy 1438 TGAATCAATTTGGCAACGATATGCTTAAGAAATCGGCTGATCAAAACAAATGAGCT 1497
 Db 1535 AGCAGCTGCTGCTGCGCTGCGAAGGAAAGTCCGCGATCAGAGAACATGGAACGA 1594
 Qy 1498 ATGATGCTATGATGATACAAATTTGCCACACTGTTATCTTATAGCAATGAATGAA 1557
 Db 1595 ACCCTGGGCACTGACCACTGTTGCTGCGCAGGGTATCCCTACAGCAAGAAATGAA 1654
 Qy 1558 GGTATGGAATATGTTCTGGGATCAATTAAGAATCCGATGATGATACAGTGTG 1617
 Db 1655 GGTATGCACTGACATGATGATGATGATGATGATGATGATGATGATGATGATG 1714
 Qy 1618 AATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
 Db 1715 AACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1774
 Qy 1678 GAGTCGATGTTGAAGAAACATAGATTTATTTT 1711

Db 1775 GAGAGCTCTATGACGACAAACAAGATTTATGCT 1808
 RESULT 10
 ID ABL02081 standard; cDNA; 1704 BP.
 AC ABL02081;
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 725.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical; gene; ss.
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US09231.
 PF 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EM;
 PI WPI; 2001-656860/75.
 DR P-PDSB; ABB57978.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX Claim 1; SEQ ID NO 725; 21pp + Sequence Listing; English.
 PS The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 1704 BP; 417 A; 445 C; 460 G; 382 T; 0 other;
 Query Match 22.1%; Score 378.6; DB 23; Length 1704;
 Best Local Similarity 53.9%; Pred. No. 2,4e-93;
 Matches 877; Conservative 0; Mismatches 729; Indels 21; Gaps 4;
 Qy 85 ACCAATGAACGGTGTGCTGAGTGAATGATGCGAAAGGCTTAAACGTTTA 144
 Db 64 AGCAATGACAAAGGTCATCGCGACACGCTACGGAAGGTGAAGGGGTGAGTGCAG 123
 Qy 145 ACTGTGACATGATCTCTACAGTTTGGAGGTTATACGATACGCGCAAGCGCATG 204
 Db 124 TCCATCTACGCAACAATCTACAGCTTGGAGGCAATCCCGTTCCGCAAGCGCGTG 183
 Qy 205 GGTAGCTGAGATTTAAGCAACCCACGACCAACACCTGCGATGCTGCTGATGTT 264
 Db 184 GCGCAGCTCGCTCAAGGCGCGCTGAGAGCAAGCAAGCTGTCATGATCAAGCGGTG 243
 Qy 265 TGCATATGAAGATGAAGTCAAGTCAAGTATTTTAAACGGCAAGTGTGCTCA 324
 Db 244 ACACATGTTGCGCGCAAGCCCTGCCAGGTCAACATCTGTTGAAGGAGTCAAGCGCAGC 303

OY	325	GAGACTGTCTAATACC	AGTGTCTTACGAAATATCTAAATCCCGAAGCAATAAAGTCCC	384
Db	304	GAGACTGTCTGTACCT	CAATGTCTACACCGAGGATTCACACAGACTCTTGCCG	363
OY	385	GTATTATATACATATG	TGGTGGTTTAAATTCGCGGAATAATCATCGATATGAT	444
Db	364	GTCTGTGTTGGATCTAT	GGCGGTGATTTCCAAATGGGAAAGCATGCGGGATCTGTAC	423
OY	445	GGTCTGATTATTTCA	TATTAAGAAAGATGTGGTTGATTAAACATCAATATCGTTGGGA	504
Db	424	AGCCCCGACTACATTA	TATGATGAACATGTCTGTAAGTCTGTAATCTCATGGTTAGGA	483
OY	505	GCCTACGTTTCTAAG	TCTTAATTAAGAAAGCTTAATGTGCCGGTAATGCCGCTT	564
Db	484	GCCCTGGGATTCCTT	ATGTCTTGACAGCAAGAACTGGAATCTCCGGAAGACCGGAGTA	543
OY	565	AAATATCAATCATG	AGCCCTTCATTTGAATTAATAATATGCGCACTTTGGGGCAAT	624
Db	544	AAGATCAATATATG	CGCTTGGCGGTGGGTCGCAACGGAATTTGCCAGTTCTTTGGTGGCAT	603
OY	625	CCCGATATATACAG	TCTTTGGTGAAGTGGCGGTGTGCTGCTACCCACTACATATG	684
Db	604	CCCGATATATTAAC	CGTTTGGTGAAGTGTGGAGGTGATCCACACATTAATATG	663
OY	685	TTAACCCAAAAACT	GGCGGTCTTTTCCATCTGTGATTAATATCGGGTAATGTATT	744
Db	664	CTGACGGATAGGCC	CAAGGCCCTATTTTCACAAAGCTATTAATATTTCTCGGATCCGCACTG	723
OY	745	TGTCATATGGCTAT	ATACCCCAATGTCA--ACATCGCCCTCACCTTAGCCAAATTTGGCC	801
Db	724	GCACCTCGGGCGAG	ACCCCAACCCCAATTAATTTGGCCCTATCGCTTGACAGGCCACT	783
OY	802	GGCTATTAAGGGTGA	GAATAATGATATGTTTGAATTTCTTATGAAGCCAGCA	861
Db	784	GGCTACACAGAGAT	GTCTACATCGGACATTTTCCCATCTCAGAAATATGTAAGGCC	843
OY	862	CAGATTTAGTAAAC	TCTGAGGAAAAAGTTTAACTCTAAGAAGCGCTACAAATAGGT	920
Db	844	AGTAGCATGTCTGA	AGGGCGCGAGATATCATCACCATGAGAGACACACAGCGTTG	903
OY	921	--CATGTTCCTTTG	STGCCACTGTGTAGGCATTAACAGCCGATGTGTCTTAACC	978
Db	904	ACCATTTTCAGCTT	TGGACCCACATCGAGCCCTATTGACTCCTCATTTGTGTATTTCC	963
OY	979	AAACATCTCGGGAAT	GTAAATCGTGGGGTAAATTCGATCCCATATGAGGT	1038
Db	964	AAGTCGCCACTGA	ATGATGCGGGACTTGTGGGCAACAGCATTTCCATGTGCTATGGA	1023
OY	1039	AACATTCATATGAG	GGTCTATTTTCACTCAATTTCTTAAGCAATGCTATGCTTT	1098
Db	1024	GGAATCTCTTGAA	AGGTCTCTCATGTTTCCGAAATGAACATGCGCGGAAGTGT	1083
OY	1099	AAGAAATTTGAAAC	TGTGTCAATTTTGTGCCAAGTGAATTTGCTGATGTGAAGCAC	1158
Db	1084	TGCCAGTGGGTGAC	TGCGGAACCTGGCCCTCAAGATGTGCCAGTGAATGACAGCA	1143
OY	1159	GCCCCAGAGACCT	TGGAATAGGGTGTCTAAATTAATAAAGGCTCATGTACAGAGAAACA	1218
Db	1144	AGAAAGACGTTTGA	ANAGAAATGACAGAGCTATTTTTCGGGATGAGAGACTCTGGCAGG	1203
OY	1219	CCAACACCTATAT	TTATATGATCTTCTCTCACTCATATTTCTGTGTTCCCATGAT	1278
Db	1204	AAGACCATATTTGG	AGATGACGCAATCTTCTGTGCAAAATATTTTCTGTGCAATGATCAT	1263
OY	1279	CGTTTGTGCAATTA	CGTTTCAATCATCACACTCCGGTACACCCGCTACTGTATCGCTT	1338
Db	1264	AGGACTTTGCTCG	GTGTCTACACAGCCCATTTGGGCCCAACATTTCTGTACCAATTC	1323
OY	1339	GACTTTCATTCGG	AAAGATCTTATCATCTCCATTCGATTAATGATGCGATGAGACGTGTGT	1398
Db	1324	GATTTCGACTCG--	AGGACTTCATATATATGCAAAATTAATACCTGTGGCGGCAAGGTG	1380

RESULT 11

ABL02066
ID ABL02066 standard; cDNA; 6175 BP.
XX
AC ABL02066;
XX
DT 26-MAR-2002 (first entry)
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 680.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
PN WO200171042-A2.
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
PI Venter JC, Adams M, Li PWD, Myers EW;
DR WPI: 2001-656860/75.
XX
DR P-PSDB: ABB57963.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1: SEQ ID NO 680; 21bp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB572072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 6175 BP; 1732 A; 1242 C; 1350 G; 1851 T; 0 other;
SQ

Query Match	21.5%;	Score 369;	DB 23;	Length 6175;
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Matches 1051; Conservative 0; Mismatches 615; Indels 263; Gaps 5;

5

OY	46	AAATGCACTGAAATAATAGTTTAAACTATACGTTTAAGCAACAAATGAACGGGTGACT	105
Db	3054	AGAACCTCAGGCATTAAGATGCCACGATATGCCAGTCGACCAATGAACAACTGTGGCC	3113
OY	106	GAACACTGAAATATGGCAAAAGTGAAGGCGTTTAAACGTTTAACTGTGTACGATGATCTTAC	165
Db	3114	GACACGGGATACGGCCAAAGTAGAGGGGATCAACGCTCTATCTCTACGATGTGGCTAC	3173
OY	166	TACAGTTTGAAGGATATACCGCTACGCCCAACGCCACGTGGGTGAGCTGAGATTTAAGCA	225
Db	3174	TTTCAGCTTCGAGGGATATCCCGTACGGCCACCCCTCGCGTGGGGAGTGGGTTTAAAGCC	3233
OY	226	CCCCAGGACCAACACCCTGGATGTGTGTCGCGATTTGTGCAATCATTAATTAATGCTCA	285
Db	3234	CCTCAGAGGCCCATTTCCCTGGAGCCAGTTTCGGAGCTGCAGCCAGCCGAAGATTAAGCC	3293
OY	286	GTCGAAGTTGATTTTATACGGGCAAGTGTGTCTCAGAGAGATTGTATACCTAAGT	345
Db	3294	GTCAGAGGTCAGTTCGCTTCGTATAGGTAGAGGGGCTCCGAGAGCTGCTCTATCTCAAT	3353
OY	346	GTCATATCAGATTAAT	360
Db	3354	GTTATACACAAACATGTGAGTAATCTTATTACTGTGTACATTAACATCGTTAAAC	3413
OY	361	-----CTAATCCGAAACTPAACG	380
Db	3414	GTAATTAACCTTAAACATTTTATTTATGTGTACATTTTAAAGTGAAACCCGACAAAGCTCG	3472
OY	381	TCCCGTTTATGATACATACATGATGTTGTTTATTAATCGGAAATCATCGATAT	440
Db	3474	CCCGTTATGTGTTGGATTACGAGAGAGGACTTCATTAATCGGAGGCCAATCGGAAATG	3533
OY	441	GTAATGTCCTGATTTATTTTCATTTAAAGAGATGTGTTGATTAACTACATCAATATCGTTT	500
Db	3534	GTAATGCCCGGATTACTTTATGAAGAAAGATGTTGTTCTGTCACAGATACACTACCGACT	3593
OY	501	GGGAGCTCT-----	509
Db	3594	TGGGGCTTTGGGTAATCTACTGTGTGCGTATGCGCAATATTTTGACTAAACTATATGA	3655
OY	510	-----AGGTTTTCTAAGTTTAAATTCAGAAACCTTATATGCCCCGATATGCGCGCC	562
Db	3654	CCTACACAGGATTTATGATGATCTTAAGTCCCGCAGCTAATGTACACGAAGAAATGCTGGCC	3712
OY	563	TTTAAAGATCAAGTATGGCCTGTCATTTGATTTAAATAATTTGCGCAACTTTGGTGCA	622
Db	3714	TCAAGGATACAGTCTCTGGCCCTCAAGTGCATCAAGAAACATTTGCGCTATTTTTCGCGGAG	3773
OY	623	ATCCGATTAATATTACAGTCTTTGTGTGAAGAGTCCGCGTCTGCTCTACCACTACATGA	682
Db	3774	ATCCCACTGATATCTGTTTGTGTGAAGAGTCTCTGAGGCGCTCTCACTCACTCAATGA	3833
OY	663	TGTTAACCGAACAACCTCGCGGCTTTTCCATCGTGTATTAATATGTCGGGTAATGCTA	742
Db	3834	TGCTAACCGATCAACACCAGAGGCTCTTTCATCGCGCATCTTGAGTGGGCACTGCA	3893
OY	743	TTTGTCCATTGGC---TAATACCCAAATGTCAACATGTCGCTTCACTTAAGCAAAATTGG	799
Db	3894	TTTTTCTTGGGCTTACACGCGGACATTAACCATATCTCTACAGATAGGCAAGCTGG	3953
OY	800	CCGCGTATTAAGGGGAGAAATATGATPAGGATTTTGGAAATTTCTATGAAGCCAGC	859
Db	3954	TTGGCTACAAAGGCGGAGGACAAACAGAGATGCTCGAGTTCCTTGCAAACTGAAGG	4013
OY	860	CACAGCAATTTAGTAAACCTTGAGGAAAAAGTTTAACTCTAGAGAGCGCTACAAATAGG	919

Db	4014	CGAGGATCTTATTCGGGTGGAGAAATATGTCCTGACACTGGAGGACGGATGAACAGA	4073
Qy	920	TCATGTTTCCTTTGGTGGCCACACTGTGGACCATATAGACCCGCTATGTGTCTTACCA	979
Db	4074	TAAATGTGGCTTTGGGCGCATCCCTGGAACTATTCACAGGCCGAATGTGATATCCA	4133
Qy	980	AACATCCTCGGGAAATGGTTAAACACTGCTGGGGTAATTCGATTACCCACTATGATGGGTA	1039
Db	4134	AGCCCTCCAAAGGAAATATATGAAAGCCGCTGGAGTAACTTCATCCCATGTTTATAGSAA	4193
Qy	1040	ACACTTCATATGAGGCTCT-----	1058
Db	4194	ACACTTCGTACGAGGGCCCTGCTGGGTTCCAGGTTAGATATTTGGAAATTTTGTGAAT	4253
Qy	1059	-----ATTTTCACTCAATTTCTTAAGCAAAATCCCATCTGTT	1097
Db	4254	TTCTTTCAATATAGTAAATTTATTTATTTTATTTACAGAGGTAAACGCTTATATGCCAGAGTCT	4313
Qy	1098	TAAAGAAATTTGGAAACTTGTGTCAATTTTGTGCCAAAGTATGGCTGATGCTGAACGAC	1157
Db	4314	GCAGAGCTGTATGCTGTGGACACCTCTCATTTCCCAAGAATTTGGCCACGAGACCCAG	4373
Qy	1158	CGCCCCAGAGACTTGGAAATGGTGTCTAAATTTAAAGGCTCAATGTTACAGGGAAC	1217
Db	4374	TAAAGAAAACCTGATTCGTGGAGTGCACGATTCGAGATGTCATCGACGCTGCTAGA	4433
Qy	1218	ACCAACAGCTGATTAATTTATTTGAT-----	1242
Db	4434	AAGCACCCCAGATTAATTTACATGATGTAAGTGTGTCACAAATTAGTGCTTACATATCAT	4493
Qy	1243	-----CTTGGCTCTCAACTCTATTTTCGTGTTCCCATGCAATCGTT	1282
Db	4494	AAGCTGTAAATTTATTTACCTGCTGTGGATTTTACACTGTCGTGTTCCGGCCCTGAAGG	4553
Qy	1283	TGTTGCATTTACGTTTCAATACACACCTCCGCTACACCCGCTACTGTATCGCTCGACT	1342
Db	4554	TGTTCCATTTCCCGAACGGCGTAGCGGCTGGAGCTCCATATATTTCTATGATATGACT	4613
Qy	1343	TCGATTCCGAAGATCTTATCATATCCCTATGTATTTAGCTAGTGGAGCTGGTGTAAAG	1402
Db	4614	TCGACTCCGAGAGACTCATATTTTTCCTGACCGCATTTAGGGGTGGACGCGGTGTCAAGG	4673
Qy	1403	GTGTTAGTCATGCTGATGAATTAACCTATTTCTTGAATCAATTTGGCCAAACGTATGC	1462
Db	4674	GGGTAGGCAATGCCGAGAGATTTTAGGTACCAATTCAGACACCTGCTGGCTGCCCGGTTGC	4733
Qy	1463	CTAAGAATCGCGTGAATACAAAAAATTTGACGTATGACTGTATATGATACATTTTG	1522
Db	4734	CGAAGGAATGCGGAGTATACAGAACATCCAAAGAACCCGTGGGCAATCTGGACCCAGTTTG	4793
Qy	1523	CCACACTGTAATCTTTATAGCAATGAATTAAGGTATGGAAATGTTTCTGGGATC	1582
Db	4794	CTGCCACGGGTAAATCCCTACACGCGAAGATCAACGGTATGGACACTCTGACCATTTGATC	4853
Qy	1583	CAATTTAAAGAAATCCGATGAAGTATACAAAGTGTGTAATTTATAGTATGAATGAATGA	1642
Db	4854	CAGTTCCGAATTCGAGAGAGGTATCAAGTGCTCAAACTCATGTATGATCGTGAAGTTCA	4913
Qy	1643	TTGATGTGCTCGAAATGGAATTAATTAACATATGGAATGATGTTTGAAGAAACATAGAG	1702
Db	4914	TCGATCTGCTCGAGTGGCCCAAAATTTGAAGGTCTGGAGAGCCCTCATATGACGCAACAAAG	4973
Qy	1703	ATTATTTT 1711	
Db	4974	ATTATTTGT 4982	
RESULT 12			
ABL02099			
ID	ABL02099 standard; cDNA: 1665 BP.		
XX			
AC	ABL02099;		
XX			

OY 1190 TTAAGAGCTCATGTTACAGAGAACACACAGCTGATATTTATGATCTTCT 1249
D 1281 TCTATCTTCAACACAGAGATGACAGATGATGAGATGTTGAGAGCCCTGAATATATTTT 1340
OY 1250 CTCACATCTATTTGTTGATCCCATGATGCTTTGTTGCAATTTGATTCATCACACT 1309
D 1341 CGCATCGGCATATTTGGACATATGCGATGCTTTATTTCTGGCCGTCATCTTATGCCC 1400
OY 1310 CCGGTACACCCGCTTACTTGTATGCTTGCATCTGATTCGAGAGATCTTATCAATCCCT 1369
D 1401 CCAAAACCCGACCATATATATGCTTTTGAATTCGACTC---CCCGCATTCATCAAT 1457
OY 1370 ATGATATATGCGTAGTGGAGAGTGTTTAAAGGTTAGTATGATGCTATGATTAACCT 1429
D 1458 TTCCGCCACTGTTGTCGGCGATGATGATGCGGAGTAGCCCATGCGATGATATAT 1517
OY 1430 ATTCTCTGGAATCAATTTGGCCAAACGATGCTTAAGAAATCGCGTAAATACAAACA 1489
D 1518 ACCTGTTTACACATCATATACCTCCCAACGATGATTAATCATGATGATTAACAAACA 1577
OY 1490 TTGAACGATACATGATATATGATACATTTGCCACCATGATGATCTTATGACAAATG 1549
D 1578 TTGAGAGATGTTGGCATGTCGATGCTTGGCTCCAGTGGAGATCCAAATTTGCCAG 1637
OY 1550 AAATTGAAGTATGGAATAATGTTCTCGGATGCCATTAAGAAATCCGATGAGATACA 1609
D 1638 AACTGGGATCTGCCAAATGGAGAGCCGTCACG-----TTAAAGAAATGCGCGTGAGA 1691
OY 1610 AGTGTGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1662
D 1692 AGTGTGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1744

RESULT 14

ABL02103 standard; cDNA; 1593 BP.

XX ABL02103:
XX AC ABL02103:
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 791.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX OS pharmaceutical; gene; ss.
XX PN Drosophila melanogaster.
XX MO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI: 2001-656860/75.
XX DR P-PSDB; ABB58000.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX PS Claim 1: SEQ ID NO 791; 21bp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1593 BP; 417 A; 394 C; 405 G; 377 T; 0 other;

Query Match 19.0%; Score 325.2; DB 23; Length 1593;
Best Local Similarity 52.9%; Pred. No. 9.9e-79;
Matches 832; Conservative 0; Mismatches 708; Indels 32; Gaps 5;

OY 111 TGAATATGGCAAGGAGGAGGCTTAAAGCTTAACTGTGATGATTTCTTACTACAG 170
D 6 TGACTGGGCTCCTGTGGGGAGGTAGAGAAACACATCTGGGAGGAGCTACTTACG 65
OY 171 TTTTGGGGTATACCGTACGCCCAACGCGACGTGGGAGCTGAGATTTAAAGCACCCCA 230
D 66 TTTGAGGAAGATACCTTCGCAAAAGCTCGGTGGAGATCTGCGCTTCAAGGCCCGGA 125
OY 231 GCGACCAACACCCGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 290
D 126 AGCATGAGAGCCATGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 185
OY 291 AGTTGATTTTATTAACGGGCAAGGTGTGGCTCAAGAGATTTCTATACCTAGATGTC 350
D 186 GACACACATGTTTTCACAAAATACGGCGGCTCAGAGAGACTCCCTTACTTAATATGTGA 245
OY 351 TAGCATATATCTAAATCCCGAAACTAAAGCTCCGCTTTTATATACATACATGATGTC 410
D 246 TGTCAAGATCTGACGCGGATGAACTGCTCCGCTGATGATGATGATGATGATGATG 305
OY 411 TTTTATATGCTGAAATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 470
D 306 CTATCAATTTGGGAGAGCTTCTCGGATATGATGATGATGATGATGATGATGATGATG 365
OY 471 TGTGCTGTTTATTAACATACATATATGTTGGAGCTGTAGTGTTCATAGTTTAAATTC 530
D 366 TGTGCTATGATGACACGCTTCTGATGATGATGATGATGATGATGATGATGATGATG 425
OY 531 AGAAGCTTATATGTCGCCGATATGCGGCTTAAAGATCAAGTCAATGCTTGCATTTG 590
D 426 TCCCAACTAAAGCTTCCCGGAAATGACAGTCTCAAGATCAAAATCATGCGCTCGATG 485
OY 591 GATTAAATATATTCGCGCAACTTGTGGGCAATCCGCTATATATATACAGTCTTGGTGA 650
D 486 GGTGCAACAAAACATCGAAGCATTTGGGGGTATTCACCAATATATACCTTTTGGCGA 545
OY 651 AAGTCCGGTGTGCTTACCCACTACATGATGTTAACCGAACAACCTGGCGCTTTT 710
D 546 AAGTCCGGGAGGAGCTCGACCACTTCTCCTACATGATGCCCAACATGAAAGTCTTAT 605
OY 711 CCATGCTGTATATTAATGTCGGGATATGCTATTTGTCATTTGGCTAATACCAATGTCA 770
D 606 CCACAACCTATGCTTATGTCGGGAGTGTGCTTGTGCGCTTGACGCAACCCAGAA 665
OY 771 ACATGCTGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 830
D 666 TAATTTGGGCTTATAGGCTTGGCCAAAATTTGGGATATACCTGTCATATAGGACAGGC 725
OY 831 TGTTTGGAATTTCTTATGAAAGCCACAGCATTTAGTAAACTTTGAGGAAATAGT 890
D 726 GATCTTTGAGTTTGTGCGATCAATGATGAGGCGGAGATGTCAGAGCCAGCAACAGT 785
OY 891 TTTACTCTAGAGAGCGTACAAATAGGTCTATTTCTTTTGGTCCACTGTTGAGCC 950
D 786 TCTCAGCAACGATGAAAGACATCATGATCTTTTTCGCTTCCGCTGATGTCGATGAA 845
OY 951 ATATCAGACCGCTGATGTTGTCTTACCAACATCCTCGGAAATAGTTAAATGCTTTC 1010

Db 846 ATATCTACCGACGACACTGTGTGCTTAACACACCGATGAACAGATGACGAATAGCTG 905
 Qy 1011 GGGTAATTCGATACCCGACTATGATGGGTACACCTTCATATGAGGGTCAATTTTCACCTC 1070
 Db 906 GACTCAGACGATACCCGATGATGTTGGAGCAGAGCTCGAGGATGGCTATTTCTATCC 965
 Qy 1071 AATTTTAAAGCAAAATCCCTATGCTTTTAAGAAATGGAACCTTGATGATTTTGTGCC 1130
 Db 966 AGAGGTTTCAAGGCGCGACCAACCTCGATGAGTGGGTACTGCAACAAATCTGCTACC 1025
 Qy 1131 AAGTAATTCGCTGATGCTGAACGACCGCCGACGACCTTGGAAATGGGTCTTAAT 1190
 Db 1026 GAGCGATCTGGT---CTTAACCTAGATCCCAAACTGGGTGAACTAGCGCTTGGAC 1081
 Qy 1191 TAAAGGCTCATGTTACAGAGAACACCAACAGCTGATTAAT-----TTTATGG 1240
 Db 1082 TGAAGAGGCGTATTTGGCGAGCAACCTGTAAACGAGCAACATGATGAAGTTCTCG 1141
 Qy 1241 ATCTTGTCTCAGATCTATTTCTGTTCCCATGCTGTTTGTGCAATTCGTTCA 1300
 Db 1142 AGCTATGCTCATATCGAGAGTCTGGCAACCTATATACAGGCGAGCTTGAACCGTGTCC 1201
 Qy 1301 ATCAACACCTCGGTACACCCGCTACTTGTATGCTGCTTGCATTCGAGATGGAATCTTA 1360
 Db 1202 GCGAATCCAGCG---CACCCAGCTATCTGTATGATTCGATTCACGATTCGAA---CTGT 1255
 Qy 1361 TCATCCCTATCGTATTTATGCTGAGTGTGAGCTGTGTTAAGGTGATGATGCTGATG 1420
 Db 1256 GCAACGCTATGAGTATCTTACTTTGGCGCATGAGATGCGAGGTGTTGTCATGCTGACG 1315
 Qy 1421 AATTAACCTATTTCTTCTGCAATCANTTGGCCAAACGATGCCAAGAAATCGCGTGAAT 1480
 Db 1316 ATCTGTGATATTTTCCACAGCATGTTGTCGATCAATCCGCTCCGATTTCTCGGAC 1375
 Qy 1481 ACMAAACAATGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1540
 Db 1376 ACAAGGTTTAAACCGAATGTCGACGCTTGGAGAGTTTGGACGCGACGAGATGCCA 1435
 Qy 1541 ATAGCAATGAATGAAGTATGAAATGTTTCTGCGATTCATTAAGAAATCCGATG 1600
 Db 1436 ACTGCGAAGTAAATCACTCAAGTTTGCACCCATGGAAGCAACCAACTTT----- 1491
 Qy 1601 AAGTATCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1660
 Db 1492 -----AAGTGTCTCAATTTGGGATCAGTTGMAATGATGCGCTCCAGAAATGG 1543
 Qy 1661 ATAGATTAAC 1672
 Db 1544 AGAAATCGAAC 1555

RESULT 15

ABLO1859 standard; cDNA; 1863 BP.

ID ABL01859:

XX ABL01859:

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide seq ID NO 59.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmaceutical; gene; ss.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI: 2001-656860/75.
 DR P-RSDB; ABB57756.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX Claim 1; SEQ ID NO 59; 21bp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcr_sequences.

SO Sequence 1863 BP; 425 A; 493 C; 523 G; 422 T; 0 other;

Query Match 18.8%; Score 321.4; DB 23; Length 1863;

Best Local Similarity 51.4%; Pred. No. 1.2e-77;

Matches 795; Conservative 0; Mismatches 746; Indels 6; Gaps 2;

Qy 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAACGATTAATGATGAAAT 60
 Db 166 ATGCAATCCAGATGGAGTGGCGATCTGCTGAATTTGGACACCACTATTTGGCCAC 225
 Qy 61 AAGTTTAACTATCTGTTTAACTCAATGAACGCTGATGATGATGATGATGATGATG 120
 Db 226 AAGATCGTCAGATATGCTCTGGCACAAAGCAAGCAAGGATGCTGACACAGGATGCG 285
 Qy 121 AAGTGAAGCGCTTAAAGCTTAACTGCT---ACGATGATCTCTACTACAGTTTGG 177
 Db 286 CAGGTGGCGGCAATGCGCAAGACACTCTACAGAGAGATGATGATGATGATGATG 345
 Qy 178 GGTATACCGTACCGCCACACCGGAGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 237
 Db 346 GAATCCCTTTTGCACAGCGCGGCGGAGGAGCTTCCGCTTCGAGCCGCCAGCACCA 405
 Qy 238 ACACCCCTGGAGTGGTGGCTGATGTTGATGATGATGATGATGATGATGATGATG 297
 Db 406 CATCCCTGTTGGGGGTGGGGATGACCTATCCGCGGCCAACGCGATGCAAAAGCAC 465
 Qy 298 TTTTAAACGGGCAAGTGTGTGCTGAGAGATGCTTATACCTAGTGTCTATACGAAT 357
 Db 466 TTCTGTCTCAGCATCTGCAAGGACGAGGATGCTGCTGATGATGATGATGATGATG 525
 Qy 358 AATCTAAATCCGAAACATAAAGCTCCGTTTATGATATATATATATATATATATATAT 417
 Db 526 CGCTGAGATGAGCAAGCCGCTCCGCTGATGATGATGATGATGATGATGATGATG 585
 Qy 418 ATCGGTAAATCATCTGATATGATGCTGATGATGATGATGATGATGATGATGATG 477
 Db 586 TTGCGGAGGCTGTGCGGATTTCTAAGATCACTACTTATGACGAAAGAGTAAAGT 645
 Qy 478 TTGATTAACATACATATCTGTTGAGCTCTAGATTTCTAAGTTTAAATCAAGAAC 537
 Db 646 GTTGTCAATTAATTAAGGTGGGCCCATTTGGCTTCACACCTCGCGGATTCGGAC 705
 Qy 538 CTTAATGTCCCGGTAATGCGGCTTAAGATCAAGTCAAGTCAAGTCAAGTCAAGTCA 597
 Db 706 TTGATGTGCGCGGAAATGCTGCTCAAGAGCAAGATGAGCCCTTCGCTGATCAGT 765

OY	598	AAATTTGGGCAACTTGGTGGCATTCCCGAATTAATTACAGTCTTTGGTGAAGTCC	657
Db	766	CAGAAATATACCCCAATTCATGAGATGCCCAAAATATATACCGTATGGGAGAGTCCG	825
OY	658	GGTCTCTCTCTACCCACTCATGATGTTAAACGGAACAATCGGGCTTTTCCATCGT	717
Db	826	GGACACACCTCCGTTTCAACGGGTTGATGACACCGAGCAAAACCCGAGGGCTGTCCACAG	885
OY	718	GGTATTACTAAATGTCGGGTAATGCTATTGTGCATTGECTAATACCAATGTCAACATCGT	777
Db	886	GCCATCATGCAATTCGGGATCCATGTTCTCGAGTGGGCAATGAGCCAAAGTGCAGTGG	945
OY	778	GCCTTACCTTAGCCAAATTTGGCCGGCTATTAAGGGTGAAGATAATATGATAGAGATTG	837
Db	946	GCATATCCGACTGGCTTCCCAATTTGGATTACTCGGGAGTGAAGAACGAAAGAAAGTGT	1005
OY	838	GAATTTCTTATGAAGACCAAGCACAAGATTAATGTTAAACTTGAGGAAAAAGTTTACT	897
Db	1006	CGATACCTTCAGAAAGCACCCGGCTCCGAATTTGCCGACAGGATATTACTTGTCTCC	1065
OY	898	CTAGAACGCGTACAAATAGTCAATGTTTCCTTTGGTCCACGTTTGAGCAATATCAG	957
Db	1066	CAGAAGAACGGCGGCGAGTACGTCTGTTTCCCTTACTCCGTTGGAACATATATTC	1125
OY	958	ACCCGATATGTGCTTAACCCAAACATCCTCGGGAATGTTAAACATGCTTTGGGTAAT	1017
Db	1126	ACCGAGGATTTGGCTTTTGGCCCGCTGCCACAGGGAATCTCCGGAATTTGGGGTAT	1185
OY	1018	TGCAATCCCACTATGATGGGTAACTCATATATGAGGGTCTATTTTCACTTCAATCTT	1077
Db	1186	GACCTGGCGGTGATCCCTGGGGGCGGCACTCCTTTGAAGTCTGTCTCTACCAAGTACC	1245
OY	1078	AAGCAATGCCATGCTTTGTTTAAAGAAATTGGAACCTGTGTCAATTTTGTGCCAAGTGA	1137
Db	1246	CTGCAGCAGCAGGAACACATGCTGAGTGGCTTTTGAAGTCTTAATCTCAGGAGATCAG	1305
OY	1138	TTGCGTGTGCTGAAACGACACCGGCCACAGACCTTGGAAATGGGTCTAAATTAATTAAG	1197
Db	1306	GAGAAAGTATCCCAAGTGGCATTTTAAAGATCTGTCTACGTCAATTTAAGTGGATATCTC	1365
OY	1198	GCTCATGTTACAGGAGAAACACCAACAGCTGATTAATTTTATGAACTTTGCTCTCACATC	1257
Db	1366	GATGATGGACACTCGAGGGCAATGAGATTCAATGATGCTGCACATATCTGCTGTAA	1425
OY	1238	TATTTTGGTTCCTCCATGCATGCTTTGTGGCAATTACGTTTAAATACACCTCGGGTACA	1317
Db	1426	CACTTTGGCATGTGCATTTCAATCCACTGATATGGCCCGGCTCAGCCAGCCGCCCAAGC	1485
OY	1318	CCCCGATCTGTAATGCCCTCGACTTCGATTCGGAAGATCTATCAATCCCATGATATT	1377
Db	1486	CCCACCTACTCTGATCCCTTCCATGTGAGACTCG--CCCAATTTCAATDACTCTCCGGCAG	1542
OY	1378	ATGCGTAGTGACGTGGTGTTAAGGGGTATTAGTCATGCTGATGAATTAACCTATTCTC	1437
Db	1543	GTGATGTGCGGAAAAACAGTTCGGGGAGTATGATCAATGCGAGAGATCTCTCTACCTTTC	1602
OY	1438	TGAATCAATTGGCCCAACGATATGCTTAAGAAATGCGGTGAATACAAACAATTAACGT	1497
Db	1603	TATCACATTTTGGCCCAACAGGTGATTAAGTCTCGATGAGTACTCAACAACATACAGAGA	1662
OY	1498	ATGACGTGTAATGATATACAAATTTGGCACACCTCGGTAATCTTTAATG	1544
Db	1663	CTGTGGGCAATGTGGTGGCAATTTGCCCGGAAGACAAATCCCAATTTG	1709

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Job time : 263.905 secs

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:24:12 ; Search time 1663.49 seconds
(without alignments)
16677.553 Million cell updates/sec

Title: US-09-776-910-5
1713
Sequence: 1 atgattcaccagttagttt.....aacatagagattatttttag 1713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:
2: em_esthum:
3: em_estin:
4: em_estm:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_hlc:
9: gb_est1:
10: gb_est2:
11: gb_hlc:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: gb_gss:
18: em_gss_hum:
19: em_gss_inv:
20: em_gss_pln:
21: em_gss_vrt:
22: em_gss_fun:
23: em_gss_mam:
24: em_gss_mus:
25: em_gss_other:
26: em_gss_pro:
27: em_gss_rod:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	315.2	18.4	778 9	AT062034 GH01076.5
2	280.8	16.4	649 9	AT1388926 GH19977.5
3	266.8	15.6	688 9	AT1403569 GH23036.5
4	256.6	15.0	671 9	AT1517692 GH28740.5
5	254.4	14.9	569 13	BI609541 RH14337.5
6	250	14.6	674 13	BI628316 RH56682.5

7	249.4	14.6	676 13	BI635372
8	248.4	14.5	673 13	BI614181
9	247	14.4	660 13	BI639486
10	246.8	14.4	672 13	BI614443
11	246.4	14.4	670 13	BI233202
12	245	14.3	648 9	AT113763
13	245	14.3	648 9	AT1403098
14	243.4	14.2	646 9	AT1109901
15	243.4	14.2	646 9	AT293416
16	242.6	14.2	526 9	AT1108080
17	241.4	14.1	516 9	AT1108156
18	239.2	14.0	658 13	BI564586
19	238.4	13.9	656 13	BI619037
20	236.8	13.8	656 13	BI614821
21	236.6	13.8	669 13	BI588370
22	236.2	13.8	656 13	BI621302
23	233.2	13.6	628 9	AT1109573
24	231.4	13.5	619 9	AT1516869
25	231	13.5	638 13	BI564361
26	230.8	13.5	628 9	AT1513346
27	230.6	13.5	630 9	AT1403830
28	230	13.4	614 12	BG641228
29	230	13.4	647 13	BI575862
30	229.6	13.4	614 9	AT1107729
31	229.6	13.4	614 9	AT1134360
32	229.2	13.4	622 9	AT1134524
33	228	13.3	633 13	BI370683
34	222.6	13.0	670 9	AT1389766
35	219.8	12.8	615 13	BI617897
36	219.2	12.8	614 13	BI588504
37	218.6	12.8	587 9	AT1517539
38	218.6	12.8	588 13	BI638519
39	218.6	12.8	607 13	BI624437
40	218.6	12.8	607 13	BI673399
41	218.6	12.8	609 13	BI607309
42	218.6	12.8	609 13	BI622392
43	218.6	12.8	609 13	BI630054
44	218.6	12.8	611 13	BI572606
45	217.8	12.7	612 13	BI631806

ALIGNMENTS

RESULT 1
LOCUS AT062034 778 bp mRNA linear EST 19-APR-2001
DEFINITION GH01076.5prine GH Drosophila melanogaster head P0T2 Drosophila melanogaster cDNA clone GH01076.5prine similar to U51050:
Drosophila melanogaster alpha esterase (aET) gene, partial cds,
mRNA sequence.
ACCESSION AT062034
VERSION AT062034.1 GI:3337873
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 778)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HMT Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP

TITLE JOURNAL
COMMENT
FEATURES
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, estfruitfly@berkeley.edu
Plate: 10 row: G column: 4
High quality sequence stop: 363.
Location/Qualifiers

QY	908	GAACAATAAGTCATGTTCTCTTTGGGCCACAGTGTAGGCATATCGACCGGTGANT	967
Db	484	GCATGACAGAGTAATAGTTGGCTTTGGGCCATCCCTGGAAACATCTTCACGCCGGAAT	543
QY	968	GTGCTTTACCCCAACATCCCTCGGAAATGGTTAAACTGCTTGGGGTAATTGATACCA	1027
Db	544	GTGTATATCCAAAGCCTCCAAAGAGATATATAAGACCGCCCTGGAGTATCTCATCCCA	603
QY	1028	CTATGATGGGTACACTTCATATGAGGCTCTATTTT	1063
Db	604	TGTTATAGGAACACTTCGTACGAGGCGCTCTGT	639
RESULT 3			
LOCUS	AI403569	688 bp	mRNA
DEFINITION	GH23036.5prime GH Drosophila melanogaster head por2 Drosophila melanogaster CDNA clone GH23036.5prime similar to U510507.		
ACCESSION	AI403569		
VERSION	AI403569.1	GI:4246656	
KEYWORDS	EST.		
SOURCE	fruit fly.		
ORGANISM	Drosophila melanogaster		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
AUTHORS	Harvey, D., Broksstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G.M.		
TITLE	BDGP/HMI Drosophila EST Project		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Stapleton, M.		
	BDGP		
	Lawrence Berkeley National Lab		
	One Cyclotron Rd, Berkeley, CA 94720, USA		
	Fax: 510 486 6798		
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu		
	Plate: 230 row: C column: 12		
	High quality sequence stop: 648.		
FEATURES	Location/Qualifiers		
source	1..688		
	/organism="Drosophila melanogaster"		
	/db_xref="taxon:7227"		
	/clone="GH23036"		
	/clone_lib="GH Drosophila melanogaster head por2"		
	/sex="male and female"		
	/dev_stage="adult"		
	/lab_host="DHS - alpha"		
	/note="Organ: head; Vector: por2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into por2. Plasmid cDNA library."		
BASE COUNT	161 a 174 c 197 g 156 t		
ORIGIN			
Query Match	15.6%;	Score 266.8;	DB 9; Length 688;
Best Local Similarity	65.4%;	Pred. No. 1.9e-63;	
Matches 391; Conservative	0;	Mismatches 207;	Indels 0; Gaps 0;
QY	1	ATGAATTCACGTTAGTTGATGAGAAATTTAAATGGAACATTAATGCAATGAAAT	60
Db	91	ATGAATTAAGAACCTCGCTTGTGCGACCTTGCAGGTGCGCCTCAAAACATCGACAT	150
QY	61	AAGTTTAAATACGTCTTAACTACATCCATGAAAGCGGTGATGCTGAACATGAATATGCG	120
Db	151	AAAGTCACCAATATGCGCCAGTCGACCAATGAACAGATTGCGCGACACGAGATCGGC	210
QY	121	AAAGTAAAGGCGTTAAAGCTTAACTGTATGATGATGATCTTACTACAGATTTTGAGGCT	180
Db	211	CAAGTGAAGGCGATCAAGGCTCTATCTCTCTAGATGATGCTCCTACTTCAAGCTTCAGGCT	270
QY	181	ATACCGTACGCCCAACCGCCACTGGGTGAGTGTAGATTTTAAAGCACCCAGCGACCAACA	240

[illegible]

Matches 376: Conservative 0: Mismatches 199: Indels 0: Gaps 0:

1 ATGATTTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAATGATGAAT 60
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 95 ATGATTAAGAACCTCGGCTTGTGGAGCGCTTGGCGCCCTCAAAACCATGACAT 154
 61 AAGTTTAACTATTCGTTTACTACCAATGAACGCTGTAGTGAATGAATATGCG 120
 11 111111 111111 111111 111111 111111 111111 111111 111111 111111
 155 AAGTCCACAGATTCGCCAGTCGACCAATGAACAGTTTGGCCGACGAGTACGCG 214
 121 AAGTGAAGGCGTTAAAGCTTAACTGTATGATGATTCCTACTACAGTTTGAAGGT 180
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 215 CAAGTAGAGGTTCAAGGCTATCTCTACGATGTCCTACTTCAAGCTTCAAGGT 274
 181 ATACCGTACGCCACACCGCCAGTGGTGAAGTATTAAGCAACCCGACCAACA 240
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 275 ATCCCGTACGCCACCGCTCGGTGGGAGTTCGCTTTAAGGCCCTCAGAGCCCAT 334
 241 CCGTGGATGATGCTGCTGATGTTGCAATCATTAAGATTAAGTCAAGTGAATTT 300
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 335 CCGTGGAGGAGTTCGCGACTGACGACCCAGATGAAGCCCTCAGGTCGAGTTC 394
 301 ATAAAGGCAAGTGTGCTGCTGAGAGTGTCTATACATGCTCTATACGAATAT 360
 11 111111 111111 111111 111111 111111 111111 111111 111111 111111
 395 GCTTTCATTAAGTGAAGGCTCGAGAGTCTGCTCTATCTCAATGATACCAACAT 454
 361 CTAATCCGCAAACTAAACGTCCTGTTTATGATATACATACATGCTGTGTTTATATC 420
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 455 GTGAAGCCGCAAGAGGCTCGCCGTTATGTTGATTCAGGAGAGAGGCTTCAATATC 514
 421 GGTGAATATCTGATATGATGCTGCTGATGATTTTCAATTAAGATGATGCTG 480
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 515 GCGGAGGCGCAATCGGAATGATGATGCGCCGATTTACTTTGAAGAAAGATGTTGCTC 574
 481 ATTAACATACATATCGTTTGGAGCTCTAGCTTTCTAAGTTTAATCAGAAGCTT 540
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 575 GTACAGATTAACGATACGACTTGGGCTTGGGATTTAAGTCTTAAGTCCCGGAGCTA 634
 541 AATGTGCCCCGTAATGCGGCTTAAAGTCAAGT 575
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 635 AATGTACAGAAATGCTGCTCAAGATCAGT 669

RESULT 5 569 bp mRNA linear EST 07-SEP-2001
 B1609541
 LOCUS RH14337.5prime RH Drosophila melanogaster normalized Head pf1c-1
 DEFINITION Drosophila melanogaster cDNA clone RH14337.5 similar to alpha-Est7:
 (GO:0004091) located on: 3R 84D5-84D5; 08/17/2001, mRNA sequence.
 G.M.

ACCESSION B1609541 GI:15505066
 VERSION B1609541.1
 SOURCE EST.
 KEYWORDS fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyngota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 569)
 Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
 J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
 R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S.,
 Mungall, C.J., Nunoo, J., Pacle, J., Paragas, V., Park, S.,
 Plouffe, S., Wan, K., Yu, C., Lewis, S.E., Celinker, S. and Rubin
 G.M.
 BDCP/HMT RH Drosophila EST Project
 Unpublished (2001)
 Contact: Stapleton, M.
 BDCP
 Lawrence, Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu

FEATURES
 source
 1. 569
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="RH14337"
 /clone_id="RH Drosophila melanogaster normalized Head
 pf1c-1"
 /sex="male and female"
 /dev_stage="Adult"
 /lab_host="DH5-alpha Tona"
 /note="Organ: head. Vector: pf1c1. Site_1: XhoI; Site_2:
 BamHI; Library was kindly generated by Piero Carninci at
 the RIKEN. The library was normalized and excised using
 Cre recombinase. Plasmid cDNA library."
 Cre recombinase. Plasmid cDNA library."

BASE COUNT 126 a 147 c 167 g 129 t

ORIGIN

Query Match 14.9%; Score 254.4; DB 13; Length 569;
 Best Local Similarity 65.5%; Pred. No. 5.1e-60;
 Matches 372: Conservative 0: Mismatches 196: Indels 0: Gaps 0:

17 GTTGTAGGAGCAATTAATGAAGATTAATGATTAATGAATTAATGATTAAT 76
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 1 GCTTTGTGAGCGCTTGGCGGCTCAAAACATGAGCATTAAGTCCAGCAATATC 60
 77 GTTAACTACCAATGAACGCTGTAGTCAAACTGAATGCAAGTGAAGGCGTTA 136
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 61 GCCAGTCCACCAATGAACAGTTTCCGACACGAGTACGCGCAAGTAGGGATCA 120
 137 AACGTTTACGTTGATGATGATGATGATGATGATGATGATGATGATGATG 196
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 121 AACGTTTACGTTGATGATGATGATGATGATGATGATGATGATGATGATG 180
 197 CCGCAGTGGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 256
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 181 CTCGGTGGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 240
 257 GTGATGTTGCAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 316
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 241 GCGACTGACAGCCAGCAAGATTAAGGCGCTGATGATGATGATGATGATG 300
 317 GTGCTCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 376
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 301 AGGCGTCCGAGGATGATGATGATGATGATGATGATGATGATGATGATG 360
 377 AACGTTCCGTTTGAATGATGATGATGATGATGATGATGATGATGATGATG 436
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 361 CTCGCGCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 437 ATATGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 496
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 421 AATGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 480
 497 GTTGGAGCTCTAGTGTGATGATGATGATGATGATGATGATGATGATGATG 556
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 481 GACTTGGGCGCTTGGGATGATGATGATGATGATGATGATGATGATGATGATG 540
 557 CCGGCTTAAAGATCAAGTCAAGTCTT 584
 111111 111111 111111 111111 111111 111111 111111 111111 111111 111111
 541 CTGGCGTCAAGATCAGTCTGCTGCTT 568

RESULT 6 674 bp mRNA linear EST 10-SEP-2001
 B1628316
 LOCUS RH5682.5prime RH Drosophila melanogaster normalized Head pf1c-1
 DEFINITION Drosophila melanogaster cDNA clone RH5682.5 similar to alpha-Est7:
 (GO:0004091) located on: 3R 84D5-84D5; 08/22/2001, mRNA sequence.
 G.M.

ACCESSION B1628316 GI:15530524
 VERSION B1628316.1

KEYWORDS	EST
SOURCE	fruit fly
ORGANISM	Drosophila melanogaster
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
AUTHORS	1 (bases 1 to 674) Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champagne, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C. J., Nuno, J., Pacle, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin, C. M.
TITLE	BDGP/HHMI RH Drosophila EST Project
JOURNAL	Unpublished (2001)
COMMENT	Contact: Stapleton, M. BDGP
FEATURES	Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu Plate: RH.566 row: G column: 10 High quality sequence stop: 558. Location/Qualifiers 1..674 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="RH56682" /clone_lib="RH Drosophila melanogaster normalized Head pFLC-1" /sex="male and female" /dev_stage="Adult" /lab_host="DHS-alpha Tona" /note="Organ: head; Vector: pFLC; Site: 1: XhoI; Site: 2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
BASE COUNT	153 a 170 c 195 g 155 t 1 others
ORIGIN	
Query Match	14.6%; Score 250; DB 13; Length 674;
Best Local Similarity	65.2%; Pred. No. 9.3e-59;
Matches	367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
1	ATGAATTCACAGTTAGTTGATGAGAAATTTAAATGGAAGATTAAATGCATTGAAAT 60
111	ATGATTAAGAACCTCGGCTTTGTGAGAGCGCTTGCGGTGGCCCTCAAAACATCGAGCAT 170
61	AAGTTTAAACTATCGTTTAACTACCAATGAACGGGTGTAGCTGAAACTAATATGGC 120
171	AAAGTCACGACATATCGCAGTCAGCAATGAACAGTTGTCCGACACGGAGTAACGCG 230
121	AAAGTGAAGGGGTTAAAGCTTTACTGTGATCGATGATTCCTACTACGTTTGAGGGT 180
231	CAGAGTGAAGGGGATTAAGACGTTATCTCTACGATGTGCCCTTACTTACGTTTGAAGGT 290
181	ATACCGTACGCCCAACCGCCAGTGGGTGAGCAGATTTTAAAGCAACCCAGCGACCAACA 240
291	ATCCGTACGCCCAACCGCCAGTGGGTGAGCAGATTTTAAAGCAACCCAGCGACCAACA 300
241	CCCTGGGATGGTGTGCGGTGATTTGTCACATCAATAAGATAGTCACTGCAAGTTATTTT 300
351	CCCTGGGATGGTGTGCGGTGATTTGTCACATCAATAAGATAGTCACTGCAAGTTATTTT 350
301	ATAAGGAGCAAGTGTGGCTCAGAGATTTCTATACCTAAGTGTCTATACGATATAT 360
411	GTCTTCGATTAAGGTAGAGGCTCCGAGGATCTCTCTATCTTAATGTGTACACCAACAT 470
361	CTAAATCCCGAATAACGTTCCCTTTAGTATACATACATAGTGTGGTTTATTTATC 420
471	GTGAAGCCCGAAGAGTGTGGCTTATGTTTGAATTCACAGGAGGAGGCTTATTTATC 530
421	GCTGAATAATCATCTGATATGTATGCTCTGTATTTATTTCAATTAAGAGATGTGTGTG 480

QY	481	ATTACATACATATATCGTTTGAGCTCTAGGTTTCTTAAGTTTAATTCAGAACCTT	540
DB	531	GGCGAGGCCAATCGGGAATGATGATGCGCCGATTACTTTATGAAAGAAATGTTGTCTC	590
QY	481	ATTACATACATATATCGTTTGAGCTCTAGGTTTCTTAAGTTTAATTCAGAACCTT	540
DB	591	GCACGATTAATCAGTACCTGGGCTCTTGGGATTTATGAGCTTAAGTCCCGAGGTA	650
QY	541	AATGTGCCCGGTAATGCGGCT	563
DB	651	AATGTACCAAGAAATGCTGGCT	673
RESULT 7			
LOCUS	B1635372		
DEFINITION	SD16705.5prine SD Drosophila melanogaster schneider L2 cell culture	676 bp	mRNA
FEATURES	port2 Drosophila melanogaster cDNA clone SD16705 5 similar to alpha-Est: FBan001112 GO: [carboxyesterase (GO:0004091); carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5; 05/18/2001		
ACCESSION	B1635372		
VERSION	B1635372.1		
KEYWORDS	EST.		
SOURCE	fruit fly.		
ORGANISM	Drosophila melanogaster		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prelygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
AUTHORS	Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.		
TITLE	BDGP/HMI Drosophila EST Project		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Stapleton, M.		
	BDGP		
	Lawrence Berkeley National Lab		
	One Cyclotron Rd, Berkeley, CA 94720, USA		
	Fax: 510 486 6798		
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu		
	Plate: SD.167 row: A column: 5		
	High quality sequence stop: 641.		
FEATURES	Location/Qualifiers		
source	1. 676		
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	/db_xref="taxon:7227"		
	/clone="SD16705"		
	/clone.lib="SD Drosophila melanogaster Schneider L2 cell culture port2"		
	/lab.host="DH5-alpha"		
	/note="Vector: port2; Site.1: EcoRI; Site.2: XhoI; Sized fractionated cDNAs were directly ligated into port2. Plasmid cDNA library."		
BASE COUNT	155 a 173 c 194 g 154 t		
ORIGIN			
Query Match	14.6%; Score 249.4; DB 13; Length 676;		
Best Local Similarity	65.2%; Pred. No. 1.4e-58;		
Matches	367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;		
QY	1	ATGAATTCACGTTAGTTGATGAGAAATTTAAATGGAAGATTAATGCAATTAAAT	60
DB	114	ATGAATTAAGAACCTCGCTTTGTGAGGCGCTTGGCGCTCMAAACCATTCAGCAT	173
QY	61	AAGTTTAAATATACGTTTAACTACCAATGAAGGAGGTGTCGGAACCTGAATATG	120
DB	174	AAAGTCACAGCAATATGCCAGTCGACCAATGAAGAGTTGTGCCGACAGGATACGC	233
QY	121	AAAGTAAAGGCGCTTAAAGCTTAACCTGTGACGATGATTCCTACTACAGTTTAAAGGT	180
DB	234	CAAGTAGAGGGATCAAGGCTATCTCTTCATGATGATGAGTGGCTACTTACGTTGAGAGGT	293
QY	181	ATACGGTACGCCCAACGCCAGTGGGTGAGCTGACATTTAAAGACACCCAGCGACCAACA	240

Db 294 ATCCGATACGCCACCTCCGGTGGGAGTTCCGTTAAGGCCCTCAGAGCCCAATT 353
 Qy 241 CCTGGGATGTGTCGATGATGTTCAATCAATTAAGATAGTCAGTCAGTATGATTT 300
 Db 354 CCTGGGACGAGTTCGCGACTGACGACGCCGGAAGTAAAGCGCTCCAGTCAGTTC 413
 Qy 301 ATTAACGGCAAGTGTGTGCTCAGAGATGTTCTATCACTAAGTGTCTAATCAATAT 360
 Db 414 GTCTGCAATAGGTAGAGGGCTCCGAGAGCTCCTCTATCTCAATGTCTACCAACAT 473
 Qy 361 CTAAATCCGAACTAAAGTCCGCTTTTATATACATATAGTGTGTGTTTATATTC 420
 Db 474 GTGAGGCCGACAGAGCTGCGCCGTTATGTTGATTCACGAGAGCGCTTCATTTTC 533
 Qy 421 GGTGAATAATCATGATATGATGTCCTGATATTTCTAATTAATTAATTAATTAAT 480
 Db 534 GCGAGGCCAATGCGGATGATGCGCGGATTAATTAATTAATTAATTAATTAAT 593
 Qy 481 ATTAACATACATATGTTTGGAGCTCTAGTCTTCTAATTAATTAATTAATTAAT 540
 Db 594 GTCAAGATACAGTACGACTTGGGCTTTGGATTTATGATCTTAAGTCCCGAGCTA 653
 Qy 541 AATGTCGCCGCTAATGCCGCT 563
 Db 654 AATGACAGGAATGCTGCGCT 676

RESULT 8 673 bp mRNA linear EST 07-SEP-2001
 B1614181
 LOCUS RH43493.5prime RH Drosophila melanogaster normalized Head pRc-1
 DEFINITION Drosophila melanogaster cDNA clone RH43493.5 similar to alpha-Est7:
 Fban0001112 GO: [carboxylesterase (GO:0004091)] carboxylesterase
 (GO:0004091) located on: 3R 84D5-84D5.1: 08/18/2001, mRNA sequence.

ACCESSION B1614181 GI:15509706
 VERSION B1614181.1
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 673)
 AUTHORS Stapleton M., Brokstein P., Hong L., Tyler D., Berman B., Carlson
 J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George
 R., Gonzalez M., Guarin H., Harris N., Li P., Liao G., Misra S.,
 Mungall C.J., Nunoo J., Pacled J., Paragas V., Park S.,
 Phouenavong S., Wan K., Yu C., Lewis S.E., Celinker S. and Rubin
 G.M.

TITLE BDGP/HMI RH Drosophila EST Project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP

Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
 Plate: RH.434 row: H column: 9
 High quality sequence stop: 553.
 Location/Qualifiers

FEATURES

1..673
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 /db_xref="taxon:7227"
 /clone="RH43493"
 /clone_1bp="RH Drosophila melanogaster normalized Head
 pRc-1"
 /sex="male and female"
 /dev_stage="Adult"
 /lab_host="DBS-alpha Tona"
 /note="Organ: head; Vector: pRc1; Site: 1; XhoI; Site: 2;
 BamHI; Library was kindly generated by Piero Carninci at
 the RIKEN. The library was normalized and excised using
 Cre recombinase. Plasmid cDNA library."

BASE COUNT 153 a 169 c 195 g 155 t 1 others
 ORIGIN

Query Match 14.5%; Score 248.4; DB 13; Length 673;
 Best local similarity 65.0%; Pred. No. 2.6e-58;
 Matches 366; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

Qy 1 ATGAATTTACAGTATGATGAGAAATTAATTAATGAAGATTAATGATTTGAAAT 60
 Db 111 ATGAATTAAGACCTCGCTTTTGAGCGCTGCGTGCGCCCTCAAAACCATGACAT 170
 Qy 61 AAGTTTAACTATCGTTTAATCAATGAAGGTTAGTGAAGTGAATATGATG 120
 Db 171 AAGTCCAGAGATGCGCAATGACCAATGAAGATTTGTCGCCGAGACGAGTACG 230
 Qy 121 AAGTGAAGGCTTAAAGTTAACTGTGATGATGATCTCTACTACATTTGAGGT 180
 Db 231 CAAGTGAAGGTTCAAGCTCTATCTCTAGATGCTCCACTTACAGTTCAGGGT 290
 Qy 181 ATACGATACCCCAACCGCCAGTGGTGAAGTTAAAGCAACCCAGCACACA 240
 Db 291 ATCCCGATACCGCCAGCTCCGTTGGGAGATTCGGTTAAGGCCCTCAGAGCCATT 350
 Qy 241 CCTGGGATGTGCTGCTGATGTCATTAAGATTAAGTCACTGCAATGATTTT 300
 Db 351 CCTGGGAGGAGTTGCGAGCTGACGACGACCCAGAGATTAAGCCGCTCCAGGTG 410
 Qy 301 ATACGGGCAAGTGTGTGCTCAGAGATTTCTATCTAATGTCCTTAATCAATAT 360
 Db 411 GTCTTCGATTAAGTAAAGGGCTCCGAGAGCTCCTATCTAATGTGTACCAACAT 470
 Qy 361 CTAAATCCGAACTAAAGTCCGCTTTTATATACATATGATGATGATTTATAT 420
 Db 471 GTGAAGCCGCAAGAGCTGCGCGGTTATGTTGATTCACGAGAGGCTTCATTA 530
 Qy 421 GGTGAATAATCATGATATGATGTCCTGATTTATTTCAATTAAGATGAGTGG 480
 Db 531 GCGAGGCCAATCGGGAATGATGCGCGGATTAATTAAGATGTTGATCTC 590
 Qy 481 ATTAACATACATATCGTTTGGAGCTCTAGTCTTCTAATTAATTAATTAAT 540
 Db 591 GTCAACATACATACGACTTGGGCTTTGGATTTATGATCTTAAGTCCCGAGCTA 650
 Qy 541 AATGTCGCCGCTAATGCCGCT 563
 Db 651 AATGTACAGGAATGCTGCGCT 673

RESULT 9 660 bp mRNA linear EST 10-SEP-2001
 B1639486
 LOCUS SD22067.5prime SD Drosophila melanogaster Schneider I2 cell culture
 DEFINITION PORT2 Drosophila melanogaster cDNA clone SD22067.5 similar to
 alpha-Est7: Fban0001112 GO: [carboxylesterase (GO:0004091)]
 carboxylesterase (GO:0004091) located on: 3R 84D5-84D5.1: 05/19/2001
 mRNA sequence.

ACCESSION B1639486 GI:15541696
 VERSION B1639486.1
 KEYWORDS EST.

SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 660)
 AUTHORS Harvey D., Brokstein P., Hong L., Evans-Holm M., Su C., Tsang G.,
 Lewis S. and Rubin G.M.

TITLE BDGP/HMI Drosophila EST Project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
471	GTGAAGCCGACAGGCGTGGCCGGTATGTTGGATTACACGGAGGAGCGCTTCAATATC	530							
QY	421 GGTGAATATCATCTGATATATGATGCTCTGATTAATTCATTAATAAGAGATGTGGTGG	480							
Db	531 GCGCAGGCGCATCGGAATGATGCGCCGGATTAATTAATGAAGAAGATCTTGTCTC	590							
QY	481 ATTAACATACAAATATGCTTGGAGCTCTAGTATTTTCAAGTTTAATTAATCAACACCT	540							
Db	591 GTCACGATACAGTACCGACTTGGGCTTTGGGATTATGAGCTTAACTCCCGCAGCTA	650							
QY	541 AATGTGCGCGGTAAATGCGGCC	562							
Db	651 AATGACCAAGAAATGCTGCC	672							
RESULT 11									
B1233202	B1233202	670 bp	mRNA	linear	EST 11-JUL-2001				
LOCUS	RE29491.prime RE Drosophila melanogaster normalized Embryo pf1c-1								
DEFINITION	Drosophila melanogaster cDNA clone RE29491 5 similar to alpha-ps7								
ACCESSION	Fban000112 located on: 3R 84D5-84D5; 04/12/2001, mRNA sequence.								
VERSION	B1233202								
KEYWORDS	B1233202.1 GI:14700784								
SOURCE	EST.								
ORGANISM	Fruit fly.								
REFERENCE	Drosophila melanogaster								
AUTHORS	Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.								
	1 (bases 1 to 670)								
	Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mitra, S., Mungall, C. J., Nuno, J., Pacleb, J., Pargass, V., Park, S., Pounenavong, S., Wan, K., Yu, C., Lewis, S. E., Celinker, S. and Rubin, G. M.								
	BCSP/HMT RE Drosophila EST Project								
	Unpublished (2001)								
	Contact: Stapleton, M.								
	BDSP								
	Lawrence Berkeley National Lab								
	One Cyclotron Rd, Berkeley, CA 94720, USA								
	Fax: 510 486 6798								
	Email: http://www.fruitfly.org/EST , estfruitfly.berkeley.edu								
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	/lab_host="DH5-alpha Tona"								
	/note="Organ: embryo; Vector: pf1c1; Site:1; Site:2 BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."								
	Cre recombinase. Plasmid cDNA library."								
BASE COUNT	152 a 168 c 194 g 155 t								
ORIGIN	1 others								
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QY	1 ATGAATTCACGCTAGTTGATGAGAAATTAATGAGAGATTAATGATCAATGAAAT	60							
Db	110 ATGATATAGAACCTCGCTTTGTGAGAGCGCTTGGCGGCTCAAAACATGAGCAT	169							
QY	61 AAGTTTAACTATCGTTTAACTACCAATGACGAGCGGTGATGCTGAACATGATATGCG	120							

Db	170	AAAGCCAGCAGTATTCGCCAGTCGACCAATGAAGAACGTTTGCCGACACGAGATACGGC	229
Qy	121	AAAGTGAAGAGCGTTTAAACGTTTAACTGTATACATGATTCCTACTACAGTTTAAAGGT	180
Db	230	CAAGTGAAGGGGTATCCAGCCGCTACTCTCTACGATGTGCCCTTACTTACGTTTCAAGGT	289
Qy	181	ATACCGTACGGCCCAACGCCACGTGGGTGAGCTGAGATTTTAAAGCACCCACGACCAACA	240
Db	290	ATCCCGTACGCCCAACGCCCTCCGGTGGGGAGTTTCCGGTTTAAAGCCCCCTACAGAGCCCAT	349
Qy	241	CCCTGGGATGGTGTGCGCTGATTTTGGCAATCATAAAGATTAAGTCAGTCCAAAGTTGATTT	300
Db	350	CCCTGGGAGCGCAAGTTCGCGACTGCGACCGCAGCCGGAAGGATTAAGGCCGTCCAGTGCAGTTC	409
Qy	301	ATAACGGCCAAAGTGTGGGCTCAGAGGATTTGCTATACCTAAAGTCTCATTCGAAATAT	360
Db	410	GTCTTCGTAAGTAGTAGAGGCTCGAGGACGCTCCTCTATTCATATGTGTACACCAACAT	469
Qy	361	CTAAATCCCGGAACATTAACGTCGCCGTTTATATACATACATAGTGCTGTGTTTATATC	420
Db	470	GTGAAGCCCGCAAGAGGCTCGCCCGGTTATGTGTTTGGATTTCACGGAGAGGCTTCATATC	529
Qy	421	GCTGAATATCTGTGATATATATGTCCTGATTTTTCATTAATAAGATGSGTGTG	480
Db	530	GCGCAGGCCAATCGGGATGTGATGCCCCGGGATTACTTTATGANAAGATGTGTCTC	589
Qy	481	ATTAACATACATATATCGTTTGGAGCTCTAGGTTTCTAAAGTTTAAATTCAGAGACCTT	540
Db	590	GTCAAGATACAGTACCGACTTGGGCTTTGGGATTTATGAGTCTTAAGTCCCGCAGCTA	649
Qy	541	AATGTGCCCCGCTAATGCCGCC	561
Db	650	AATGTACCGAGAAATGTCTGC	670
RESULT 12			
LOCUS	GH10213	648 bp	EST 19-APR-2001
DEFINITION	GH10213.Sprime GH Drosophila melanogaster head por2 Drosophila melanogaster cDNA clone GH10213 Sprime similar to U51050;		
ACCESSION	Drosophila melanogaster alpha esterase (aE7) gene, partial cds, mRNA sequence.		
VERSION	A1113763		
KEYWORDS	A1113763.1 GI:3514566		
SOURCE	EST.		
ORGANISM	fruit fly.		
REFERENCE	Drosophila melanogaster		
AUTHORS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
TITLE	1 (bases 1 to 648)		
JOURNAL	Harvey, D., Brokslein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G.M.		
COMMENT	BDGP/HHMT Drosophila EST Project		
	Unpublished (2001)		
	Contact: Stapleton, M.		
	BDGP		
	Lawrence Berkeley National Lab		
	One Cyclotron Rd Berkeley, CA 94720, USA		
	Fax: 510 486 6796		
	Email: http://www.fruitfly.org/EST , est@fruitfly.berkeley.edu		
	Plate: 102 row: B column: 1		
	High quality sequence stop: 435.		
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Best Local Similarity 65.0%; Pred. No. 2.3e-57;
Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, estfruitfly@berkeley.edu
Plate: 224 row: F column: 4
High quality sequence stop: 533.
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Matches 362; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

RESULT 14 646 bp mRNA linear EST 19-APR-2001
LOCUS A1109901
DEFINITION GH09292.Sprime GH Drosophila melanogaster head port2 Drosophila
melanogaster cDNA clone GH09292 Sprime similar to U51050:
Drosophila melanogaster alpha esterase (aef) gene, partial cds,
mRNA sequence.
ACCESSION A1109901
Lawrence Berkeley National Lab


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VERSION      AI109901.1  GI:3478225
KEYWORDS     EST.
SOURCE       fruit fly.
ORGANISM     Drosophila melanogaster
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              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 646)
AUTHORS      Harvey, D., Broksstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
              Lewis, S., and Rubin, G. M.
              BDGP/HHMI Drosophila EST project
TITLE        Unpublished (2001)
JOURNAL      Contact: Stapleton, M.
COMMENT      BDGP
              Lawrence Berkeley National Lab
              One Cyclotron Rd, Berkeley, CA 94720, USA
              Fax: 510 486 6798
              Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
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QY 181 ATACGCTACGCCAACCCGACGATGGTGAAGTATTAAGCAACCCGACGACCAACA 240
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Db 269 ATCCCTACGCCACCTCCGCTGGTGGGAGTGTGGGTTTAAGGCCCTCAAGAGCCCATTT 328
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QY 241 CCTGGAGTGTGTGCTGATGTTGCAATCAATAAGTAAAGTCAAGTCAAGTCAAGTCAAGT 300
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Db 389 GCTCTGATTAAGGTAGAGGCTCCGAGGACCTCTATCTATCTATCTATCTATCTATCTAT 448
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QY 361 CTAAATCCGAACCTAAAGCTCCGCTTTAGTATACATACATAGTGTGTGTTATATTC 420
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RESULT 15
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LOCUS        LP06524.5prine LP Drosophila melanogaster larval-early pupal pot2
DEFINITION   Drosophila melanogaster cDNA clone LP06524.5prine similar to
              051050: Drosophila melanogaster alpha esterase (aef) gene, partial
              cds, mRNA sequence.
ACCESSION    AI293416
VERSION      AI293416.1  GI:3942823
KEYWORDS     EST.
SOURCE       fruit fly.
ORGANISM     Drosophila melanogaster
              Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 646)
AUTHORS      Harvey, D., Broksstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
              Lewis, S., and Rubin, G. M.
              BDGP/HHMI Drosophila EST project
TITLE        Unpublished (2001)
JOURNAL      Contact: Stapleton, M.
COMMENT      BDGP
              Lawrence Berkeley National Lab
              One Cyclotron Rd, Berkeley, CA 94720, USA
              Fax: 510 486 6798
              Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
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Best Local Similarity 64.8%; Pred. No. 6.4e-57;
Matches 361; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

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3	1706.6	99.6	1713	4	US-09-068-960-1	Sequence 1, Appl1
4	1706.6	99.6	1713	4	US-09-068-960-3	Sequence 3, Appl1
5	1698.6	99.2	1713	2	US-08-669-924-1	Sequence 1, Appl1
6	1698.6	99.2	1713	2	US-09-068-960-7	Sequence 7, Appl1
7	1673.4	97.7	1713	2	US-08-669-924-2	Sequence 2, Appl1
8	951.8	55.6	1710	4	US-09-068-960-14	Sequence 14, Appl1
9	181.2	10.6	1584	3	US-08-747-221B-51	Sequence 51, Appl1
10	181.2	10.6	1584	3	US-08-747-221B-52	Sequence 52, Appl1
11	181.2	10.6	1584	4	US-09-005-051-51	Sequence 51, Appl1
12	181.2	10.6	1584	4	US-09-005-051-52	Sequence 52, Appl1
13	181.2	10.6	2007	3	US-08-747-221B-36	Sequence 36, Appl1
14	181.2	10.6	2007	3	US-08-747-221B-38	Sequence 38, Appl1
15	181.2	10.6	2007	4	US-09-005-051-36	Sequence 36, Appl1
16	181.2	10.6	2007	4	US-09-005-051-38	Sequence 38, Appl1
17	143.8	8.4	1590	3	US-08-747-221B-23	Sequence 23, Appl1
18	143.8	8.4	1550	3	US-09-005-051-21	Sequence 21, Appl1
19	143.8	8.4	1650	3	US-08-747-221B-21	Sequence 21, Appl1
20	143.8	8.4	1650	3	US-08-747-221B-22	Sequence 22, Appl1
21	143.8	8.4	1650	4	US-09-005-051-21	Sequence 21, Appl1
22	143.8	8.4	1650	4	US-09-005-051-22	Sequence 22, Appl1
23	143.8	8.4	1792	3	US-08-747-221B-18	Sequence 18, Appl1
24	143.8	8.4	1792	3	US-08-747-221B-20	Sequence 20, Appl1
25	143.8	8.4	1792	4	US-09-005-051-18	Sequence 18, Appl1
26	143.8	8.4	1792	4	US-09-005-051-20	Sequence 20, Appl1
27	140.2	8.2	1650	3	US-08-747-221B-60	Sequence 60, Appl1

C	28	140.2	8.2	1.550	3	US-08-747-221B-61	Sequence 61, Appl
C	29	140.2	8.2	1.650	4	US-09-005-051-60	Sequence 60, Appl
C	30	140.2	8.2	1.550	4	US-09-005-051-61	Sequence 61, Appl
C	31	140.2	8.2	2.144	3	US-08-747-221B-57	Sequence 57, Appl
C	32	140.2	8.2	2.144	3	US-08-747-221B-59	Sequence 59, Appl
C	33	140.2	8.2	2.144	4	US-09-005-051-57	Sequence 57, Appl
C	34	140.2	8.2	2.144	4	US-09-005-051-59	Sequence 59, Appl
C	35	139.6	8.1	1.515	3	US-08-747-221B-16	Sequence 16, Appl
C	36	139.6	8.1	1.515	3	US-08-747-221B-17	Sequence 17, Appl
C	37	139.6	8.1	1.515	4	US-09-005-051-16	Sequence 16, Appl
C	38	139.6	8.1	1.515	4	US-09-005-051-17	Sequence 17, Appl
C	39	139.6	8.1	1.982	3	US-08-747-221B-13	Sequence 13, Appl
C	40	139.6	8.1	1.982	3	US-08-747-221B-15	Sequence 15, Appl
C	41	139.6	8.1	1.982	4	US-09-005-051-13	Sequence 13, Appl
C	42	139.6	8.1	1.982	4	US-09-005-051-15	Sequence 15, Appl
C	43	87.2	5.1	1.684	3	US-09-136-421-11	Sequence 11, Appl
C	44	87.2	5.1	1.684	3	US-07-927-851-11	Sequence 11, Appl
C	45	87.2	5.1	2.989	1	US-08-453-323-1	Sequence 1, Appl

ALIGNMENTS

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1 RESULT 1
2 US-09-068-960-5
3 ; Sequence 5, Application US/09068960A
4 ; Patent No. 6235515
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org
7 ; TITLE OF INVENTION: MALATHION CARBOXYLSTERASE
8 ; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
9 ; CURRENT APPLICATION NUMBER: US/09/068,960A
10 ; CURRENT FILING DATE: 1998-05-20
11 ; EARLIER APPLICATION NUMBER: PCT/AU96/00746
12 ; EARLIER FILING DATE: 1996-11-22
13 ; EARLIER APPLICATION NUMBER: AU 6751
14 ; EARLIER FILING DATE: 1995-11-23
15 ; NUMBER OF SEQ ID NOS: 43
16 ; SOFTWARE: PatentIn Ver. 2.0
17 ; SEQ ID NO 5
18 ; LENGTH: 1713
19 ; TYPE: DNA
20 ; ORGANISM: Lucilia cuprina
21 US-09-068-960-5

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Query Match	Similarity	100.0%	Score 1713:	DB 4:	length 1713:
Best Local	Similarity	100.0%	Pred. No. 0:		
Matches 1713:	Conservative	0:	Mismatches	0:	Indels 0: Gaps 0
Oy	1	ATGAATTCACAGCTAGTTGATGAGAAATTTAAATGGAAGATTAAATGCATTGGAAAT	60		
Db	1	ATGAATTCACAGCTAGTTGATGAGAAATTTAAATGGAAGATTAAATGCATTGGAAAT	60		
Oy	61	AAATTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTACGTGAAACTGAATATGCG	120		
Db	61	AAATTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTACGTGAAACTGAATATGCG	120		
Oy	121	AAAGTGAAGAGCGGTTAAACGTTTAACTGTACAGATGATTCCTACTACAGTTTGGAGGT	180		
Db	121	AAAGTGAAGAGCGGTTAAACGTTTAACTGTACAGATGATTCCTACTACAGTTTGGAGGT	180		
Oy	181	ATACCGTACGCCCAACCGCACTGGGTGAGCTTAAAGACACCCAGGACCACA	240		
Db	181	ATACCGTACGCCCAACCGCACTGGGTGAGCTTAAAGACACCCAGGACCACA	240		
Oy	241	CCCTGGGATGGTGCCTGGATGTTGGCAATCATAAAGATAACTCAGTCGAATGATTTT	300		
Db	241	CCCTGGGATGGTGCCTGGATGTTGGCAATCATAAAGATAACTCAGTCGAATGATTTT	300		
Oy	301	ATAACGGCAAGAGTGTGGGCTCAGAGATTTCTATACCTAAGTGTCTATACGATAT	360		
Db	301	ATAACGGCAAGAGTGTGGGCTCAGAGATTTCTATACCTAAGTGTCTATACGATAT	360		


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Db 361 CTAATCCGGAACCTAAGCTCCGCTTTAGTATACATGATGCTGTTTATATC 420
QY 421 GGTGAATAATCATGCTGATATGATGCTGCTGATTTTCAAAAAGAGTGTG 480
Db 421 GGTGAATAATCATGCTGATATGATGCTGCTGATTTTCAAAAAGAGTGTG 480
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QY 601 AATGTCGCCGCTAATCCGCGCTTAAGATCAAGTCATGCGCTTGCATTGATAAAT 600
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QY 781 TTACCTTACCCAAATTTGGCGGCTATAGGGGTAGAGATATATAGATGTTTGGAA 840
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Db 841 TTTCTTATGAAGCCAAAGCCACAGATTTAGTAAACCTTGAGGAAAAAGTTTAACTCTA 900
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Db 1021 ATACCCATATGATGCTGCTTACCTTATGAGGCTCATTTTTCACCTTCAATTTCTTAAG 1080
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QY 1381 CTAATCCGGAACCTAAGCTCCGCTTTAGTATACATGATGCTGTTTATATC 1440
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QY 1441 AATCAATTTGGCCAAAGCTATGCTTAAGAAATCCGCTGATACAAACAAATTTGAAGTATG 1500
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Db 1681 TCGATGTTGAAAAACATAGATTTATTTTATG 1713

RESULT 2
US-09-068-960-9
; Sequence 9, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/NU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-9

Query Match 99.7%; Score 1708.2; DB 4; Length 1713;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1710; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATTTCAAGCTTATGATGAGAAATTTAAATGGAAGTTAAATGCAATTGAAAT 60
Db 1 ATGAATTTCAAGCTTATGATGAGAAATTTAAATGGAAGTTAAATGCAATTGAAAT 60
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Db 721 ATACTAATGTGGGTAAATGCTATTTGTCATTTGCTAAATACCAATGTCACATGTCGC 780
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Db 781 TTACCTTAGGCAATTTGGCGGCTATAGGTTGAGATTAATGATTAAGATGTTTGGAA 840
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Db 841 TTTCTTATGAAGCCACAGAGATTAGTAAACTTGAAGAAAGTTTAACTCTA 900
Qy 901 GAAGAGCTACAAATTAAGTATGCTTTCTTTGCTCCACTGTTGACCATATGACACC 960
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RESULT 3
US-09-068-960-1
: Sequence 1, Application US/09068960A
: Patent No. 623515
: GENERAL INFORMATION:
: APPLICANT: Commonwealth Scientific and Industrial Resch. Org.
: TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
: FILE REFERENCE: Attorney Docket No. 623515 50179-051
: CURRENT APPLICATION NUMBER: US/09/068,960A
: EARLIER FILING DATE: 1998-05-20
: EARLIER FILING DATE: 1996-11-22
: EARLIER FILING DATE: AU 6751
: NUMBER OF SEQ. ID NOS: 43
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 1713
: TYPE: DNA
: ORGANISM: Lucilia cuprina
US-09-068-960-1

Query Match 99.6%; Score 1706.6; DB 4; Length 1713;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGATTTTCAACGTTAGTTGATGAGAAATTAATGAAGATTAATGATGAAT 60
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 RESULT 4
 US-09-068-960-3
 ; Sequence 3, Application US/09068960A
 ; Patent No. 623515
 ; GENERAL INFORMATION:
 ; APPLICANT: Commonwealth Scientific and Industrial Rarch. Org.
 ; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
 ; FILE REFERENCE: Attorney Docket No. 623515 50179-051
 ; CURRENT APPLICATION NUMBER: US/09/068,960A
 ; EARLIER FILING DATE: 1998-05-20
 ; EARLIER APPLICATION NUMBER: PCT/AU96/00746
 ; EARLIER FILING DATE: 1996-11-22
 ; EARLIER APPLICATION NUMBER: AU 6751
 ; EARLIER FILING DATE: 1995-11-23
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 1713
 ; TYPE: DNA
 ; ORGANISM: Lucilia cuprina
 US-09-068-960-3
 Query Match 99.64; Score 1706.6; DB 4; Length 1713;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1709; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 601 AATGTCGCCGGTAATGCCGCCCTTAAGATCAAGTCATGCGCTTGCAATGGATTTAAAAAT 660
Db 601 AATGTCGCCGGTAATGCCGCCCTTAAGATCAAGTCATGCGCTTGCAATGGATTTAAAAAT 660
Qy 661 GCTGCTCTACCCACTACATGATGTTAAACCAACAACTCGCGGCTTTTCATCGTGTG 720
Db 661 GCTGCTCTACCCACTACATGATGTTAAACCAACAACTCGCGGCTTTTCATCGTGTG 720
Qy 721 AATCAATGTCGGGTAAATGCTATTTGTCATTTGGCTAATACCAATGTCATCGTCC 780
Db 721 AATCAATGTCGGGTAAATGCTATTTGTCATTTGGCTAATACCAATGTCATCGTCC 780
Qy 781 TTCACTTAGCAAAATTTGGCGGCTATTAAGGTGAGATTAATGATTAAGATGTTTGGAA 840
Db 781 TTCACTTAGCAAAATTTGGCGGCTATTAAGGTGAGATTAATGATTAAGATGTTTGGAA 840
Qy 841 TTTCTTATGAAGCCCAAGCCACAGAGATTAGTAAAACTTGAGAAAGTTTAACTCTA 900
Db 841 TTTCTTATGAAGCCCAAGCCACAGAGATTAGTAAAACTTGAGAAAGTTTAACTCTA 900
Qy 901 GAAGAGCGTACAAATAGGTCATGTTTCTTTGCTCCACTGTTGAGCCATATCAGACC 960
Db 901 GAAGAGCGTACAAATAGGTCATGTTTCTTTGCTCCACTGTTGAGCCATATCAGACC 960
Qy 961 GCTGATTTGTCCTTACCCAAACATCTCGGGAAATGTTAAACGCTTGCGGTAAATCG 1020
Db 961 GCTGATTTGTCCTTACCCAAACATCTCGGGAAATGTTAAACGCTTGCGGTAAATCG 1020
Qy 1021 ATACCCACTATGATGGGTAGACACTTCATATGAGGGTCTATTTTCTCAATCTTAAAG 1080
Db 1021 ATACCCACTATGATGGGTAGACACTTCATATGAGGGTCTATTTTCTCAATCTTAAAG 1080
Qy 1081 CAAATGCTATGCTTGTTAAGGAATGGAACCTGTCAATTTTGTGCCAAGTCAATG 1140
Db 1081 CAAATGCTATGCTTGTTAAGGAATGGAACCTGTCAATTTTGTGCCAAGTCAATG 1140
Qy 1141 GCTGATGCTGAAGCGACCGCCCAAGAGACTTGAATGGGTCAAAATTAAGAAAGCT 1200
Db 1141 GCTGATGCTGAAGCGACCGCCCAAGAGACTTGAATGGGTCAAAATTAAGAAAGCT 1200
Qy 1201 CATGTTACAGAGAAACCAACAGCTGATTAATTTATGATCTTGTCTCACAATCTAT 1260
Db 1201 CATGTTACAGAGAAACCAACAGCTGATTAATTTATGATCTTGTCTCACAATCTAT 1260
Qy 1261 TTTGCGTCCCAATGATCGTTTGTGCAATTAAGCTTTCATCAGCTCCGGTACACC 1320
Db 1261 TTTGCGTCCCAATGATCGTTTGTGCAATTAAGCTTTCATCAGCTCCGGTACACC 1320
Qy 1321 GTCTACTTGTATCGCTGACCTGATTCGAGAGATCTTATCAATCCCTATCGTATTAG 1380
Db 1321 GTCTACTTGTATCGCTGACCTGATTCGAGAGATCTTATCAATCCCTATCGTATTAG 1380
Qy 1381 CGTAGTGAACGTGTGTTAAGGGTGTAGTCAATGCTGATGAATTAACCTATTTCTG 1440
Db 1381 CGTAGTGAACGTGTGTTAAGGGTGTAGTCAATGCTGATGAATTAACCTATTTCTG 1440
Qy 1441 AATCAATTTGCCAAACGATAGCTTAAAGATCGCTGAATACAAACAAATGAAGTATG 1500
Db 1441 AATCAATTTGCCAAACGATAGCTTAAAGATCGCTGAATACAAACAAATGAAGTATG 1500
Qy 1501 ACTGATATGATGATCAATTTGCGCACCTGTAATCCTTATAGCAATGAATTAAGGT 1560
Db 1501 ACTGATATGATGATCAATTTGCGCACCTGTAATCCTTATAGCAATGAATTAAGGT 1560
Qy 1561 ATGAAAAATGTTTCCCTGGATCAATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
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Db 1561 ATGAAAAATGTTTCCCTGGATCAATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
Qy 1621 ATTAGTATGATTAAGAAATGATGATGTCCTGTAATGATTAAGATTAACATGGAG 1680
Db 1621 ATTAGTATGATTAAGAAATGATGATGTCCTGTAATGATTAAGATTAACATGGAG 1680
Qy 1681 TCGATGTTGAAAAACATAGATTTATTTAG 1713
Db 1681 TCGATGTTGAAAAACATAGATTTATTTAG 1713

RESULT 5
US-08-669-524-1
; Sequence 1, Application US/08669524
; Patent No. 5843758
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, Robyn J.
; APPLICANT: NEWCOMB, Richard D.
; APPLICANT: ROBIN, Geoffrey C.
; APPLICANT: BOYCE, Thomas M.
; APPLICANT: CAMPBELL, Peter M.
; APPLICANT: PARKER, Anthony G.
; APPLICANT: OAKESHOT, John G.
; APPLICANT: SMYTH, Kerrie A.
; TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: Lowe Price Leblanc & Becker
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,524
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Price, Robert L.
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 1451-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1124
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-669-524-1

Query Match 99.2%; Score 1698.6; DB 2; Length 1713;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGATTTTCAACGTTAGTTGATGAGAAATTAAGAAATGAAGATTAATGCTTGAAT 60
Db 1 ATGATTTTCAACGTTAGTTGATGAGAAATTAAGAAATGAAGATTAATGCTTGAAT 60
Qy 61 AAGTTTAAACTATGTTTAACTACCAATGAAAGGTGATGTAAGTGAATATATGCG 120
Db 61 AAGTTTAACTATGTTTAACTACCAATGAAAGGTGATGTAAGTGAATATATGCG 120
Qy 121 AAAGTGAAGGCGTTAAACGTTTAACTGTATGATGATTCCTACTACAGTTTGAAGGT 180
Db 121 AAAGTGAAGGCGTTAAACGTTTAACTGTATGATGATTCCTACTACAGTTTGAAGGT 180
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QY 181 ATACCGTACGCCAACCGCAGTGGGTGAGCTGAGATTTAAAGCACCCGAGCACCACA 240
DB 181 ATACCGTACGCCAACCGCAGTGGGTGAGCTGAGATTTAAAGCACCCGAGCACCACA 240
QY 241 CCCGCGGATGCTGCTGATGTTTGCATCATTAAGATTAAGTCAAGTGTGATTTT 300
DB 241 CCCGCGGATGCTGCTGATGTTTGCATCATTAAGATTAAGTCAAGTGTGATTTT 300
QY 301 ATACCGGCAAAAGTGTGGCTCAGAGATGCTATACCTAAGTGTCTATACGATTAAT 360
DB 301 ATACCGGCAAAAGTGTGGCTCAGAGATGCTATACCTAAGTGTCTATACGATTAAT 360
QY 361 CTAATATCCGAAACCTAAGCTCCGCTTTAGTATACATACATGCTGCTGTTTATATC 420
DB 361 CTAATATCCGAAACCTAAGCTCCGCTTTAGTATACATACATGCTGCTGTTTATATC 420
QY 421 GGTGAATATCATGCTATATGATGCTGCTGATTTATTCATTAAGATGCTGCTG 480
DB 421 GGTGAATATCATGCTATATGATGCTGCTGATTTATTCATTAAGATGCTGCTG 480
QY 481 ATTAACATATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 ATTAACATATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 AATGCGCGGCTAATGCGCGCTTAAAGATCAAGTCAAGTCAAGTCAAGTCAAGT 600
DB 541 AATGCGCGGCTAATGCGCGCTTAAAGATCAAGTCAAGTCAAGTCAAGTCAAGT 600
QY 601 AATGCGCGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 601 AATGCGCGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 GCTGCTCTTACCCATCATGATGTTTAAACGCAAACTGCGGCTCTTCCATCGGCT 720
DB 661 GCTGCTCTTACCCATCATGATGTTTAAACGCAAACTGCGGCTCTTCCATCGGCT 720
QY 721 ATACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 ATACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 TTTACCTTACCCAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 781 TTTACCTTACCCAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 TTTCTTATGAAGCAAGCAGAGATTTAGTAAACTTGAAGAAAGTTTAACTCTA 900
DB 841 TTTCTTATGAAGCAAGCAGAGATTTAGTAAACTTGAAGAAAGTTTAACTCTA 900
QY 901 GAAGAGCGTACAAATAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 GAAGAGCGTACAAATAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 GCTGATGCTGCTTACCCAAACCTCTGCGGAAATGCTTAAACTGCTGCGGATTTG 1020
DB 961 GCTGATGCTGCTTACCCAAACCTCTGCGGAAATGCTTAAACTGCTGCGGATTTG 1020
QY 1021 ATACCCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1021 ATACCCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 CAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1081 CAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1141 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 1141 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 CATGTTACAGAGAAACCAACAGCTGATTAATTTTATGATCTTCTCTCATCTAT 1260
DB 1201 CATGTTACAGAGAAACCAACAGCTGATTAATTTTATGATCTTCTCTCATCTAT 1260
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QY 1261 TTTGCTTCCCATGATGCTGTTTGTTCATTAAGTCAATGATGCTGCTGCTGCTGCTG 1320
DB 1261 TTTGCTTCCCATGATGCTGTTTGTTCATTAAGTCAATGATGCTGCTGCTGCTGCTG 1320
QY 1321 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
DB 1321 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1381 CGTAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1381 CGTAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1441 AATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1441 AATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1501 ACTGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1501 ACTGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
DB 1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY 1621 ATTAGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1621 ATTAGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 TCGATGTTGAAATACATGAGATTTATTTAG 1713
DB 1681 TCGATGTTGAAATACATGAGATTTATTTAG 1713

RESULT 6
US-09-068-960-7
; Sequence 7, Application US/09068960A
; Patent No. 623515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
; FILE REFERENCE: Attorney Docket No. 623515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; NUMBER OF SEQ. ID NOS: 43
; SOFTWARE: Patentln Ver. 2.0
; SEQ. ID NO 7
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-7

Query Match 99.2%; Score 1698.6; DB 4; Length 1713;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTTAAATGGAAGATTTAAATGATGAAAT 60
DB 1 ATGAATTTCAACGTTAGTTGATGAGAAATTTAAATGGAAGATTTAAATGATGAAAT 60
QY 61 AAGTTTTTAACTATGCTTTAACTACCAATGAACGCTGCTAGCTGAACCTGAATATG 120
DB 61 AAGTTTTTAACTATGCTTTAACTACCAATGAACGCTGCTAGCTGAACCTGAATATG 120
QY 121 AAGTGAAGCGCTTAAAGCTTTAACTGCTGACGATGATTTCTACTACAGTTTGAG 180
DB 121 AAGTGAAGCGCTTAAAGCTTTAACTGCTGACGATGATTTCTACTACAGTTTGAG 180
QY 181 ATACCGTACGCCAACCGCAGTGGGTGAGCTGAGATTTAAAGCACCCGAGCACCACA 240
DB 181 ATACCGTACGCCAACCGCAGTGGGTGAGCTGAGATTTAAAGCACCCGAGCACCACA 240
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Db 181 ATACCGTACGCCCAACCCGCAATGGGTGAGCTGAGATTAAAGACCCAGCCAGCACCAACA 240
Oy 241 CCCGCGGATGGTGGCGGATGTTGGCAATCATTAAGATTAAGTCTGTCAGTATATTT 300
Db 241 CCCGCGGATGGTGGCGGATGTTGGCAATCATTAAGATTAAGTCTGTCAGTATATTT 300
Oy 301 ATAAAGGCGCAAGTGTGGGTGAGAGATGTCATATCTATAGTGTATATAGCAATAT 360
Db 301 ATAAAGGCGCAAGTGTGGGTGAGAGATGTCATATCTATAGTGTATATAGCAATAT 360
Oy 361 CTAAATCCCGAACTAAACGTCCTTTAGTATACATACATGCTGTGTTTATATAC 420
Db 421 GGTGAATATCATGATATGATGTCCTGATTTATTCATTAAGAGATGCTGTG 480
Oy 481 ATTAACATACATATCTTTGGAGCTGAGTCTTCTAAGTTTAAATTCAGAAAGCTT 540
Db 481 ATTAACATACATATCTTTGGAGCTGAGTCTTCTAAGTTTAAATTCAGAAAGCTT 540
Oy 541 AATGCGCCGGTAATGCGGCTTAAAGATCAATGATGCTGCTGATTTAAAT 600
Db 541 AATGCGCCGGTAATGCGGCTTAAAGATCAATGATGCTGCTGATTTAAAT 600
Oy 601 AATGCGCCGGTAATGCGGCTTAAAGATCAATGATGCTGCTGATTTAAAT 660
Db 601 AATGCGCCGGTAATGCGGCTTAAAGATCAATGATGCTGCTGATTTAAAT 660
Oy 661 GGTGCTCTACCCACTACATGATGTTAAACGCAACGAGCTGCTTTCCATGCTGT 720
Db 661 GGTGCTCTACCCACTACATGATGTTAAACGCAACGAGCTGCTTTCCATGCTGT 720
Oy 721 ATACTAATGTCGGTAATGCTATTTGTCATGCTGCTAATACCAATGTCACATGCTGC 780
Db 721 ATACTAATGTCGGTAATGCTATTTGTCATGCTGCTAATACCAATGTCACATGCTGC 780
Oy 781 TTCACCTTAGCCAAATTTGGCGGCTAATAAGGTGAGATTAAGATGATGTTTGA 840
Db 781 TTCACCTTAGCCAAATTTGGCGGCTAATAAGGTGAGATTAAGATGATGTTTGA 840
Oy 841 TTTCTTATGAAGCCAGAGCAGATTTAGTAAACTTGAGAGAAAGTTTAACTGA 900
Db 841 TTTCTTATGAAGCCAGAGCAGATTTAGTAAACTTGAGAGAAAGTTTAACTGA 900
Oy 901 GAAGAGCGTACAAATTAAGTCTATTTCTTTGCTCCACTGTTGAGCCATATAGACC 960
Db 901 GAAGAGCGTACAAATTAAGTCTATTTCTTTGCTCCACTGTTGAGCCATATAGACC 960
Oy 961 GGTGATGTCCTTACCCAAACATCTCGGGAAATGTTAAACGCTTGGGTAATTCG 1020
Db 961 GGTGATGTCCTTACCCAAACATCTCGGGAAATGTTAAACGCTTGGGTAATTCG 1020
Oy 1021 ATACCCACTATGATGGTAAACCTTCATATGAGGCTATTTTCTCACTTCAATTCCTAG 1080
Db 1021 ATACCCACTATGATGGTAAACCTTCATATGAGGCTATTTTCTCACTTCAATTCCTAG 1080
Oy 1081 CAAATGCTATGCTTGTTAAGGAATGGAACCTTGTCAATTTTGTGCCAAGTAATG 1140
Db 1081 CAAATGCTATGCTTGTTAAGGAATGGAACCTTGTCAATTTTGTGCCAAGTAATG 1140
Oy 1141 GGTGATGTCGAAGCGAGCCGCCAGAGACCTTGAAGGCTGCTAAATTAAGAGCT 1200
Db 1141 GGTGATGTCGAAGCGAGCCGCCAGAGACCTTGAAGGCTGCTAAATTAAGAGCT 1200
Oy 1201 CATGTTACAGAGAAACCAACACCTGATATTTATGATCTTGTGCTCAGATCTAT 1260
Db 1201 CATGTTACAGAGAAACCAACACCTGATATTTATGATCTTGTGCTCAGATCTAT 1260
Oy 1261 TTTCTGTTCCCGATCATGTTTGTGCAATTAACGTTTCAATCAGACCTCGGTACACC 1320
Db 1261 TTTCTGTTCCCGATCATGTTTGTGCAATTAACGTTTCAATCAGACCTCGGTACACC 1320

Oy 1321 GTCATCTGTATGCTGCTGACCTGATTCGAGAGATCTTATCAATCCCTATGATATG 1380
Db 1321 GTCATCTGTATGCTGCTGACCTGATTCGAGAGATCTTATTAATCCCTATGATATG 1380
Oy 1381 GGTAGTGACGTCGTGTTAAGGCTGTATGTCATGCTGATGAATTAACCTATTTCTG 1440
Db 1381 GGTAGTGACGTCGTGTTAAGGCTGTATGTCATGCTGATGAATTAACCTATTTCTG 1440
Oy 1441 AATCAATGGCCAAACGATATGCTTAAAGATCGCTGATATCAAAACATTTGACGATG 1500
Db 1441 AATCAATGGCCAAACGATATGCTTAAAGATCGCTGATATCAAAACATTTGACGATG 1500
Oy 1501 ACTGATATGATATCAATTTGCCCACACTGATATCCCTTATAGCAATGAATTAAGT 1560
Db 1501 ACTGATATGATATCAATTTGCCCACACTGATATCCCTTATAGCAATGAATTAAGT 1560
Oy 1561 ATGAAATGTTTCTGCGATCCATTTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
Db 1561 ATGAAATGTTTCTGCGATCCATTTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
Oy 1621 ATTAGTATGAATTAAGATGATGTCCTGAAATGATTAAGATTAACATGCGAG 1680
Db 1621 ATTAGTATGAATTAAGATGATGTCCTGAAATGATTAAGATTAACATGCGAG 1680
Oy 1681 TCGATGTTGAAACATAGATTTATTTAG 1713
Db 1681 TCGATGTTGAAACATAGATTTATTTAG 1713

RESULT 7
US-08-669-524-2
; Sequence 2, Application US/08669524
; Patent No. 5843758
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, Robyn J.
; APPLICANT: NEWCOMB, Richard D.
; APPLICANT: ROBIN, Geoffrey C.
; APPLICANT: BOYCE, Thomas M.
; APPLICANT: CAMPBELL, Peter M.
; APPLICANT: PARKER, Anthony G.
; APPLICANT: OAKESHOTT, John G.
; APPLICANT: SMYTH, Kerrie A.
; TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe Price Leblanc & Becker
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669, 524
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Price, Robert L.
; REGISTRATION NUMBER: 22,695
; REFERENCE/DOCKET NUMBER: 1451-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single


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;      TOPOLOGY: linear
;      MOLECULE TYPE: DNA (genomic)
US-08-669-524-2

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Query Match	97.78;	Score 1673.4;	DB 2;	Length 1713;
Best Local Similarity	97.98;	Pred. No. 0;		
Matches 1677; Conservative	0;	Mismatches 36;	Indels 0;	Gaps 0

OY	1	ATGAATTCACGCTTGGTTGATGGAAGAAATTAAGATGAAGATTAAATCATCTTGAAAT	60
Db	1	ATGAATTCACGCTTGGTTGATGGAAGAAATTAAGATGAAGATTAAATCATCTTGAAAT	60
OY	61	AAGTTTAAACATATCGTTTAACTACCAATGAACGGTGTAGCTGAACACTGAATATAGCG	120
Db	61	AAGTTTAAACATATCGTTTAACTACCAATGAAGGGGTGATGAACCTGAATATAGCG	120
OY	121	AAATGAAAGCGGCTTAAAGCTTTAACTGTGTGCAATGATTTCTACTACAGTTTGAAGGGT	180
Db	121	AAATGAAAGCGGCTTAAAGCTTTAACTGTGTGCAATGATTTCTACTACAGTTTGAAGGGT	180
OY	181	ATACCGTAGCCGACCAAGCCGACGAGTGGTGAAGCTTTAAAGCAAGCCGACGACCAACA	240
Db	181	ATACCGTAGCCGACCAAGCCGACGAGTGGTGAAGCTTTAAAGCAAGCCGACGACCAACA	240
OY	241	CCCGGGATGGTGGGTGATTTGGTCATCTCAATTAAGATGAAGTACAGTCAAGTTGATTTT	300
Db	241	CCCGGGATGGTGGGTGATTTGGTCATCTCAATTAAGATGAAGTACAGTCAAGTTGATTTT	300
OY	301	ATACGGGGCAAAAGTGTGGCTCAGAGATGTGTATACCTTAAGTGTCTATACCAATAT	360
Db	301	ATTAACGGGCAAAAGTGTGGCTCAGAGATGTGTATACCTTAAGTGTCTATACCAATAT	360
OY	361	CTAAATCCGGAATTAAGCTCCCGTTTATAGTATACATCATGAGTGGTGTATATATC	420
Db	361	CTAAATCCGGAATTAAGCTCCCGTTTATAGTATACATCATGAGTGGTGTATATATC	420
OY	421	GGTGAATAATCATCGTGAATGTATGTGCTGATTAATTTCAATTAAGAGATGTGTGTG	480
Db	421	GGTGAATAATCATCGTGAATGTATGTGCTGATTAATTTCAATTAAGAGATGTGTGTG	480
OY	481	ATTAACTACAAATATCGTTTGGGAGCGTAAAGTTTCTAAGTTTAAATTCAGAAAGACTT	540
Db	481	ATTAACTACAAATATCGTTTGGGAGCTCTAAGTTTCTAAGTTTAAATTCAGAAAGACTT	540
OY	541	AATGTGCCCGGTAAATGCGCGGCTTTAAAGATCAAGTCANTGGCTTCATGTGATTAAGAT	600
Db	541	AATGTGCCCGGTAAATGCGCGGCTTTAAAGATCAAGTCANTGGCTTCATGTGATTAAGAT	600
OY	601	AATTCGGCCAACTTTGGTGGCAATCCCGAATAATATACAGTCTTGGTGAAGTCCGGT	660
Db	601	AATTCGGCCAACTTTGGTGGCAATCCCGAATAATATACAGTCTTGGTGAAGTCCGGT	660
OY	661	GCTGCGTACCCACTACATAGATGTTAAACGAACAACATCGGAGTCTTTCCATGNTGTT	720
Db	661	GCTGCGTACCCACTACATAGATGTTAAACGAACAACATCGGAGTCTTTCCATGNTGTT	720
OY	721	ATACCTAATGTGGGTAAATGCTATTTGTCATTTGGCTAATATACCAATGCAATAGTGTGCC	780
Db	721	ATACCTAATGTGGGTAAATGCTATTTGTCATTTGGCTAATATACCAATGCAATAGTGTGCC	780
OY	781	TTACACTTAAGCCAAATTTGGCGGCTAATAAGGTGAGANTATGATTAAGGATTTTGGAA	840
Db	781	TTACACTTAAGCCAAATTTGGCGGCTAATAAGGTGAGANTATGATTAAGGATTTTGGAN	840
OY	841	TTTTCTTATGAAGCCAGCCACAGGATTTAGTAAACTTGAGSAAAAAATTTTAACTCTA	900
Db	841	TTTTCTTATGAAGCCAGCCACAGGATTTATATAAACTTGAGSAAAAAATTTTAACTCTA	900
OY	901	GAAGAGCGTACAAATTAAGTGTATGTTTCCTTTGGTCCCACTGTGAGCATATAGACG	960
Db	901	GAAGAGCGTACAAATTAAGTGTATGTTTCCTTTGGTCCCACTGTGAGCATATAGACG	960
OY	961	GCATATGTGTATCCCAACATCTTCGGAAATGGTTAAAACTCCTTGGGGTATATTCG	1020

Db	961	GTGATGTGTCTTACCCAAACATCTCTCGGAAATGTTAAANTGCTTGGGGTAAATTCG	1020
Qy	1021	ATACCCACTATGATGGGTAAACACTTCATATGAGGGTCTATTTTTCATTCATTTCTTAAG	1080
Db	1021	ATACCCACTATGATGGGTAAACACTTCATATGAGGGTCTATTTTTCATTCATTTCTTAAG	1080
Qy	1081	CAAAATGCGCTATGCTTGTTAAGAATTTGAAACTTGTGTCAATTTTGTGCCAAGGAATG	1140
Db	1081	CAAAATGCGCTATGCTTGTTAAGAATTTGAAACTTGTGTCAATTTTGTGCCAAGGAATG	1140
Qy	1141	GCATATCTGACAGCACCGCCGCCAGACCTTGGAATGGTGTCTAAATTAATAAAGGCT	1200
Db	1141	GCATATCTGACAGCACCGCCGCCAGACCTTGGAATGGTGTCTAAATTAATAAAGGCT	1200
Qy	1201	CATGTTACAGAGAAACACCAACAGCTGATATTTTATGATCTTTTGTCTTCACATCTAT	1260
Db	1201	CATGTTACAGAGAAACACCAACAGCTGATATTTTATGATCTTTTGTCTTCACATCTAT	1260
Qy	1261	TTTCGGTTCCTCCCAACGATACGTTTGTGCAATTAACGTTTAAACACACCTCGGTACACC	1320
Db	1261	TTTCGGTTCCTCCCAACGATACGTTTGTGCAATTAACGTTTAAACACACCTCGGTACACC	1320
Qy	1321	GTCACCTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCGTATCTATATG	1380
Db	1321	GTCACCTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCGTATCTATATG	1380
Qy	1381	CGTACGTGACGTGGTGTTAAGGGGTAGTCATGATGATTAACCTATTTCTTCGG	1440
Db	1381	CGTACGTGACGTGGTGTTAAGGGGTAGTCATGATGATTAACCTATTTCTTCGG	1440
Qy	1441	AATCAATGGGCAACACGTATGCCCTAAAGATTCGCGTGAATACAAACAATGACGATG	1500
Db	1441	AATCAATGGGCAACACGTATGCCCTAAAGATTCGCGTGAATACAAACAATGACGATG	1500
Qy	1501	ACTGCTATATGATATCAATTTGCCACACAGCGTAAATCCCTATATGCAATGAATGAGGT	1560
Db	1501	ACTGCTATATGATATCAATTTGCCACACAGCGTAAATCCCTATATGCAATGAATGAGGT	1560
Qy	1561	ATGGAATGTTTCTCGTGGATCCCAATTAAGAAATCCGATGACACTATACAAGTGTGAAT	1620
Db	1561	ATGGAATGTTTCTCGTGGATCCCAATTAAGAAATCCGATGACACTATACAAGTGTGAAT	1620
Qy	1621	ATTAGTGAATGAATGAANAATGATTGATGTGCTGAAATGATTAAGATTAAACAATGGGAG	1680
Db	1621	ATTAGTGAATGAATGAANAATGATTGATGTGCTGAAATGATTAAGATTAAACAATGGGAG	1680
Qy	1681	TCGATGTTGAAAAACATAGAGATTTATTTTAAAG	1743
Db	1681	TCGATGTTGAAAAACATAGAGATTTATTTTAAAG	1743

```

? RESULT 8
? US-09-068-960-14
? Sequence 14, Application US/09068960A
? Patent No. 6235515
? GENERAL INFORMATION:
? APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org
? TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
? FILE REFERENCE: Attorney Docket No. 6235515 50179-051
? CURRENT APPLICATION NUMBER: US/09/068,960A
? CURRENT FILING DATE: 1998-05-20
? EARLIER APPLICATION NUMBER: PCR/AU96/00746
? EARLIER FILING DATE: 1996-11-22
? EARLIER APPLICATION NUMBER: AU 6751
? EARLIER FILING DATE: 1995-11-23
? NUMBER OF SEQ ID NOS: 43
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 14
? LENGTH: 1710
? TYPE: DNA
? ORGANISM: Musca domestica
? US-09-068-960-14

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Query Match 55.6%; Score 951.8; DB 4; Length 1710;
 Best Local Similarity 73.2%; Pred. No. 1.3e-264;
 Matches 1220; Conservative 0; Mismatches 447; Indels 0; Gaps 0;

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OY 44 TTAATGATGAAATAATGTTTAACTATGTTTAACTACCAATGAAGAGGTGTAG 103
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DB 44 TTAATGATGATGTTTAAATATACAAACTACCGTCTGATCAATGAAGAACCAATTA 103
OY 104 CTGAATCGAATATGCAAGTGAAGGCTTAAAGCTTAACTGTACGTGATTCCT 163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 104 TCGATACGTAATATGACAAATTAAGGCTTAAAGCTGAAATGACCTCTACGTATCTT 163
OY 164 ACTAGATTTTGGGGTATACCGTACGCCAACCGCGTGGAGTGGAGTGAATTAAG 223
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 164 ACTAGATTTTGGAGATATACCGTATACCGTATGCTAAGCTTCAGTGGATGAATTCAGG 223
OY 224 CACCCGAGGACCAACACCGTGGATGTGCTGATTTGTAATCAATGAAGTAACT 283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 224 CACCCGAGGCGCTGTACCATGTGGAGGCTGATGATGCTGTGGCCAGCCAAAGAT 283
OY 284 CAGTCAAGTATTTTAAAGGGCAAGTGTGCTGACAGAGATTTCTATACCTAA 343
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 284 CAGTCAAGACAGATTTCAATAGTGGCAAAACCCAGAGTGGAGATTTCTATACCTGA 343
OY 344 GTGTATATCAATATCAATCCGAAACTAAAGCTCCGTTTAACTATACATACATG 403
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 344 ATGTATATACCAATGACTTGAACCCAGAACAAAGGCTCTTATGTTTCAATCATTG 403
OY 404 GTGTGTTTTTATATCGGTGAAATATCATGTAATATGATGCTGATTTTCAATTA 463
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 404 GCGGAGATTTTATTTTCCGCAAGCAAACTGTAAGTGGTTGCTCCGACTTATATGA 463
OY 464 AAAAGAGTGTGTATATCAATACATATATGTTGGAGACTAGTTTTCTAAGTT 523
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 464 AAAAGAGTGTGTATATCAATATATGTTGGAGACTAGTTTTCTAAGTT 523
OY 524 TAAATTCAGAAAGACCTTAAATGTCGCGTAATGCGGCTTAAAGTCAAGTACGCT 583
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 524 TGAATTCGAAATATCATATGTCGCGCAACGCTGCTCAAGATCAAGTAATGCTT 583
OY 584 TGCATTTGATTAATAATTAATGCGCAACTTTGTTGGCAATCCGATAATATTAAGTCT 643
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 584 TGAATTCGATTAATAATTAATGCGCAACTTTGTTGGCAATCCGATAATATTAAGTCT 643
OY 644 TTGTGGAAGTCCGCTGCTGCTACCCACTATGATGTTAAACCGAACCAACTCGCG 703
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 644 TCGGGAAGTCTGCTGCGGCTCAACCCATTAATGATGATTAACCGAACCAACTCGCG 703
OY 704 GTCTTTTCATGATGATTAATGATGCGGTAATGCTATTTGCTCATTTGCTAATACC 763
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 704 GTCTTTTCATGATGATTAATGATGCGGTAATGCTATTTGCTCATTTGCTAATACC 763
OY 764 AATGTCACATGCTGCTTACCTTACCAATTAATGCGGCTTAAAGGCTGAATTAATG 823
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 764 AATGTCACATGCTGCTTACCTTACCAATTAATGCGGCTTAAAGGCTGAATTAATG 823
OY 824 ATAAGATTTTGAATTTCTTATGAAGAACCAAGCAGAGATTTAGTAAACTTGAGC 883
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 824 AAAAGATATCTGGAATTTCTTAAATGAAGCAATCCATGATTTGATCAAGAGAGC 883
OY 884 AAAAGTTTAACTCTGTAAGAGGCTACAAATGAAGTCAATTTCTTTGCTCCACG 943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 884 CACAAGTTTTCACACCCGAAAGATGCAAAATGAAGTCAATTTCTTTGACACACG 943
OY 944 TTGACCATATCAGACCGCTGATTTGCTTACCCAAACATCTCGGGAATAGTTAAAG 1003
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 944 TGAAGCATATACGACGCGCTGTGTATCCAAACCAATCAAGAAATGGAAGA 1003
OY 1004 CTGCTTGGGATATTCGATACCATATGATGCTGAACACTTCATATGAGGCTTATTTT 1063
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1004 GCGCTGGGAAATTCGATACCATGATGAGCAATACCTCTCAAGAGGTTTGCCTT 1063

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OY 1064 TCACCTCAATTTCTTAAGCAAAATGCCATGCTTGTAAAGCAATTTGAACCTGTGCAAT 1123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1064 CCAATTCATTTTCCCAACATATCCGGAGGTTGTAAAGAGTTTGAATCTCTGTCAAT 1123
OY 1124 TTGTGCCAAGTGAATTTGCTGATGTAACGACGCGCCCAAGAGACTTTGGAATGGCTG 1183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1124 ATGTGCTGGGAGTGTGGCTGACAGTGAACGCGAGTGGCCCGAAACCTGGAGAGGCTG 1183
OY 1184 CTAAATTTAAAGAGCTCATGTTTACAGGAGAAACCAACACTGATTAATTTTATGATC 1243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1184 CCATTTGTAAAAAGGCCCAATGTGATGGGGAACACCTTGTGATTAATTTTATGAGAC 1243
OY 1244 TTGTGCTCACAATCTATTTCTGTTCCCATGATCGTGTGTTGCAATACGTTTCAATC 1303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1244 TTGTGCTCATTCTTATTTCTTCCCTTCCCTGATGATGCTTCTACATTTGCGCTTCAAC 1303
OY 1304 ACACCTCGGTACACCGCTCTACTGTATGCTGTGACCTTGTGGAATGGAAGATCTTATCA 1363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1304 ACACAGCTGGACCTCCCATTTTATTTGTATCGTTGATTTGATTCGAAGAATATATTA 1363
OY 1364 ATCCCTATGCTTATGCTGATGACGCTGTGTTAAGGCTGTAGTCTGCTGATGAAT 1423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1364 ACCCTATGCTATTTATGCTGTTTGGCGCTTAAAGGTGAACCTGCGATGAGC 1423
OY 1424 TAACCTATTTCTTGAATCAATTTGGCCAAACGTAATGCTTAAAGATGCGGTAATACA 1483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1424 TAACCTATTTCTTGAATCAATTTGGCCAAACGTAATGCTTAAAGATGCGGTAATACA 1483
OY 1484 AAACATTTGAACGATATGACTGTATATGATGATCAATTTTGCACACACTGTTAATCTTATA 1543
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1484 AAACATTTGAACGATATGACTGTATATGATGATGATCAATTTTGCACACACTGTTAATCTTATA 1543
OY 1544 GCAATGAATTTGAAGTATGAGAAATGTTTCTGCGATCCATTAAGAAATCCGATGAG 1603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1544 GCAATGAATTTGAAGTATGAGAAATGTTTCTGCGATCCATTAAGAAATCCGATGAG 1603
OY 1604 TTATCAAGTGTGTAATTAATGATGATTAATGAATTAATGATGCTGTAATGATGA 1663
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1604 TCTATTAAGTTTAATATATGCGGATGATTAATGAATTTGATGATTTTGCAGAAATGATGA 1663
OY 1664 AGATTAAACATGAGGATGATGTTTGAAGAAACATGAGATTTATTT 1710
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1664 AATTAACATGAGGCAATGATATTTGATTAATGAAGAAATGTTT 1710

```

RESULT 9
 US-08-747-221B-51
 : Sequence 51, Application US/08747221B
 : Patent No. 6063610
 : GENERAL INFORMATION:
 : APPLICANT: Silver, Gary W.
 : APPLICANT: Wisniewski, Nancy
 : TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
 : TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
 : NUMBER OF SEQUENCES: 66
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Carol Talkington Verser, Ph.D.
 : ADDRESSEE: Heska Corporation
 : STREET: 1825 Sharp Point Drive
 : CITY: Fort Collins
 : STATE: Colorado
 : COUNTRY: USA
 : ZIP: 80525
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: Windows 95
 : SOFTWARE: WordPerfect for Windows, Version 7.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/747,221B
 : FILING DATE: No. 6063610ember 12, 1996
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:


```

NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1584
US-08-747-221B-51

Query Match      10.6%; Score 181.2; DB 3; Length 1584;
Best Local Similarity 56.4%; Pred. No. 1.7e-42;
Matches 361; Conservative 0; Mismatches 273; Indels 6; Gaps 1;

QY 116 ATGGCAAGTAAAGGCGTTAAAGCTTAAGTGTACGATGATGCTTCTACTACAGTTTG 175
DB 29 AAGTACTTTAAAGGAAAGAGCAAAATTAAGTAAAGAAAGAAATGCTTCCATAGTATT 88
QY 176 AGGATATACCGTACGCCCAAGCCAGTGGGTAGCTGAGATTAAAGCAAGCCAGCGAC 235
DB 89 CTGGAATTCATATGCGCAAACTCCTGTAGTGTCTAAGATTAAAGCCACCTCAACCTG 148
QY 236 CAACACCCCTGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 295
DB 149 CAAACACCTTGGTCAAGGTTCTTGTAGTAAAGAAAGGAATAGTTGATGATCACTAC 208
QY 296 ATTTTAACGGGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 355
DB 209 ATTTTAATTAAGAAATTAAGTAAAGGAGGCTTAAGTGTGTGTGTGTGTGTGTGTGT 268
QY 356 ATATCTAATATCCCAAGCAATTAAGCTCCGTTTGTATATCAATACATGATGATGAT 415
DB 269 CAAAAACATCAGAAATATCACTTCTTCCAGTAAATGATGATGATGATGATGATGAT 328
QY 416 TTATCGGTGAATATCATCGATATGATGATGATGATGATGATGATGATGATGATGATG 475
DB 329 TCATGGATATGCAATATGATATGATGATGATGATGATGATGATGATGATGATGATG 388
QY 476 TGTGATTAACATACATATCGTTGGAGCTGTAGTTTCTAAGTTTAAATTCAGAG 535
DB 389 TTCTGTTACTTCAATATATGATATGATGATGATGATGATGATGATGATGATGATGAT 448
QY 536 ACCTTAATGTGCGGATATGCGGCTTAAAGATCAAGTCAATGCGCTTGCATGATGAT 595
DB 449 AA-----GCGCTGCAAGTGTGTTGATGAGCAGGTGAAGCTCTTAATATGGGTAA 502
QY 596 AAAATATATGGCGCACTTGTGTGCAATCCGATATATTAAGTCTTGTGGTGAAGT 655
DB 503 AAACATATATGATCTTGTGTGAGTACCCCAACATATGATCTATTTTGGAGATCAG 562
QY 656 CCGGTCTGCTTACCATCATATGATGATGATGATGATGATGATGATGATGATGATGAT 715
DB 563 CAGGTGTGCAAGTGTCTATATGATGATGATGATGATGATGATGATGATGATGATGAT 622
QY 716 GTGTATATCAATATGCGGATATGATGATGATGATGATGATGATGATGATGATGATG 755
DB 623 AAGCATCTCACAAAGTGAAGTCTTTAATCTTGGGCG 662

RESULT 10
US-08-747-221B-52/c
; Sequence 52, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
```

```

APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: Carol Talkington Verser, Ph.D.
ADDRESS: Hesk Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610eember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-747-221B-52

Query Match      10.6%; Score 181.2; DB 3; Length 1584;
Best Local Similarity 56.4%; Pred. No. 1.7e-42;
Matches 361; Conservative 0; Mismatches 273; Indels 6; Gaps 1;

QY 116 ATGGCAAGTAAAGGCGTTAAAGCTTAAGTGTACGATGATGCTTCTACTACAGTTTG 175
DB 1556 AAGTACTTTAAAGGAAAGAGCAAAATTAAGTAAAGAAAGAAATGCTTCCATAGTATT 1497
QY 176 AGGATATACCGTACGCCCAAGCCAGTGGGTAGCTGAGATTAAAGCAAGCCAGCGAC 235
DB 1496 CTGGAATTCATATGCGCAAACTCCTGTAGTGTCTAAGATTAAAGCCACCTCAACCTG 1437
QY 236 CAACACCCCTGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 295
DB 1436 CAAACACCTTGGTCAAGGTTCTTGTAGTAAAGAAAGGAATAGTTGATGATCACTAC 1377
QY 296 ATTTTAACGGGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 355
DB 1376 ATTTTAATTAAGAAATTAAGTAAAGGAGGCTGAAGTGTATTAATGATGATG 1317
QY 356 ATATCTAATATCCCAAGCAATTAAGCTCCGTTTGTATATCAATACATGATGATGATG 415
DB 1316 CAAAAACATCAGAAATATCACTTCTTCCAGTAAATGATGATGATGATGATGATGAT 1257
QY 416 TTATCGGTGAATATCATCGATATGATGATGATGATGATGATGATGATGATGATGATG 475
DB 1256 TCATGGATATGCAATATGATATGATGATGATGATGATGATGATGATGATGATGATG 1197
QY 476 TGTGATTAACATACATATCGTTGGAGCTGTAGTTTCTAAGTTTAAATTCAGAG 535
DB 1196 TTCTGTTACTTCAATATATGATATGATGATGATGATGATGATGATGATGATGATGAT 1137
QY 536 ACCTTAATGTGCGGATATGCGGCTTAAAGATCAAGTCAATGCGCTTGCATGATGAT 595
DB 1136 AA-----GCGCTGCAAGTGTGTTGATGAGCAGGTGAAGCTCTTAATATGGGTAA 1083
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NAME/KEY: CDS
LOCATION: 11..1594
US-09-005-051-36

Query Match 10.6%; Score 181.2; DB 4; Length 2007;
Best Local Similarity 56.4%; Pred. No. 1.9e-42;
Matches 361; Conservative 0; Mismatches 273; Indels 6; Gaps 1;

QY 116 ATGGCAAGTGAAGCGTTAAAGCTTAACTGTACGATGCTCTACTACAGTTTG 175
DB 39 AAGGTACTTTAAAGAGAAAGACCAATTAAGTAAAGAAAGAAATGTTCATAGTTATT 98
QY 176 AGGGTATACCGTACGCCCAACCCGAGTGAGCTGAGATTAAAGCACCACGAC 235
DB 99 CTGGAAATTCATATGCGCAACCTCTGTAGTATCTAAGATTAAAGCACCACCTG 158
QY 236 CAACACCCCTGCGTGTGCGGATTTGCAATCATTAAGTACAGTCAAGTTG 295
DB 159 CAGAACCTTGTCAGGTGTTCTTGATGCTAGTAAAGAGGAATAGTGTATCAGTAC 218
QY 296 ATTTTAAAGGCAAGTGTGTGCTAGAGATTGCTATACCTAAGTGTATACGA 355
DB 219 ATTTTAAAGGCAAGTGTGTGCTAGAGATTGCTATACCTAAGTGTATACGA 278
QY 356 ATATCTAATCCCGAACTAAAGCTCCGTTTGTATACATACATGCTGCTTTTA 415
DB 279 CAAAAACATCAGAAATACCTCTTCCAGTAAATGATGATGATGAGAGAGGCTCT 338
QY 416 TTATGCGTGAATATCATGCTATGATGATGATGATGATGATGATGATGATG 475
DB 339 TCATGGGATCTGGAATAGTATGATGATGATGATGATGATGATGATGATG 398
QY 476 TGTGATTAACATACATATGCTGATGATGATGATGATGATGATGATGATG 535
DB 399 TTCTGTTACTTTCATATATGATGATGATGATGATGATGATGATGATGATG 458
QY 536 ACCTTAATGTCCCGGTAATGCCGCTTAAAGATCAAGTATGATGATGATGATG 595
DB 459 AA-----GCGCTGGCAATGTTGTTGATGACCAAGTTGAAGCTCTAATAATGGTAA 512
QY 596 AAAATTAATGGCCCACTTTGTTGCAATCCGATTAATTAATTAATTAATTAAT 655
DB 513 AAAACAAATTAATGATCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 572
QY 656 CCGGTGCTGCTTACCCACTACATGATGATGATGATGATGATGATGATGATG 715
DB 573 CAGGTGCGAAGTGTCTATTTGATGATGATGATGATGATGATGATGATGATG 632
QY 716 GTGTATACTAATGTCCGGTAATGCTATTTGCTCAATTGGC 755
DB 633 AAGCATCTCACAAGTGAAGTGTCTTTAATCTCTTGGGC 672

Search completed: April 11, 2003, 08:51:22
Job time : 46.518 secs

Db 500 TTAATTACAGATTGAACGCTCTTCGGTTTCCTGTCATGACACACACA-----AAATCC 553

Query Match	4.6%	Score 78.8	DB 9	Length 1611
Best Local Similarity	50.4%	Fred. No. 2.7e-10		
Matches 278	Conservative	0	Mismatches 262	Indels 12
			Gaps	3
Qy 177	GGGATACCGCTACGCCCAACCGCCAACTGGGTGACGTGAGATTAAAGCACCCACGGACAC	236		
Db 78	GGGATTCCTTACGGCCGAACACTGGCGGAAATATGCTTCGGGGACCCCGGGCCGC	137		
Qy 237	AACACCTGGGATGCTGTGGTGTGTTGCA---ATCATAAAGATAAGTCATGCAAGT	293		
Db 138	CAGAAATGGAGCGCGCTGGCGCATTTGTCATGTTCCGGTGAAGTAGCTTCTCAGCCAAC	197		
Qy 294	TGATTTTATTAACGGGCAAACTGTGTGGCTCAGAGGATTTCTATACCTAATGTCTATAC	353		
Db 198	GTACTCTCTGCGACAAATTAAGATTCGCGGTCAGAGACTCCTTAACCGATGCTGTGCG	257		
Qy 354	GAAATATCTAATATCCGGAACCTAAGCTCCGTTTATATCAATACATGGTGGTGTTT	413		
Db 258	G-----CGTATTCGCAAGAAAGCTCTCTGTGGGTGATCTCCACGGGGTTCTT	311		
Qy 414	TATTTTCGCTA---AAATCAATCGCTGATATGATATGCTCTCGATTATTTCAATTAAGA	470		

	Query Match	3.7%;	Score 63.8;	DB 10;	Length 1967;	
	Best Local Similarity	55.0%;	Fred. No. 2.3e-06;			
	Matches 191;	Conservative	0;	Mismatches 147;	Indels 9;	Gaps 3.
OY	325 GAGATTTGCTACTACAGTGTCTATTACGANTTAATCTAAATCCCGAAGCAACTMAAGTCGCC	384				
Db	437 GAACACGGTTTATATCTAAATGATGATGCAGCACCCTAACCC---AAAAAGTCCACT	493				
OY	385 GTTTTAGTATACATACATGCTGTGTTTTATTATCCGGGAATAATCATCGATATGTAT	444				
Db	484 GTATTGATATGAGATTATGTGTGGTGGTTTCAAACCTGGACATCATCTTTMACATGTTTG	553				
OY	445 GGTCCTGATTATTTTCATTAAAAGA---TGNGGTGTGATTAAACATCAATATCGTTTG	501				
Db	554 GATGSCAAGTTTCGGCTCGGGTTGAAGACAGTATTGTAGTGTCAATGACATATAGGGTG	613				
OY	502 GGAGCTCTAGSGTTTTCTTAAGTTTAAATTCAGAGACCTTAATGTCCCGGTAATGCCGCG	561				
Db	614 GGTCGCCCTAGSATTCTTAGCTT---GCCAGGAAATCTCGAGGCTCCAGGGACATGGGT	670				
OY	562 CTTAAAGATCAAGTCATGCGCTTGCAATGGATTAATAAATAATATGGCCAACTTTGGTGC	621				
Db	671 TTAATTGATCAACAAGCTGGCGCTTCAGGTGGCTTCMAAAAATAATATGACACCGTTGGTGA	730				
OY	622 AATCCGATTAATATTACAGTCTTTGGTGAAGAATGCCGGTCTGCCCTC	668				

Db 721 AATCCTAAAGTGAACCTCTCTTGGAGAAAGTGCAGGAGCAGCTTC 777

RESULT 4

US-09-880-107-2271
; Sequence 2271, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2271
; LENGTH: 2381
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474
US-09-880-107-2271

Query Match

3.7%; Score 63.8; DB 10; Length 2381;
Best Local Similarity 55.0%; Pred. No. 2.6e-06;
Matches 191; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

Qy 325 GAGAGTTGCTATACCTACGTCGTATAGCATATATCTAAATCCCGAATCAAGTCC 384
Db 427 GAGAGCTGTTTATATCTAAATGATGATCCAGCACCCTAAAC---AAAAATGCCACT 483
Qy 385 GTTTAGTATACATACATGCGTGGTGTATTTATTCGGTGAATATCATCGTATAT 444
Db 484 GTATTGATATGATTTAATGCTGCTGCTTCAACTGGAACATCATCTTTATGTTAT 543
Qy 445 GGTCTGATTTATTCATTAAGAAAG---TGTGCTGTTGATTAACATACATATCGTTG 501
Db 544 GATGGCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
Qy 502 GGAGCTAGGTTTCTAAGTTTAATTCAGAAAGCTTAATGTCGCCGTAATGCCGC 561
Db 604 GGTGCCCTAGGATTTCTTAGCTTT---GCCAGGAATCCTGAGGCTCCAGGAAATGGGT 660
Qy 562 CTTAAGATCAAGTATGCGCTTGCATTGGATTAAATTAATTTGGCCACTTGTGGC 621
Db 661 TTATTGATCAACAGTCTCTTCATGCTGCTTCAAAAAAATATAGCAGCCTTGTGGA 720
Qy 622 AATCCGATTAATTAACAGTCTTGTGTAAGTGGCGGTGCTGCTC 668
Db 721 AATCCTAAAGTGAACCTCTCTTGGAGAAAGTGCAGGAGCAGCTTC 767

RESULT 5

US-09-748-739A-3
; Sequence 3, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
; NAME/KEY: CDS
; LOCATION: (214)....(1935)
US-09-748-739A-3

Query Match

3.7%; Score 63.8; DB 10; Length 2416;
Best Local Similarity 55.0%; Pred. No. 2.6e-06;
Matches 191; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

Qy 325 GAGAGTTGCTATACCTACGTCGTATAGCATATATCTAAATCCCGAATCAAGTCC 384
Db 481 GAGAGCTGTTTATATCTAAATGATGATCCAGCACCCTAAAC---AAAAATGCCACT 537
Qy 385 GTTTAGTATACATACATGCGTGGTGTATTTATTCGGTGAATATCATCGTATATGAT 444
Db 538 GTATTGATATGATTTAATGCTGCTGCTTCAACTGGAACATCATCTTTATGTTAT 597
Qy 445 GGTCTGATTTATTCATTAAGAAAG---TGTGCTGTTGATTAACATACATATCGTTG 501
Db 598 GATGGCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
Qy 502 GGAGCTAGGTTTCTAAGTTTAATTCAGAAAGCTTAATGTCGCCGTAATGCCGC 561
Db 658 GGTGCCCTAGGATTTCTTAGCTTT---GCCAGGAATCCTGAGGCTCCAGGAAATGGGT 714
Qy 562 CTTAAGATCAAGTATGCGCTTGCATTGGATTAAATTAATTTGGCCACTTGTGGC 621
Db 715 TTATTGATCAACAGTCTCTTCATGCTGCTTCAAAAAAATATAGCAGCCTTGTGGA 774
Qy 622 AATCCGATTAATTAACAGTCTTGTGTAAGTGGCGGTGCTGCTC 668
Db 775 AATCCTAAAGTGAACCTCTCTTGGAGAAAGTGCAGGAGCAGCTTC 821

RESULT 6

US-09-748-739A-5
; Sequence 5, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
; NAME/KEY: CDS
; LOCATION: (214)....(1935)
US-09-748-739A-5

Query Match

3.7%; Score 63.8; DB 10; Length 2416;
Best Local Similarity 55.0%; Pred. No. 2.6e-06;
Matches 191; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

Qy 325 GAGAGTTGCTATACCTACGTCGTATAGCATATATCTAAATCCCGAATCAAGTCC 384
Db 481 GAGAGCTGTTTATATCTAAATGATGATCCAGCACCCTAAAC---AAAAATGCCACT 537


```

Db      775  AATCTTAAGTGTACTCTTTGGACGAAGTGCAGGACGCTC 821

RESULT 8
US-09-748-739A-16
; Sequence 16, Application US/09748739A
; Patent No. US20020119489A.1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-I-X 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-748-739A-16

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Query Match	3.7%	Score 63.8	DB 10	Length 2416
Best Local Similarity	55.0%	Pred. No. 2.6e-067	Indels	Gaps
Matches 191	Conservative	0	Mismatches 147	
QY	325	GAGGATGTCATACCTAAGTGTGTATACCAATTAATCTAAATCCGGAAGTAAACGTC	384	
Db	481	GAAGACGTGTTATATCTAATATGTATGATTCGACGACCTAAAC---AAAAATGGCACT	537	
QY	385	GTTTATGATATACATACATGGTGGTGGTTTATATGCGGAAATCATCGATATGAT	444	
Db	538	GTTTATGATATGATTTATGGTGGTGGTGGTTTCAACCTGGAACTCATCTTATACCTGTTAT	597	
QY	445	GGTCCGATATTTTCATTAATAAAGA---TGCGTGTGATTAACTATACATATCGTTG	501	
Db	598	GATGGCAAGTTCTCGCTGGCTGGTTGAAGAGTTATGTACTGTCAATGACATATAGSGTG	657	
QY	502	GGAGCTCTAGCTTTTCTAGTTTAATTCACAAACCTTAATGTGCCGCTAATCCGCG	561	
Db	658	GGTCCCTAGATCTTACCTTT---GCCAGAAATCTCGAGCTCCAGGAAACATGGGT	714	
QY	562	CTTAAATCAATCAATGGCTTGCATTCGATTGATTAATAAATAATTCGCCCACTTGGTGGC	621	
Db	715	TTATTTATATACAGTTGGCTCTTCAGTGGGTTCAAAAAATAATATAGCAGCTTGGTGGTA	774	
QY	622	AATCCGATATATTTACAGCTCTTTGTGTAAGTGGCGGTGGTGGCTC	668	
Db	775	AATCCTAAAGTGAACCTCTTTGGAGAAAGTGCAGAGCAGCTTC	821	
RESULT 9	US-09-893-519A-112			
	; Sequence 112, Application US/09893519A			
	; Publication No. US20030027243A1			
	GENERAL INFORMATION:			
	APPLICANT: ANADYS PHARMACEUTICALS, INC.			
	APPLICANT: THOMPSON, Craig			
	APPLICANT: MOORE, Jeffrey			
	APPLICANT: BURMAN, Ed T.			
	APPLICANT: BRADLEY, John			
	APPLICANT: DESILVA, Thamara			
	APPLICANT: HARRIS, Sandra			
	APPLICANT: KOMARNITSKY, Svetlana			
	APPLICANT: MENDILLO, Marc			
	APPLICANT: MOORE, Daniel			
	APPLICANT: MCCOY, Melissa			
	APPLICANT: SANDERSON, Karen			
	APPLICANT: HAO, Tariq			
	APPLICANT: ZHU, Shuhao			
	APPLICANT: LONG, Fan			
	APPLICANT: DAVIDOV, Eugene			

;; TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
;; FILE REFERENCE: 0342/16548-US2
;; CURRENT APPLICATION NUMBER: US/09/893,519A
;; CURRENT FILING DATE: 2001-06-28
;; PRIOR APPLICATION NUMBER: US 60/215,164
;; PRIOR FILING DATE: 2000-06-29
;; PRIOR APPLICATION NUMBER: US 60/224,457
;; PRIOR FILING DATE: 2000-08-10
;; NUMBER OF SEQ ID NOS: 146
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 112
;; LENGTH: 2444
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: Human Genbank/NM_000055
;; DATABASE ENTRY DATE: 2001-02-03
;; RELEVANT RESIDUES: (1)..(2444)
US-09-893-519A-112

Query Match 3.7%; Score 63.8; DB 9; Length 2444;
Best Local Similarity 55.0%; Pred. No. 2,6e-06;
Matches 191; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

QY 325 GAGGATGCTATACCTAGTGTCTATACGAATTAATCTAAATCCGGAACCTAAAGCTCC 384
DB 509 GAAGACTGTTATATCTAATATGATGATTCAGACCACTAAACC---AAAAATGCCACT 565
QY 385 GTTTTAGTATACATCATGCTGGTGGTTTATATCGGTGAATAATCATGATATGAT 444
DB 566 GTATTGATATGATGATTTATGCTGGTGGTTTCAACCTGCAACATCTTACATGTTAT 625
QY 445 GGTCCTGATTTTTCATTAAGAAAG---TGTGCTTGTATATACATACATATGCTTGG 501
DB 626 GATGCCAATTTCTGGCTGGCTGGAGAGATTATGATGTCATGATGATAGGGTG 685
QY 502 GGAGCTAGAGTTTCTAAGTTTAATTCAGAGACCTTAATGTCGCCGATATGCCGC 561
DB 686 GGTGCCCTAGGATTTCTACTT---GCCAGAAATCTCGAGGCTCCAGGAACATGGGT 742
QY 562 CTTAAGATCAAGTACGCTTGCATTTGATTAATAAATATGCGCCACTTTGGTGC 621
DB 743 TATTGATCAACAGTGTGCTTCAGTGGGTTCAAAAAAATATGACAGCCTTGGTGA 802
QY 622 AATCCGATATATTACAGCTTTGTGTAAGTGGCGTGCCTC 668
DB 803 AATCTAAAGTGTACTCTCTTTGGAGAAAGTGAAGGACGCTTC 849

RESULT 10
US-09-974-300-1107
;; Sequence 1107, Application US/09974300
;; Patent No. US20020146721A1
;; GENERAL INFORMATION:
;; APPLICANT: Berka, Randy M.
;; APPLICANT: Clausen, Ib Groth
;; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
;; TITLE OF INVENTION: Expression
;; FILE REFERENCE: 10085,500-US
;; CURRENT APPLICATION NUMBER: US/09/974,300
;; CURRENT FILING DATE: 2001-10-05
;; PRIOR APPLICATION NUMBER: 09/680,598
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 60/279,526
;; PRIOR FILING DATE: 2001-03-27
;; NUMBER OF SEQ ID NOS: 8481
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1107
;; LENGTH: 657
;; TYPE: DNA
;; ORGANISM: Bacillus licheniformis
US-09-974-300-1107

Query Match 3.5%; Score 59.4; DB 10; Length 657;
Best Local Similarity 50.1%; Pred. No. 1.7e-05;
Matches 175; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 377 AACGCCCTTTAGTATACATACATGCTGGTGTATATCGG---TGAAATCATC 433
DB 30 ATCTGCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 89
QY 434 GTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 493
DB 90 CGCTATGACGGGACTACGCTTGCAGAACGGAAGGATGCTGTCACCATCAAT 149
QY 494 ATCGTTGGAGCTCTAGGTTTCTAAGTTTAATTCAGAACACCTTAATGTCGCCGTA 553
DB 150 ATGCGCTGCTCGTTCGTTGGTGTGATCTATCTCTCATTTATGATCTCTACAGAGA 209
QY 554 ATGCGGCTTAAAGTCAATGATGCTGCTGATGATGATGATGATGATGATGATGATGAT 613
DB 210 ATCTTGGCTCTGATCAATCGCGCTCTGAGTGGTGAAGAACATATCGCTTCT 269
QY 614 TTGGTGGCATATCCATATATATACAGTCTTGGTGAAGTCCGCTGCTTACCC 673
DB 270 TTGGGGGAGACCGTCAATCAATGATGATGATGATGATGATGATGATGATGATGATG 329
QY 674 ACTACATGATGATTAACCGAACACCGCGCTTTCATGCTGAT 722
DB 330 CTTCGCTTTTGGCGATGCCGAAGCAAGGGCTTTTCAACAGCCAT 378

RESULT 11
US-08-781-986A-43
;; Sequence 43, Application US/08781986A
;; Publication No. US20030054436A1
;; GENERAL INFORMATION:
;; APPLICANT: Charles Kunsch
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5255
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/781,986A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Benson, Bob
;; REGISTRATION NUMBER: 30,446
;; REFERENCE/DOCKET NUMBER: PB248BP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 43:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3606 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
US-08-781-986A-43
Query Match 3.3%; Score 56.4; DB 7; Length 3606;
Best Local Similarity 52.1%; Pred. No. 0.00027;

	Matches	176;	Conservative	0;	Mismatches	156;	Indels	6;	Gaps	2
QY	335	GAGCATTTGCTAATACCTTAAGTGTCTATAACGAATAATCTAAATCCCGAACAATCTGCC	384							
Db	2729	GAAAGCTGTTTAATCAATAATAT---TTGGAAACAACAATAAATGATCAGACGAAAGAACCCT	2785							
QY	385	GTTTTAGATACATCAATGAGTGTCGTTTATTATCCGGTAAATCATCGTATATGAT	444							
Db	2786	GTCAATCATTTATTTTATTTATGGTGATGTTTGAATAATGGTCAATGTCACGCCCAACTCTAT	2845							
QY	445	GGTCCTGATTAATTTTCAT--TAAAAAGCATGTGCTGTGATTAACATACATATCGTTG	501							
Db	2846	CACCGGCACATTTAGTACAAAATAACGACATTAATCGTATTACATGCAATATATCGTTTA	2905							
QY	502	GGAGCTTAGAGTTTCTAAGTTTAAATTCAGAGAACCTTAATGTGCCGGTAATGCCGCG	561							
Db	2906	GGCCGATTAAGCATTTTATGACTGTGCATATTTTAAATGAATTTTTCATTCACATTAATGCG	2965							
QY	562	CTTAAAGATCAAGTCATAGCCCTTGATATGGATTTAAAAAATTAATTCGCCCAACTTTGGTGGC	621							
Db	2966	CTTTTCAGATCAAAATCAAATGCTCAATAAATGGGGGCATCAATTTATGTAATCTCGTGCGC	3025							
QY	622	AATCCGATTAATATTACAGCTTTGGTGTGAAGTCCGCG	659							
Db	3026	GACGCTAATTAACATTACTTTAATGGGTGACGTGTCAGG	3063							

```

RESULT 12
US-09-934-323-3
: Sequence 3, Application us/099934323
: Patent No. us20020150910A1
: GENERAL INFORMATION:
: APPLICANT: CUTLIS, RORY A. J.
: TITLE OF INVENTION: A NOVEL HUMAN CARBOXYLLESTERASE
: FILE REFERENCE: FAMILY MEMBER AND USES THEREOF
: CURRENT APPLICATION NUMBER: US/09/934,323
: CURRENT FILING DATE: 2001-08-21
: PRIOR APPLICATION NUMBER: US 60/226,774
: PRIOR FILING DATE: 2000-08-21
: NUMBER OF SEQ. ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 3
: LENGTH: 2508
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-934-323-3

```

Query Match	3.38;	Score 56;	DB 10;	Length 2508;
Best Local Similarity	53.7%;	Pred. No. 0.00028;		
Matches 116;	Conservative 0;	Mismatches 100;	Indels 0;	Caps 0

QY	530	CAGAAAGCCTTAATGTCGCGGGTAAATCCGGCCCTTAAGAAGTCAAGTCATGGCCCTGCATT	589
Db	671	CCGGGGACCAAGCTGCACAAMGGCAACATATGGGCTCCCTGGACCGAGATCCAGGCCCTGGCCT	730
QY	590	GGATTTAAAAATATTTGGCGCCAACTTTGGTGGCAATCCCGATTAATATATACAGTCTTTGGTG	649
Db	731	GGCTCAGTGAAMAAACATGCGCCACTTTGGGGGCGAACCCCGAGCGTATCACCATCTTTGGTT	790
QY	650	AAAGTCCCGGTCGTCCTCTACCCACATACATGATGTTAAACGGAACAACCTCGCGGTCCTTT	709
Db	791	CCGGGGGAGGGGCTCCTCGGCTCAACCTTGTGATCCCTCCACCAATTCAGAAGGGCTGT	850
QY	710	TTCATCGTGTATACTAATGTCCGGGTAAATCTATT	745
Db	851	TCCAGAAGGCCATGCGCCAGAGTGGCACCGCCCATTT	886

RESULT 13
US-09-934-323-1
; Sequence 1, Application US/09934323
; Patent No. US20020150910A1

```

: GENERAL INFORMATION:
: APPLICANT: Curtis, ROY A. J
: TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
: FILE OF INVENTION: FAMILY MEMBER AND USDS THEREOF
: FILE REFERENCE: 10448--081001
: CURRENT APPLICATION NUMBER: US/09/934,323
: CURRENT FILING DATE: 2001-08-21
: PRIOR APPLICATION NUMBER: US 60/226,774
: PRIOR FILING DATE: 2000-08-21
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 4667
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (420)...(2924)
: US-09-934-323-1

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Query Match	3.38;	Score 56;	DB 10;	Length 4667;
Best Local Similarity	53.7%;	Pred. No. 0.0004;		
Matches 116;	Conservative	0;	Mismatches 100;	Indels 0;
			Gaps	0;

OY	530	CAGAAAGCCTTAATGTCGCCGGTAAATGCACCAATCGCCCTTGCAATT	589
Db	1090	CCGGGGACCCAGCGTCCAAGAAGCAACTATGTGGCTCTCTGGACCAAGATCCAGGCCCTGCGCT	1149
OY	590	GGATTTAAAAAATAATTGGCCCACTTTGGTGGCAATCCCATATAATACATGCTTTGGTG	649
Db	1150	GCGTCAGTAGAAAACATGCGCCACTTTGGGGGGCACCCGACGGGTATACACATCTTTGGTT	1209
OY	650	AAAGTCCCGGTGCTGCTCTTACCCTACTACATGATGTTAAACGACAACMAACTGGCGGCTT	709
Db	1210	CCGGGGCAGGGGGCCCTCCTGGGTCAACCTTGTGATCTCCACCACATTCAGAAGGGCGTG	1269
OY	710	TCCATGCTGGTATACTAAATGCGGGTAATGCTATTT	745
Db	1270	TTCAGAAAGGCCATGCCCCAGATGTGGGACCGGCATTT	1305

RESULT 14
 US-09-418-176-1
 : Sequence 1, Application US/09418176
 : Publication No. US20030040040A1
 : GENERAL INFORMATION:
 : APPLICANT: Das, Goutam
 : TITLE OF INVENTION: DNA Molecules for Expression of
 : TITLE OF INVENTION: Polypeptides
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: White & Case
 : STREET: 1155 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: United States
 : ZIP: 10036-2787
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/418,176
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/624,398
 : FILING DATE: 04-Apr-1996
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: PCI/SE96/00318
 : FILING DATE: 12-Mar-1996
 : PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9501939-4
FILING DATE: 24-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Thelma A. Chen Cleland
REGISTRATION NUMBER: 40,948
REFERENCE/DOCKET NUMBER: 1103326-0206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8200
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2428 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: mammary gland
FEATURE:
NAME/KEY: CDS
LOCATION: 82..2319
OTHER INFORMATION: /Product= "bile-salt-stimulated
OTHER INFORMATION: lipase"
FEATURE:
NAME/KEY: exon
LOCATION: 985..1173
FEATURE:
NAME/KEY: exon
LOCATION: 1174..1377
FEATURE:
NAME/KEY: exon
LOCATION: 1378..1575
FEATURE:
NAME/KEY: exon
LOCATION: 1576..2415
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 151..2316
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 2397..2402
FEATURE:
NAME/KEY: repeat_region
LOCATION: 1736..2283
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..81
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1736..1788
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1789..1821
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1822..1854
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1855..1887
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1888..1920
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1921..1953
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1954..1986
FEATURE:
NAME/KEY: repeat_unit

LOCATION: 1987..2019
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 2020..2052
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 2053..2085
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NAME/KEY: repeat_unit
LOCATION: 2119..2151
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NAME/KEY: repeat_unit
LOCATION: 2152..2184
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 2185..2217
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 2218..2250
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 2251..2283
PUBLICATION INFORMATION:
AUTHORS: Nilsson, Jeanette
AUTHORS: Blackberg, Lars
AUTHORS: Carlsson, Peter
AUTHORS: Enerback, Sven
AUTHORS: Hernehl, Olle
AUTHORS: Bjursell, Gunnar
TITLE: cDNA cloning of human milk
TITLE: bile-salt-stimulated lipase and evidence for its
TITLE: identity to pancreatic carboxylic ester hydrolase
JOURNAL: Eur. J. Biochem.
VOLUME: 192
PAGES: 543-550
DATE: Sept.-1990
US-09-418-176-1

Query Match 3.2%; Score 55.4; DB 9; Length 2428;
Best Local Similarity 52.9%; Pred. No. 0.00039;
Matches 119; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 530 CAGAGACCTTAATGTCGCCGTAATGCCGCTTAAGATCAAGTCATGCTTGCAATT 589
DB 608 CTGGGGAGCGCAATCTGCAGGTAATGATGCTTCGGGATCAGACATGGCATTCCTT 667
QY 590 GGATTAAATAATATGCGGCACCTTTGGTGGCAATCCGATTAATTAAGTCTTGGTG 649
DB 668 GGGTGAAGAGGATATTCGGGCTTCGGGGGAGCCCAACACATCAGCTCTTGGGG 727
QY 650 AAAGTCCCGCTGCTGCTTACCCACTACATGATGTTAACCGAACAACCTCGGCTCTT 709
DB 728 ACTGCTGCTGAGGTGCACAGCTCTCTCTCAGACACCTCTCCCTACACAAAGGGGCTCA 787
QY 710 TCCATCGTGTACTAATGTCGGGTAATGCTAATGTTTTCCTTCCTGG 754
DB 788 TCCGGGAGCCATCAGCCAGAGCGGCTGGCCCTGATGTCCTCGGG 832

RESULT 15
US-09-969-347-220
Sequence 220, Application US/09969347
Patent No. US20020115085A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
FILE REFERENCE: 689290-69
CURRENT APPLICATION NUMBER: US/09/969,347
CURRENT FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: US/60/237,598
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: US/60/237,604
 PRIOR FILING DATE: 2000-10-03
 NUMBER OF SEQ ID NOS: 318
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 220
 LENGTH: 2428
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-969-347-220

Query Match 3.28; Score 55.4; DB 10; Length 2428;
 Best Local Similarity 52.98; Pred. No. 0.00039;
 Matches 119; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

```

OY 530 CAGAGACCTTAATGTGCGCGTAATGCCGCTTAAGATCAAGTCATGGCCTTGCTT 589
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 608 CTGGGACGCCCAATCTGCGAGTAAGTATGCTTGGATCAGACATGGCCATTGCTT 667
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 590 GGATTAAATAATTTGCGCACTTTGTGCGCATCCCGAATATATACAGCTTTGTG 649
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 668 GGGTAAGAGAAATATCGGGCTTCGGGGGGAACCCACACATCAGCGCTTGGGG 727
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 650 AAGTCCCGTGTGCTCTACCCACTACATGATGTTAACCGAACTGCGGCTTT 709
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 728 AGTCTGTGAGGTGCGAGCTCTCTGCAAGACCTCTCCCTACACAAAGGGCTCA 787
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 710 TCCATCGTGTATCTAATGTGCGGTATGCTATTGTCCATTTG 754
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 788 TCCGGGAGGCATCAGCCAGAGGGGCTGCGCTGAGTCCCTGGG 832
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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 Job time : 108.528 secs

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:59:47 ; Search time 2944.03 Seconds

(without alignments)
16933.650 Million cell updates/sec

Title: US-09-776-910-7

Perfect score: 1713
Sequence: 1 atgaattcaacgttagttt.....aacatagagattatttttag 1713

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_hlg:*
3: gb_in:*
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16: em_fun:*
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18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rod:*
36: em_hlg_mam:*
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40: em_hlgo_mus:*
41: em_hlgo_other:*
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Pred. No. is the number of results predicted by chance, to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1713	100.0	1713	6 AR062837	AR062837 Sequence
2	1713	100.0	1713	6 AR153441	AR153441 Sequence
3	1713	100.0	2240	3 LCUS5636	US6636 Lucilia cup
4	1703.4	99.4	1713	6 AR153442	AR153442 Sequence
5	1701.8	99.3	1713	6 AR153438	AR153438 Sequence
6	1701.8	99.3	1713	6 AR153439	AR153439 Sequence
7	1698.6	99.2	1713	6 AR153440	AR153440 Sequence
8	1683	98.2	1713	6 AR062838	AR062838 Sequence
9	987.2	57.6	2175	3 AF133082	AF133082 Musca dom
10	959.4	56.0	2175	3 AF133082	AF133082 Haematobi
11	956.6	55.8	1710	6 AR153445	AR153445 Sequence
12	678.8	39.6	2017	3 AY051473	AY051473 Sequence
13	377	22.0	2660	3 AY121675	AY121675 Drosophila
14	375.4	21.9	2820	3 DMU51050	US1050 Drosophila
15	370.6	21.6	57335	2 AC015272	AC015272 Drosophila
16	370.6	21.6	188459	3 AC008312	AC008312 Drosophila
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18	370.6	21.6	309023	3 AE003671	AE003671 Drosophila
19	363.8	21.2	1962	3 AY051497	AY051497 Drosophila
20	323	18.9	2122	3 AY058637	AY058637 Drosophila
21	306.2	17.9	1906	3 AY058345	AY058345 Drosophila
22	302	17.6	13044	2 AC014297	AC014297 Drosophila
23	302	17.6	117743	2 AC008098	AC008098 Drosophila
24	302	17.6	173373	3 AC008349	AC008349 Drosophila
25	302	17.6	307363	3 AE003457	AE003457 Drosophila
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27	280	16.3	1205	3 AF216215	AF216215 Drosophila
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32	238.2	13.9	188459	3 AC008312	AC008312 Drosophila
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34	238.2	13.9	309023	3 AE003671	AE003671 Drosophila
35	231.2	13.5	1724	3 AY069743	AY069743 Drosophila
36	229.2	13.4	2401	3 DMU51054	US1054 Drosophila
37	225.8	13.2	933	3 AF216216	AF216216 Drosophila
38	225.8	13.2	1836	3 COSERES1	Z32694 C. quinquef
39	225.6	13.2	3447	3 DMU51052	US1052 Drosophila
40	220.8	12.9	1630	2 COSERES2	Z32695 C. quinquef
41	215.6	12.6	84252	2 AC009207	AC009207 Drosophila
42	213.6	12.5	1401	3 CPU43544	U43544 Culex pipie
43	209	12.2	6028	3 AF177382	AF177382 Culex tri
44	206.4	12.0	1401	3 CPU43546	U43546 Culex pipie
45	201.4	11.8	1401	3 CPU43545	U43545 Culex pipie

ALIGNMENTS

RESULT 1	AR062837	1713 bp	DNA	PAT 29-SEP-1999
LOCUS	AR062837			
DEFINITION	Sequence 1 from patent US 5843758.			
ACCESSION	AR062837			
VERSION	AR062837.1	GI:5990528		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 1713)			
AUTHORS	Russell,R.Joyce., Newcomb,R.David., Robin,G.Charlesde.Quetteville., Boyce,T.Mark., Campbell,P.Malcolm., Parker,A.Gerard., Oakesholt,J.Graham. and Smyth,K.-A.			
TITLE	Enzyme based bioremediation			

JOURNAL Patent: US 5843758-A 1 01-DEC-1998;
 FEATURES Location/Qualifiers
 source 1..1713
 BASE COUNT 516 a 305 c 370 g 522 t
 ORIGIN

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 Best local Similarity 100.0%; Pred. No. 0;
 Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 121 AAGGTGAAGCGCTTAACGCTTAAGCTGTAGATGATGCTACTACAGTTTGAAGGT 180
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 DB 181 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTAAAGCACCAGCAGCAACA 240
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 DB 841 TTTCTTATTAAGCAAGCCAGACAGATTTAATAAATCTTGAGAAAAAAGTTTAACTCTA 900
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 QY 1261 TTCTGCTCCCATGCTGATGCTTTGTTGAATTAACGTTTCAATCACACCTCCGGTACACC 1320
 DB 1261 TTCTGCTCCCATGCTGATGCTTTGTTGAATTAACGTTTCAATCACACCTCCGGTACACC 1320
 QY 1321 GTCTACTTATGCTGCTTGCACCTTGTGGAAGATCTTATTAATCCCTATGCTATATG 1380
 DB 1321 GTCTACTTATGCTGCTTGCACCTTGTGGAAGATCTTATTAATCCCTATGCTATATG 1380
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 LOCUS DEFINITION
 ACCESSION ARI53441
 VERSION ARI53441.1 GI:15120973
 KEYWORDS
 SOURCE
 ORGANISM
 UNKNOWN.
 UNCLASSIFIED.
 REFERENCE
 1 (bases 1 to 1713)
 Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
 Robin, G. Charlesde, Quetleville., Claudianos, C., Smyth, K. A.,
 Boyce, T. Mark., Oakeshott, D. Graham. and Brownlie, D. Colin.
 Malathion carboxylesterase
 TITLE JOURNAL Patent: US 6235515-A 7 22-MAY-2001;
 FEATURES Location/Qualifiers
 source 1..1713

BASE COUNT 516 a /organism="unknown"
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 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 VERSION
 U5636.1
 KEYWORDS
 GI:1336079
 ORGANISM
 Lucilia cuprina.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Oestroidea; Calliphoridae; Lucilia.
 TITLE
 1 (bases 1 to 2240)
 Newcomb R.D., East P.D., Russell R.J. and Oakeshott J.G.
 Isolation of alpha cluster esterase genes associated with
 organophosphate resistance in *Lucilia cuprina*
 JOURNAL
 Insect Mol. Biol. 5 (3), 211-216 (1996)
 MEDLINE
 96392952
 PUBMED
 8799740
 REFERENCE
 2 (bases 1 to 2240)

AUTHORS Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
TITLE cDNA cloning, baculovirus-expression and kinetic properties of the
esterase, E3, involved in organophosphorus resistance in *Lucilia*
cuprina
JOURNAL Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)
MEDLINE 97215578
PUBMED 9061925
REFERENCE 3 (bases 1 to 2240)
AUTHORS Newcomb, R.D., Campbell, P.M., Ollis, D.L., Cheah, E., Russell, R.J. and
Oakeshott, J.G.
TITLE A single amino acid substitution converts a carboxylesterase to an
organophosphorus hydrolase and confers insecticide resistance on a
blowfly
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997).
MEDLINE 97352821
PUBMED 9207114
REFERENCE 4 (bases 1 to 2240)
AUTHORS Campbell, P.M., Newcomb, R.D., Russell, R.J. and Oakeshott, J.G.
TITLE Two different amino acid substitutions in the α -esterase, E3,
confer alternative types of organophosphorus insecticide resistance
in the sheep blowfly
JOURNAL Unpublished
REFERENCE 5 (bases 1 to 2240)
AUTHORS Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
TITLE Direct Submission
JOURNAL Submitted (24-Apr-1996) Richard D. Newcomb, Molecular Genetics,
HortResearch, Private Bag 92 169, Auckland, New Zealand
FEATURES
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exon 1540..>2010
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DB 718 GGTGAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 777
QY 481 ATTAATATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
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DB 958 GGTGCTCTACCCAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1017
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Qy 961 GCTGATTTGTCTTACCCAAACATCTCGGAAATGTTAAACGCTGGGGTAATTCG 1020
Db 1258 GCTGATTTGTCTTACCCAAACATCTCGGAAATGTTAAACGCTGGGGTAATTCG 1317
Qy 1021 ATACCACATATGATGGGTACACTTCATATGAGGGTCTATTTTTCACCTCAATCTTAAG 1080
Db 1318 ATACCACATATGATGGGTACACTTCATATGAGGGTCTATTTTTCACCTCAATCTTAAG 1377
Qy 1081 CAATGCTCTATGCTTTTAAGGAATGGAACCTGTGCAATTTTGTGCCAAGTGAATG 1140
Db 1378 CAATGCTCTATGCTTTTAAGGAATGGAACCTGTGCAATTTTGTGCCAAGTGAATG 1437
Qy 1141 GCTGATGCTGAAGCAGCCGCCAGAGACCTTGGAAATGGGTGCGTAAATATAAAGGCT 1200
Db 1438 GCTGATGCTGAAGCAGCCGCCAGAGACCTTGGAAATGGGTGCGTAAATATAAAGGCT 1497
Qy 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTTATGATCTTGTCTCACATCTAT 1260
Db 1498 CATGTTACAGAGAAACACCAACAGCTGATATTTTATGATCTTGTCTCACATCTAT 1557
Qy 1261 TTTGTTGTTCCCATGATGCTTTTGTGCAATTTAGCTTCAATCACACCTCCGGTACACC 1320
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Qy 1381 CGTAGTGACGCTGTTTAAAGGGTGTATGATGCTGATGATTAACCTATTTCTTCTG 1440
Db 1678 CGTAGTGACGCTGTTTAAAGGGTGTATGATGCTGATGATTAACCTATTTCTTCTG 1737
Qy 1441 AATCAATTTGGCCAAACGATATGCTTAAGAAATCGCGTGAATACAAACAAATGAACGTAATG 1500
Db 1738 AATCAATTTGGCCAAACGATATGCTTAAGAAATCGCGTGAATACAAACAAATGAACGTAATG 1797
Qy 1501 ACTGATATGATGATTAATTTGGCCACGCTGTATCTTATAGCAATGAATTTGAAGT 1560
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Qy 1561 ATGGAATATGTTCTCTGGGATCAATTAAGAAATCCGAGAGATTAACAAGTGTGTAAT 1620
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Qy 1621 ATTAGTGACGAATTAAGAAATGATGATGCTGCTGAATGATTAAGATTAACAATGGGAA 1680
Db 1918 ATTAGTGACGAATTAAGAAATGATGATGCTGCTGAATGATTAAGATTAACAATGGGAA 1977
Qy 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713
Db 1978 TCGATGTTGAAAAACATAGAGATTTATTTAG 2010

RESULT 4
AR153442 1713 bp DNA linear PAT 08-AUG-2001
LOCUS AR153442
DEFINITION Sequence 9 from patent US 6235515.
ACCESSION AR153442
VERSION AR153442.1 GI:15120974
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Roblin, G. Charlesde, Ouetterville., Claudinon, C., Smyth, K. A.,
Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, D. Colin.
Malatlon carboxylesterase
Patent: US 6235515-A 9 22-MAY-2001;
location/Qualifiers
1. 1713
source

BASE COUNT 515 a 305 c 370 g 523 t
ORIGIN
Query Match 99.4%; Score 1703.4; DB 6; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 121 AAAGTGAAGCGTTTAAAGCTTTAAGCTGTACAGATGATGATCTTACAGTTTGAAGGT 180
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Qy 961 GCTGATTTGTCTTACCCAAACATCTCGGGAATATGTTAAACGCTTGGGGTAATTCG 1020


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Db 961 GCTGATTTGTCCTTACCCAAACATCTCGGGAATGGTTAAACCTGCTGGGTAATCG 1020
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Db 1081 CAAATGCCATGCTTGTATGAGGAATTTGGAACCTTGTCATATTTTGCCCAAGTAATG 1140
QY 1141 GCTGATGCTGAACGACCCGCCAGAGACCTTGGAATGGGGCTAAATTAATAAAGGCT 1200
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QY 1681 TCGATGTTGAATAACATAGAGATTTATTTAG 1713
Db 1681 TCGATGTTGAATAACATAGAGATTTATTTAG 1713

RESULT 5
ARI53438 1713 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 1 from patent US 623515.
DEFINITION ARI53438
ACCESSION ARI53438
VERSION ARI53438.1 GI:15120970
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
UNCLASIFIED.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce, Newcomb, R. David, Campbell, P. Malcolm,
Rodin, G. Charles, Quetleville, Claudianos, C., Smyth, R. A.,
Boyce, T. Mark, Oakeshott, J. Graham, and Brownlie, J. Colin.
Maltolion carboxylesterase
Patent: US 623515-A 1 22-MAY-2001;
TITLE JOURNAL
FEATURES location/Qualifiers
SOURCE 1..1713
BASE COUNT 515 a 304 c 370 g 524 t
ORIGIN

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Query Match 99.3% Score 1701.8: DB 6: Length 1713:
 Best Local Similarity 99.6%: Pred. No. 0:
 Matches 1706: Conservative 0: Mismatches 7: Indels 0: Gaps 0:

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Db 901 GAAGAGCTACAAATTAAGTGTATGTTCTTTGTTGCCACGCTTGAGCATATCAGAC 960
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Db 961 GCTGATTTGCTTACCAACATCTCGGAAATGTTAAACTGTTGGGTAATTCG 1020

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QY 1021 ATACCCATATGATGGGTAACTTCATATGAGGGCTATTATTTTCTTCAATCTTAAG 1080
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DB 1621 ATTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
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DB 1681 TCGATGTTGAAACATAGAGATTATTTAG 1713

RESULT 6
AR153439 1713 bp DNA linear PAT 08-AUG-2001
LOCUS AR153439
DEFINITION Sequence 3 from patent US 6235515.
ACCESSION AR153439
VERSION AR153439.1 GI:15120971
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
Roblin,G.Charlesde,Queteville., Claudianos,C., Smyth,K.-A.,
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
TITLE Malathion carboxylesterase
JOURNAL Patent: US 6235515-A 3 22-May-2001;
FEATURES Location/Qualifiers
source 1..1713
/organism="unknown"

BASE COUNT 515 a 306 c 370 g 522 t
ORIGIN
Query Match 99.3%; Score 1701.8; DB 6; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY 181 ATACCGTACGCCCAACCGCCAGTGGGTGATGATGATGATGATGATGATGATGATGATGATG 240
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QY 361 CTAAATCCCGAACTAAACGTCCTTTTATGATGATGATGATGATGATGATGATGATGATG 420
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QY 421 GGTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
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RESULT 7
ARI53440 1713 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 5 from patent US 6235515.
DEFINITION ARI53440
ACCESSION ARI53440
VERSION ARI53440.1 GI:15120972
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Roblin, G. Charlesde. Queteville., Claudianos, C., Smyth, K. A.,
Boyce, J. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin.
TITLE Malathion carboxylesterase
JOURNAL Patent: US 6235515-A 5 22-MAY-2001;
FEATURES Location/Qualifiers
1..1713
source /organism="Unknown"

BASE COUNT 516 a 305 c 369 g 523 t
ORIGIN

Query Match 99.2%; Score 1698.6; DB 6; Length 1713;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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DB 61 AAGTTTAACTATGCTTTTAACTACCAATGAAAGGAGGATGAGAAATGATATGCG 120
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DB 541 AATGTCGCCGCTAATGCGGCTTAAGATCAAGTATGCTGCTGATTAATAAT 600
QY 601 AATTTGCCCAACTTTTGGTGCAATCCGATTAATATTAATGATGATGATGATGATGATGATGATGATGAT 660
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QY 661 GCTGCTCTACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 GCTGCTCTACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 ATTCTATGTCGGGTATGCTATTTGTCATGCTGCTAATACCAATGTCATGCTGCC 780
DB 721 ATTCTATGTCGGGTATGCTATTTGTCATGCTGCTAATACCAATGTCATGCTGCC 780
QY 781 TTACCTTTAGCCAAATTTGGCGGCTATTAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 TTACCTTTAGCCAAATTTGGCGGCTATTAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TTTCTTATGAAGGCAAGCCACAGGATTTAGTAAACCTTGAGAAAAGTTTAACTCTA 900
DB 841 TTTCTTATGAAGGCAAGCCACAGGATTTAGTAAACCTTGAGAAAAGTTTAACTCTA 900
QY 901 GAAGAGGCTCAATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 GAAGAGGCTCAATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 GCTGATTTGTCTTACCAACATCTCTGCGGAAATGTTTAAACCTGTTGGGTAATTCG 1020
DB 961 GCTGATTTGTCTTACCAACATCTCTGCGGAAATGTTTAAACCTGTTGGGTAATTCG 1020
QY 1021 ATACCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 ATACCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 CAATGCTATGCTTGTAAAGAAATGTAATTTGTGCCAAGTGAATG 1140
DB 1081 CAATGCTATGCTTGTAAAGAAATGTAATTTGTGCCAAGTGAATG 1140

Db 1081 CAAATGCTATGCTGTTAAGAAATGGAAACTGTGTCATTTTGTGCCAAGTAATG 1140
Oy 1141 GGTGATGCGAAGCGACCGCCCAAGACCTGGAAATGGCGTCTAAATTAATAAGCT 1200
Db 1141 GGTGATGCGAAGCGACCGCCCAAGACCTGGAAATGGCGTCTAAATTAATAAGCT 1200
Oy 1201 CATGTTACAGAGAAACCAACACAGCTGATATTTATGATCTTGTCTCAGATCTAT 1260
Db 1201 CATGTTACAGAGAAACCAACACAGCTGATATTTATGATCTTGTCTCAGATCTAT 1260
Oy 1261 TTCTGGTTCCTCCATGATGCTTTGTTGCAATTAGCTTCAATCAGACCTCCGGTACCC 1320
Db 1261 TTCTGGTTCCTCCATGATGCTTTGTTGCAATTAGCTTCAATCAGACCTCCGGTACCC 1320
Oy 1321 GGTCTACTGTATGCTGTGATGCTTTGATTCGGAAGATCTTATTAATCCCTATGTAATG 1380
Db 1321 GGTCTACTGTATGCTGTGATGCTTTGATTCGGAAGATCTTATTAATCCCTATGTAATG 1380
Oy 1381 GGTAGTGAAGCGTGTGTTAAGGCTGTAGTCACTGATGATTAACCTATTTCTTGG 1440
Db 1381 GGTAGTGAAGCGTGTGTTAAGGCTGTAGTCACTGATGATTAACCTATTTCTTGG 1440
Oy 1441 AATCAATTTGGCCAAACGATGCTTAAGAAATCGCTGAATACAAACAAATGACGTATG 1500
Db 1441 AATCAATTTGGCCAAACGATGCTTAAGAAATCGCTGAATACAAACAAATGACGTATG 1500
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Db 1501 ACTGATATGATGATCAATTTGCCACACTGCTATCCCTATAGCAATTAAGT 1560
Oy 1561 ATGAAATGTTTCTGGGATCCATTAAGAAATCGGAGATGATACAAAGTGTGAT 1620
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Oy 1621 ATTAGTGAAGATTAAGAAATGATGATGCTGTAAGTGAATTAACATGGA 1680
Db 1621 ATTAGTGAAGATTAAGAAATGATGATGCTGTAAGTGAATTAACATGGA 1680
Oy 1681 TCGATGTTGAAGAAATGATGATTAATTTAG 1713
Db 1681 TCGATGTTGAAGAAATGATGATTAATTTAG 1713

RESULT 8
AR062838 1713 bp DNA linear PAT 29-SEP-1999
LOCUS AR062838
DEFINITION Sequence 2 from patent US 5843758.
ACCESSION AR062838
VERSION AR062838.1 GI:5990529
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT 506 a 299 c 363 g 515 t 30 others
ORIGIN

Query Match 98.2%; Score 1683; DB 6; Length 1713;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1683; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Oy 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAGATTAATGCAATTAAT 60
Db 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAGATTAATGCAATTAAT 60

Oy 61 AAGTTTTAACTATGCTTTAACTACCAATGAAGCGGTGATGAAACGTAATAGGC 120
Db 61 AAGTTTTAACTATGCTTTAACTACCAATGAAGCGGTGATGAAACGTAATAGGC 120
Oy 121 AAGTGAAGGCGTTAAACGTTAACTGATGATGATGATGATGATGATGATGATGAT 180
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Oy 181 ATACGTTACGCCAACCGGCACTGGTGAAGATTAATTAAGCAACCCAGGACACA 240
Db 181 ATACGTTACGCCAACCGGCACTGGTGAAGATTAATTAAGCAACCCAGGACACA 240
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Oy 301 ATACGCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
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Oy 361 CTAATTCGCCAAGCTAAGCTCCGTTTATGATACATACATGATGATGATGATGAT 420
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Oy 421 GGTGAAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 421 GGTGAAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Oy 481 ATTAACATACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 ATTAACATACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Oy 541 AATGTCGCCGATTAAGCGGCTTAAGATCAAGTATGATGATGATGATGATGATGAT 600
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Oy 601 AATTCGCCAAGCTTGGTGGCAATCCGATATATTAACAGTCTTGGTGAAGTGGCG 660
Db 601 AATTCGCCAAGCTTGGTGGCAATCCGATATATTAACAGTCTTGGTGAAGTGGCG 660
Oy 661 GCTGCTCTACCCACTACATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 GCTGCTCTACCCACTACATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Oy 721 ATACTAATGTCGGTAAATGCTATTTGTCATGATGATGATGATGATGATGATGATGAT 780
Db 721 ATACTAATGTCGGTAAATGCTATTTGTCATGATGATGATGATGATGATGATGATGAT 780
Oy 781 TTACCTTACGCAAAATTTGCGGCTATTAAGGATGATGATGATGATGATGATGATGAT 840
Db 781 TTACCTTACGCAAAATTTGCGGCTATTAAGGATGATGATGATGATGATGATGATGAT 840
Oy 841 TTCTTTTGAAGCCAGCCAGATTTAATTAACCTTGAGGAAAGATTTTAACTCTA 900
Db 841 TTCTTTTGAAGCCAGCCAGATTTAATTAACCTTGAGGAAAGATTTTAACTCTA 900
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Db 901 GAAGAGCGTAAATTAAGTCTATGTTTCTTTGTCCTGCTGCTGCTGCTGCTGCTGCT 960
Oy 961 GCTGATGTTGTTTACCCCAACATCTCGGGAAGATGATTAAGTGAAGTGAAGTGAAG 1020
Db 961 GCTGATGTTGTTTACCCCAACATCTCGGGAAGATGATTAAGTGAAGTGAAGTGAAG 1020
Oy 1021 ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Oy 1081 CAAATGCTTATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1081 CAAATGCTTATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Oy 1141 GCTGATGCTGAAGCGACCGCCCAAGACCTTGGAAATGGGTGCTAAATTAAGGCT 1200


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Db 1141 GCTGATNCTGACGACCCGCCAGAGACCTTGGAAATGGTGCTAAATTAAGAGCT 1200
Qy 1201 CATGTTACAGGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTGCACATCAT 1260
Db 1201 CATGTTACAGGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTGCACATCAT 1260
Qy 1261 TTCTGTTCCCATGATGCTTTGTTGCAATATGCTTTCAATACACCTCCGGTACACCC 1320
Db 1261 TTCTGTTCCCATGATGCTTTGTTGCAATATGCTTTCAATACACCTCCGGTACACCC 1320
Qy 1321 GTCTACTGTTATGCTTTGCTTGCATTTGATTTGGAAGATCTTATTAATCCCTATGCTATATG 1380
Db 1321 GTCTACTGTTATGCTTTGCTTGCATTTGATTTGGAAGATCTTATTAATCCCTATGCTATATG 1380
Qy 1381 CGTAGAGGACGCTGCTTGAAGGCTGTAGCTGATGATGAATTAACCTATTTCTCTCGT 1440
Db 1381 CGTAGAGGACGCTGCTTGAAGGCTGTAGCTGATGATGAATTAACCTATTTCTCTCGT 1440
Qy 1441 AATCAATTTGGCCAAACGCTATGCTTAAGAAATCGCTGAATACAAACAAATTTGAACCTATG 1500
Db 1441 AATCAATTTGGCCAAACGCTATGCTTAAGAAATCGCTGAATACAAACAAATTTGAACCTATG 1500
Qy 1501 ACTGATATATGATGATACAAATTTGCCACACTGTAATCTTATAGCAATGAATTTGAAGGT 1560
Db 1501 ACTGATATATGATGATACAAATTTGCCACACTGTAATCTTATAGCAATGAATTTGAAGGT 1560
Qy 1561 ATGGAATAATGTTCTCTGCGGATTCATTAAGAAATTCGAGAACATTAATGATTTTGAAT 1620
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Db 1621 ATTAGTACGAATTTGAATAATGATTTGCTGCTGAATAGATTAAGATTAACATGAGGAA 1680
Qy 1681 TCGATGTTTGAATAACATGATTAATTTTAA 1713
Db 1681 TCGATGTTTGAATAACATGATTAATTTTAA 1713

RESULT 9
AF133341 2160 bp mRNA 1linear INV 17-AUG-2000
LOCUS Musca domestica carboxylesterase MdaE7 (mdaE7) mRNA, complete cds.
DEFINITION AF133341
ACCESSION AF133341
VERSION AF133341.1 GI:4768932
KEYWORDS Musca domestica.
SOURCE Musca domestica.
ORGANISM Musca domestica.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoidae; Muscidae; Musca.
1 (bases 1 to 2160)
Claudianos, C., Russell, R.J. and Oakeshott, J.C.
The same amino acid substitution in orthologous esterases confers
organophosphate resistance on the house fly and a blowfly
Insect Biochem. Mol. Biol. 29 (8), 675-686 (1999)
JOURNAL MEDLINE 99381228
PUBMED 10451921
REFERENCE 2 (bases 1 to 2160)
AUTHORS Claudianos, C., Russell, R.J. and Oakeshott, J.C.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-1999) Entomology, CSIRO, Clunies Ross, Canberra,
ACT 2601, Australia
FEATURES
source
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/organism="Musca domestica"
/strain="Rutgers Diazlino-R (R+)"
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/chromosome="II"
/dev_stage="4 day third instar larvae"
1..2160
/gene="MdaE7"
gene

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CDS
217..1929
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ae7 alpha esterase; organophosphate resistance"
/codon_start=1
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/protein_id="AAB29685.1"
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VKRMVYDSDYSFESPIYAKPVGELRFAKORPVPWEGVDCGPNRVSQDETIS
GKPTSEECCLINLYTNDLNPDKRPVWFTHGDEITGEANRMWFGDPMKRPVIL
VTVOYRLGVLEFLSLKSNLVPNGAGLKDQVMALEWYKSNIANRGGVDVITPGES
AGGASTHYMITEEOTRGLFHRGIMMSGMSMASTECOSRALTMARKVYKGDNEK
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SAMGSIPTLIGNTSYELFLKSIKQYEVLEKLESGVNVVPMWLEDSERAPLE
RAIYIKAHVHGEPPTLNPMEISCYFELFPMHREFLOLRFNHAGPFIYLRDFDS
EELINPYRIMRGRGVKVSNADELTIFPNHILSKRLPKREKRTIERMWCITFEA
TTGKPYSDIAGMENTLWDPILKSDVYKCLNIGDELKVMQDLPENDKIKOVASIFDKK
KELF"
polyA_signal 2115..2120
BASE COUNT 661 a 440 c 466 g 593 t
ORIGIN
Query Match 57.6%; Score 987.2; DB 3; Length 2160;
Best local similarity 73.5%; Pred. No. 6.3e-210;
Matches 1259; Conservative 0; Mismatches 453; Indels 0; Gaps 0;
Qy 1 ATGAATTTCAAGCTTATGTTGATGAGAAATTAATGGAAGATTAATGCTTGAAT 60
Db 217 ATGAATTTCAAGCTTATGTTGATGAGAAATTAATGGAAGATTAATGCTTGAAT 276
Qy 61 AAGTTTAACTATGCTTAACTACCAATGAAGAGCGTGTAGCTGAATGATGCTG 120
Db 277 AATTAACCAACACTACCGCTGTGATACCAATGAAGAGCGTGTAGCTGAATGATGCTG 336
Qy 121 AAAGTGAAGCGGTTAAAGCTTAACTGTGACAGATGATTTCTACTACAGTTTGAAGGT 180
Db 337 CAATTAAGGCTGTAAAGCAATGAGCAGCTCTACGATGATTTCTACTACAGTTTGAAGGT 396
Qy 181 ATACGCTAGCGCCCAACGCGCAGTGGGTGAGTGAATTAAGAGCAGCCAGGACCAACA 240
Db 397 ATACGCTAGCGCCCAACGCGCAGTGGGTGAGTGAATTAAGAGCAGCCAGGACCTGTA 456
Qy 241 CCCGCGATGCTGTGCGTATGTTGCAATCATTAAGATTAAGTCAAGTGAATTTT 300
Db 457 CCATGGGAGGCTGTACGTATGCTGTGGGCCAGCCACAGATCGGTACAGACATTTTC 516
Qy 301 ATACGCGCAAGCTGTGTGCTAGAGATTTGCTATACCTAAGTGTCTATACGAATAT 360
Db 517 ATAAAGTGGCAAAACCCACAGGTTGGAGGATGCTATACCTGAATGTGATACCAATGAC 576
Qy 361 CTAATCCCGCAAACTAAAGCTCCGTTTATGATACATCAATGCTGTGTTTATATAC 420
Db 577 TTAACCCCAACAAAAGCCTCTGTTATGTTTATATCATGATCGGAGATTTTATTTTC 636
Qy 421 GGTGAATAATCATGATATATATGCTGCTGATTTATTTAATAAAGATGTGTGTTG 480
Db 637 GGGGAAGCAAAATGTAAGTGTGTTGGCCGACTTATTAAGAAACCCGCGTCTTG 696
Qy 481 ATTAACATCAATATGTTTGGAGCTTAGTCTTCTAAGTTTAATTCAGAGACCTT 540
Db 697 GTAACGTCGAATATGTTTGGGTGTGTTGCTTCTTAAGCTGAATAACGAAATCTTC 756
Qy 541 AATGCGCGGTAATGCGCGCTTAAGATCAATGATGCGCTTGGGTTGATTAATAAT 600
Db 757 AATGTCGCCGCAACGCTGCGCTCAAGATCAATGATGCGCTTGGAGTGGTCAAGAGT 816
Qy 601 AATTTGCCCAACTTTGTTGGCAATCCCGATTAATTAACATCTTTTGTGAAGTGGCGGT 660
Db 817 AATATTGCCAATTTGTTGGTGGATGATGACAAATTAACGCTCTTGGCGCAAGTGGCTGT 876

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OY	661	GC	CCCTCCTCACCACCTCAGATGTTAAACGACAAACACCGCGCTTTCCATCGTGT	720
Db	877	GG	GGCTCCTCACCACCTCAGATGTTAAACGACAAACACCGCGCTTTCCATCGTGT	936
OY	721	AT	ACTAATATGTCGGGTATGCTATTTTGGCCATGCGGCTTAATACCAATGTACATGTGCC	780
Db	937	AT	CAATGATGTCGGGTATGCTATTTTGGCCATGCGGCTTAATACCAATGTACATGTGCC	996
OY	781	TT	CACCTTACGCCAAATTGGCCGGCTATAGGGTGAGAGATATGATAGGATGTTTGGAA	840
Db	997	CT	CACCACTATGGCCAAACCTGTTGGCTATAGGGGAGAGACAATGAAAAAGATTCCTGGAA	1056
OY	841	TT	TCTTATGAAAGCCCAAGCCACAGAGATTTAATAAACTTGAGAAAAATTTTAACTGA	900
Db	1057	TT	CTCTAATGAAAGCCCATTCCTATGATTTGATTAAGAGAGAGCCACAACTTTTGACACC	1116
OY	901	GA	AGAGCGCTACAATAATAGTCATGATGTTCTTTTGGTCCACTGTTGAGCATATCAGAC	960
Db	1117	GA	AGAAATATGCAAAATTAAGTCATGATGTTCTTTTGGACCCACTGTATACCAACAGACA	1176
OY	961	GC	TGATTTGTCCTTACCCAAACAATCCCGGGAAATGGTAAACACCTTGCGGGTAAATCG	1020
Db	1177	GC	CGACTGTGTGGTACCCAAACCAATCAGAGAAATGTGAAGCGCCCTGGGGAAATTCG	1236
OY	1021	AT	ATACCACTATGATGGGTAAACACTTCATATAGGGTCTATTTTCTACTTCATTTCTAAG	1080
Db	1237	AT	ATACCACTATGATGGGTAAACACTTCATATAGGGTCTATTTTCTACTTCATTTCTAAG	1296
OY	1081	CA	AATTCGCTATGCTTGTGTTAAGAAATTTGAACACTTGTGTCAATTTTGTGCCAAGTAA	1144
Db	1297	CA	ATATCCGGAGGTGTGTTAAGAAATTTGAACACTTGTGTCAATTTTGTGCCAAGTAA	1356
OY	1141	GC	TGATGCTGTAACACACCGCCGCCAGAGACCTTGGAAATGGGTCTAAATTTAAAGAGCT	1200
Db	1357	GC	TGACATGTAAGCAGTGGCCCGGGAAACCTGTGAGAGGGTCCATTTGTAAAGAGCC	1416
OY	1201	CA	TGTTCACGAGAAACACCAACAGCTGATTAATTTATGATCTTGTCTCTACATCTAT	1260
Db	1417	CA	TGTTCACGAGAGAAACACCTACTCTGGAATTTTATGAGAGCTTGTCTCTATTTCTAT	1476
OY	1261	TT	TTCGTTGCCCATGCAATCTTTGTCGATTAACGTTCAATCACACCGCGTACACC	1320
Db	1477	TT	TCCTCTTCCCATGCAATCTCTTCTCTCAATTTGCGCTTACACACACAGTGGACCTCC	1536
OY	1321	GT	CTACTTGTATCGCTTCGACTTTGATTTGGGAAGATCTTAATTAATCCATCGATTAAG	1380
Db	1537	AT	TATTTTGTATCGCTTTCGATTTTCGATTCGAGAAATTAATTAACCCATCGATTAAG	1596
OY	1381	CG	TATGAGACGTGTGTTAAGGGTGTAGTCATGCTGATGATTAATTAACCTATTTCTTGG	1444
Db	1597	CG	TATTTGACGTGTGTTAAGGGTGTAGTCATGCTGATGATTAATTAACCTATTTCTTGG	1656
OY	1441	AA	TAATCAATTTGGCCAAACGTATGCTTAAGAAATCCCGTGAATACAAACATTTAAGCTAT	1500
Db	1657	AA	TAATCAATTTTGTGAAGACCTGTCGAAAGGAAGCGGGATATACAAACATTTAAGCATT	1716
OY	1501	AC	TGTATATGATATACAAATTTGCCACACTGTGTAATCTTATAGCAGTAAGATTAAGCT	1560
Db	1717	GT	TGGCATTTTGTGAGAGAAATTTGCCACACCGGCAAAACATACAGCAATGATTTACCGGC	1776
OY	1561	AT	GAAATATGTTTCTGAGGATATCAATTAACAAATCGAGAGATATCAAGATGTTGAT	1620
Db	1777	AT	GAAAAACCTCACCTTGGGATCCCATTAATAAAATTCGATGATGTCTATTAAGTTTAAT	1836
OY	1621	AT	TATAGTACGAATTTGAAATGATTTGATGTCCTGGAATGGATGAAGTATTAACATGGGA	1680
Db	1837	AT	CGCGCATGTAATTTGAAGATTTGATGATTTGCCAAGAAATGATTAATTAACATGGGA	1896
OY	1681	TC	GATGTTTGAAGAAACATTAAGATTTATTTTA	1712
Db	1897	AG	TATATTCGATTAAGAAAGAAATGTTTTTTA	1928

RESULT 10	AF139082	2175 bp	mrna	linear	INV 20-OCT-2000
LOCUS	AF139082				
DEFINITION	Haemacobia irritans irritans alpha E7 esterase (ae7) mRNA, complete cds.				
ACCESSION	AF139082				
VERSION	AF139082.1				
KEYWORDS					
SOURCE	Haematobia irritans irritans.				
ORGANISM	Haematobia irritans irritans. Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; Muscidae; Haematobia.				
REFERENCE	1 (bases 1 to 2175) Guerrero, F.D.				
AUTHORS	Cloning of a horn fly cDNA, Hialphae7, encoding an esterase whose transcript concentration is elevated in diazinon-resistant flies				
TITLE	Insect Biochem. Mol. Biol. 30 (11), 1107-1115 (2000)				
JOURNAL	2043807				
MEDLINE	10989298				
PUBMED	2 (bases 1 to 2175) Guerrero, F.D.				
REFERENCE	Direct Submission				
AUTHORS	Submitted (30-MAR-1999) USDA-ARS, Knippling-Bushland U.S. Livestock				
TITLE	Insects Research Laboratory, 2700 Fredericksburg Rd., Kerrville, TX				
JOURNAL	78028, USA				
FEATURES					
source	1..2175 location/Qualifiers /organism="Haematobia irritans irritans" /strain="Camp Cooley 4/97" /sub_species="irritans" /db_xref="taxon:75445" /clone="HF41CC" /note="Hyethroid and diazinon-resistant" 1..2175 /gene="ae7" 282..1994 /gene="ae7" /note="similar to Lucilia cuprina and Drosophila melanogaster alpha E7 esterases" /codon_start=1 /product="alpha E7 esterase" /protein_id="AA14517.1" /db_xref="GI:6502939" /translation="MNFNVSFLEKIRKICVENKILNRLITNETHIIVDEYKIKG VKRLIYVDSPYSPEGIIPYAKPYGELRFAPOHPVMDVCQDCBASRSYOTDFTS GNSGSEDCILYINVTNNIMDTRPVLVPGFGFCGEANRNYGADFIKDDYVE ITVRLRGVTEQLNSLENLNPONALIKQVWALRIKKNKCSFGCDPDCITLFGES AGASTHYMTTEQARCLFHHAVLMSTJALCVIAHHTQCQHRGTIARIYKGENNR DVPYFLMKANDYDLAREHRYLVNBEELRDVMEFAFGTEPYETIPDCVLKPKRNEMLK TAMNSIPTLLIGNTSYGLFLISVGKNPMLIKELTEFECYVGEVLVEDRSSSESL EILSLIKLYVGETPTLESFTELCSDPEYFVPMHREPLQLRNHHVGSPIYLYRPDPS EELINRLIMYRGVGVGASHTDELDTLPYPMMLSKRMPKRSREKRTETRMGIWFOFA TTGCPYSEIENGMENTTWDLSIKSDVEYKCMNIGDELKFLIDPEMERLKWQSVFNKK RELFL"				
gene					
CDS					
BASE COUNT	690 a 365 c 435 g 685 t				
ORIGIN					
Query Match	56.0%; Score 959.4; DB 3; Length 2175;				
Best Local Similarity	72.5%; Pred. No. 1e-203;				
Matches 1242; Conservative	0; Mismatches 471; Indels 0; Gaps 0;				
1	ATGAATTTCAACGCTAGTTTGATGAGAGAATAATTAAGAGATTAAATGCAATGAATAAT 60				
282	ATGAATTTCAATGTCAGCTCTTGAGAGAAATTAAGATGGAATAATTAAGTGTGGAATAAT 341				
61	AAGTTTAACTATCGTTTAACATCAATGAAGAAACGGGTGAGCTGGAACATGAATATGCG 120				
342	AAATTTTAACTACCGGCTATTATACCAATGAAGAACGCAATATTGCGATACGGAATATGGA 401				
121	AAAGTGAAGGCGTTAAACGTTTAACTGTGACGATGATTCCTACTACATGTTTGAGGCT 180				
402	AAATTAAGGCTTAAACGTTTGACATCTACATGAGTGAGCTATTCACAGCTTGAAGGT 461				

Oy 181 ATACCGTACCCCAACCCGCTGGGTGAGTGTATTTAAAGCACCACGACACACA 240
 Db 462 ATACCATATGCGCAACCTCCGTGTGGGCAATTAGATTTAAAGCTCCACCAAGCTGTC 521
 Oy 241 CCGTGGATGTGTGCGGTATTTGCAATCATAAAGATAGAGTGCAGTGTGATTTT 300
 Db 522 CCTTGGATGTGAGTTAAAGATTTGTTCATGCTGCTCCCTGGGTTCACCAAGATTTTC 581
 Oy 301 ATACGGCCAAAGTGTGTGCTCAGAGATGTGCTATACCTAAAGCTATACCAATAT 360
 Db 582 ATATCCGCACTCAAGTGTGGAGTGTGTTATATTTGAATGCTATACCAATAT 641
 Oy 361 CTAAATCCGCAACTAAAGTGTGCTTTTATATACATACATGCTGTGTTTATATC 420
 Db 642 TTAAATATGATACAAAAGTGTGCTTTTGTCTTCTCATAGTGTGTTTCTTCTTGT 701
 Oy 421 GGTGAATATCATGCTGATATGATGTGCTGATTTTCAATTTAAAGATGTGTTG 480
 Db 702 GCGGAGCTAATAGAACTATATGCGCTGATATTTCAATTAAGAGAGCTGTCTC 761
 Oy 481 ATTAACATATCATGCTGTGAGCTCTAGGTTTCTAAGTTTAAATTCAGAGACTT 540
 Db 762 ATTAACATATCATGCTGTGAGCTCTAGGTTTCTAAGTTTAAATTCAGAGACTT 821
 Oy 541 AATGTCCTGCTAATGCTGCTTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 600
 Db 822 AATGTCCTGCTAATGCTGCTTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 881
 Oy 601 AATGTCCTGCTAATGCTGCTTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 660
 Db 882 AATGTCCTGCTAATGCTGCTTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 941
 Oy 661 GCTGCTTACCCGCTAATGCTGCTTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 720
 Db 942 GCTGCTTACCCGCTAATGCTGCTTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1001
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 Db 1062 TTACCTTACCCGCTAATGCTGCTTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1121
 Oy 841 TTCTTATGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 900
 Db 1122 TTCTTATGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1181
 Oy 901 GAAGGCTAATGAAGTGTGCTGCTTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 960
 Db 1182 GAGGAACTGTGATAGTGTGCTGCTTAAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1241
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 Db 1242 CCAAGCTGTGCTTAAAGTGTGCTTAAAGTGTGCTTAAAGTGTGCTTAAAGTGTGCT 1301
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Oy 1261 TTCTGCTTCCCATGCAAGTGTGCTTCAATACGTTTCAATACAGCTCCGCTACACC 1320
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 DEFINITION Sequence 14 from patent US 6235515.
 ACCESSION AR153445
 VERSION AR153445.1 GI:15120977
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1710)
 AUTHORS Russell, R. Joyce, R. Newcomb, R. David, Campbell, P. Malcolm, Robin G. Charlesde, Queteville, Claudianos, C., Smyth, K. A., Boyce, T. Mark, Oakeshott, J. Graham, and Brownlie, J. Collin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 6235515-A 14 22-MAY-2001;
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RESULT 12
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 AY051473
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 VERSION
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 SOURCE
 ORGANISM
 Drosophila melanogaster.
 Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1710)
 AUTHORS
 Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J.,
 Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R.,
 Gonzalez,M., Guarin,H., Li,P., Liao,G., Miranda,A., Mungall,C.J.,
 Yu,C., Pacle,D., J., Paragas,V., Park,S., Phouanavong,S., Wan,K.,
 Yu,C., Lewis,S.E., Rubin,G.M. and Celinker,S.
 DIRECT SUBMISSION
 JOURNAL
 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA
 COMMENT
 Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Berkeley, CA 94720
 This clone was sequenced as part of a high-throughput process to
 sequence clones from Drosophila gene collection 1 (Rubin et al.,
 Science 2000). The sequence has been subjected to integrity checks
 for sequence accuracy, presence of a poly A tail and contiguity
 within 100 kb in the genome. Thus we believe the sequence to
 reflect accurately this particular cDNA clone. However, there are
 artifacts associated with the generation of cDNA clones that may
 have not been detected in our initial analyses such as internal
 priming, priming from contaminating genomic DNA, retained introns
 due to reverse transcription of unsliced precursor RNAs, and
 reverse transcriptase errors that result in single base changes.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our web site
 (<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.
 location/qualifiers
 1. 2017
 /organism="Drosophila melanogaster"
 /strain="y; cn bw sp"
 /db_xref="taxon:7227"
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 ACCESSION AC015272
 VERSION AC015272.1 GI:6436063
 KEYWORDS HTG; HTG3_PHASE2.
 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 57335)
 AUTHORS Adams, M. and Venter, J.C.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
 Rockville, MD, USA
 COMMENT This sequence was identified as CDL-10213452 by the submitter.
 For further information on this sequence e-mail to fly@celera.com.
 * NOTE: This is a 'working draft' sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
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 source location/qualifiers
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 Matches 1052; Conservative 0; Mismatches 614; Indels 263; Gaps 5;
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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2003, 22:58:21 ; Search time 246.905 Seconds
(without alignments)
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Title: US-09-776-910-7

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues 4370478

Total number of hits satisfying chosen parameters:

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

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5	1679.4	98.0	1713	16	AAQ91565
6	1677.8	97.9	1713	16	AAQ91563
7	1676.2	97.9	1713	16	AAQ91562
8	956.6	55.8	1710	18	AAAT68597
9	678.8	39.6	2001	23	ABLO2067

10	380.2	22.2	1704	23	ABLO2081	Drosophila melanog
11	370.6	21.6	6175	23	ABLO2066	Drosophila melanog
12	366.6	21.4	1665	23	ABLO2099	Drosophila melanog
13	363.8	21.2	1792	23	ABLO4689	Drosophila melanog
14	323	18.9	1863	23	ABLO1859	Drosophila melanog
15	320.4	18.7	1593	23	ABLO2103	Drosophila melanog
16	313	18.3	1791	23	ABLO1933	Drosophila melanog
17	306.2	17.9	1878	23	ABLO1947	Drosophila melanog
18	304.2	17.8	1719	23	ABLO2101	Drosophila melanog
19	302	17.6	3856	23	ABLO10332	Drosophila melanog
20	302	17.6	67279	23	ABLO7668	Drosophila melanog
21	266.8	15.6	1809	24	ABAO50480	Drosophila cell cy
22	238.2	13.9	4320	23	ABLO4688	Drosophila melanog
23	231.2	13.5	1727	23	ABLO1943	Drosophila melanog
24	230.2	13.4	4242	23	ABLO2102	Drosophila melanog
25	225.6	13.2	5008	23	ABLO2080	Drosophila melanog
26	200.4	11.7	4294	23	ABLO2098	Drosophila melanog
27	200.4	11.7	4294	23	ABLO2100	Drosophila melanog
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32	191.6	11.2	2613	23	ABLO19064	Drosophila melanog
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40	169.2	9.9	4288	23	ABLO1942	Drosophila melanog
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ALIGNMENTS

RESULT 1	AAQ91561	standard; cDNA: 1713 BP.
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AC	AAQ91561	
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XX		
DT	22-DEC-1995	(first entry)
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DE	OP-sensitive esterase E3 LC743 clone.	
XX		
KW	Esterase; E3; bioremediation; organophosphate; carbamate;	
KW	Insecticide; pesticide; water decontamination; meat decontamination;	
KW	ss.	
XX		
OS	Lucilia cuprina.	
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XX		
PD	20-JUL-1995.	
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PF	13-JAN-1995;	95WO-AU00016.
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PR	13-JAN-1994;	94AU-0003347.
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
XX		
PI	Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;	
PI	Parker AG, Robin GC, Russell RJ, Smyth K;	

XX
DR WPI: 1995-263870/34.
P-PSDB: AAR78142.
XX
PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
PT eliminate residues of organo:phosphate and carbamate pesticides from
PT water, meat etc.
XX
XX Claim 5: Page 12-17; 38pp; English.
XX
XX cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA
XX library was amplified using cluster-specific esterase primers.
XX Isolated clone Ic743, a probable full-length cDNA, was expressed
XX using a baculovirus vector in insect cells and shown to encode
XX an OP-susceptible E3 esterase, useful in bioremediation.
XX
XX Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other:
SQ
Query Match 100.0%; Score 1713; DB 16; Length 1713;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATTTCAACGTTAGTTGATGAGCAAAATTAATGCAAGTTAAATGCAATGAAAT 60
DB 1 ATGAATTTCAACGTTAGTTGATGAGCAAAATTAATGCAAGTTAAATGCAATGAAAT 60
QY 61 AAGTTTAACTATCGTTTAACTACCAATGAAACGTTGAGCTGAACTGAATATGCG 120
DB 61 AAGTTTAACTATCGTTTAACTACCAATGAAACGTTGAGCTGAACTGAATATGCG 120
QY 121 AAGTGAAGGCGTTAAACGTTTAACTGATGATGATTCCTACCTGAGTTTGAAGGT 180
DB 121 AAGTGAAGGCGTTAAACGTTTAACTGATGATGATTCCTACCTGAGTTTGAAGGT 180
QY 181 ATACCGTACGCCAACCGCCAGTGGTGAAGATTAAAGCACCACGACACACA 240
DB 181 ATACCGTACGCCAACCGCCAGTGGTGAAGATTAAAGCACCACGACACACA 240
QY 241 CCTGGGATGATGCTGCTGATTTGTCATCTATTAAGTAAAGTAAAGTAAAGTAAAGT 300
DB 241 CCTGGGATGATGCTGCTGATTTGTCATCTATTAAGTAAAGTAAAGTAAAGTAAAGT 300
QY 301 ATACCGGCGAAAGTGTGCTGAGAGATGCTATACCTAAGTGTATACGAATAT 360
DB 301 ATACCGGCGAAAGTGTGCTGAGAGATGCTATACCTAAGTGTATACGAATAT 360
QY 361 CTAAATCCGAAACTAAACGTCCTGTTTAACTATACATGATGATGATGATGATGATG 420
DB 361 CTAAATCCGAAACTAAACGTCCTGTTTAACTATACATGATGATGATGATGATGATG 420
QY 421 GGTGAATATCATGCTGATATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 421 GGTGAATATCATGCTGATATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 481 ATTAACATACAAATATCGTTTGGAGCTCTAGGTTTCTAAGTTAAATTCAGAACCTT 540
DB 481 ATTAACATACAAATATCGTTTGGAGCTCTAGGTTTCTAAGTTAAATTCAGAACCTT 540
QY 541 AATGCGCCGCTAATGCGCGCTTAAAGATCAAGTCAATGCGCTTGGCTGATTAATAAT 600
DB 541 AATGCGCCGCTAATGCGCGCTTAAAGATCAAGTCAATGCGCTTGGCTGATTAATAAT 600
QY 601 AATGCGCGCACTTGTGTGCGCAATCCGATATATACGCTTGTGTAAGATGCGCGT 660
DB 601 AATGCGCGCACTTGTGTGCGCAATCCGATATATACGCTTGTGTAAGATGCGCGT 660
QY 661 GCTGCTTACCGCATACATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 GCTGCTTACCGCATACATGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 721 ATACTAATGCTGCGTAATGCTATTTGTCATGCGCTAATACCAATGCAACATGCGTCC 780
DB 721 ATACTAATGCTGCGTAATGCTATTTGTCATGCGCTAATACCAATGCAACATGCGTCC 780

QY 781 TTCACCTTAGCCAAATTTGGCCGCTATTAAGCTGAGATATGATGATGATGATGATG 840
DB 781 TTCACCTTAGCCAAATTTGGCCGCTATTAAGCTGAGATATGATGATGATGATGATG 840
QY 841 TTTCTTATGAAGCCACACGAGATTAATTAAGTGAAGAAATTTTAAGTCTTA 900
DB 841 TTTCTTATGAAGCCACACGAGATTAATTAAGTGAAGAAATTTTAAGTCTTA 900
QY 901 GAAGAGCTGACAAATTAAGTCTATTTCTTTGCTCCACTGTTGAGCCATACAGCC 960
DB 901 GAAGAGCTGACAAATTAAGTCTATTTCTTTGCTCCACTGTTGAGCCATACAGCC 960
QY 961 GCTGATGCTGATGCTTACCAACATCTCGGGAATGTTAAACGCTGGGGTAATTCG 1020
DB 961 GCTGATGCTGATGCTTACCAACATCTCGGGAATGTTAAACGCTGGGGTAATTCG 1020
QY 1021 ATACCCACTATGATGAGGTAACACTTATATGAGGCTATTTTCTCAATCTTAAG 1080
DB 1021 ATACCCACTATGATGAGGTAACACTTATATGAGGCTATTTTCTCAATCTTAAG 1080
QY 1081 CAATGCTATGCTTGTGTAAGAAATGAAACCTGTGTCAATTTTGTGCAAGTAAATG 1140
DB 1081 CAATGCTATGCTTGTGTAAGAAATGAAACCTGTGTCAATTTTGTGCAAGTAAATG 1140
QY 1141 GCTGATGCTGATGCTTACCAACATCTCGGGAATGTTAAACGCTGGGGTAATTCG 1200
DB 1141 GCTGATGCTGATGCTTACCAACATCTCGGGAATGTTAAACGCTGGGGTAATTCG 1200
QY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTTGCTGCAATCTAT 1260
DB 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTTGCTGCAATCTAT 1260
QY 1261 TTTCTGTTCCCATGATGCTTGTGTAAGAAATGAAACCTGTGTCAATTTTGTGCAAG 1320
DB 1261 TTTCTGTTCCCATGATGCTTGTGTAAGAAATGAAACCTGTGTCAATTTTGTGCAAG 1320
QY 1321 GTCCTGTTCCCATGATGCTTGTGTAAGAAATGAAACCTGTGTCAATTTTGTGCAAG 1380
DB 1321 GTCCTGTTCCCATGATGCTTGTGTAAGAAATGAAACCTGTGTCAATTTTGTGCAAG 1380
QY 1381 CGTAGTGACGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
DB 1381 CGTAGTGACGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1441 AATCAATGCGCAACGATGCTTAAAGATGCGCTGATTAACAAACATTAAGCAATG 1500
DB 1441 AATCAATGCGCAACGATGCTTAAAGATGCGCTGATTAACAAACATTAAGCAATG 1500
QY 1501 ACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
DB 1501 ACTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
QY 1561 ATGGAATATGCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1620
DB 1561 ATGGAATATGCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1621 ATTAGTGACGAATTAAGAAATGATGATGATGATGATGATGATGATGATGATGATG 1680
DB 1621 ATTAGTGACGAATTAAGAAATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
DB 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
RESULT 2
AAT68596
ID AAT68596 standard; DNA: 1713 BP.
AC AAT68596;
XX
XX 08-AUG-1997 (first entry)

XX LC-alpha-E7 malathion susceptible esterase clone Lc743.
XX Malathion carboxylesterase; organophosphate; insecticide.
KW pesticide; remediation; bioremediation; decontamination; esterase;
KW ss.
XX *Lucilia cuprina*.
XX
FH Key Location/Qualifiers
FT primer_bind complement (1..26)
FT /tag- a
FT /note- "Lc743 5' primer"
FT primer_bind 1686..1713
FT /tag- b
FT /note- "Lc743 3' primer"
FT mutation 752
FT /tag- c
FT /note- "base 752 is T in resistant clones
FT (Trp to Leu mutation)"
FT mutation 1344
FT /tag- d
FT /note- "base 1344 is C in resistant clones
FT (silent mutation)"
FT mutation 1362
FT /tag- e
FT /note- "base 1362 is C in resistant clones
FT (silent mutation)"
FT mutation 1599
FT /tag- f
FT /note- "base 1599 is T in resistant clones
FT (silent mutation)"
FT mutation 1629
FT /tag- g
FT /note- "base 1629 is T in resistant clones
FT (silent mutation)"
XX MO9719176-A1.
XX
XX 29-MAY-1997.
XX
XX 22-NOV-1996; 96MO-AUD00746.
XX
XX 23-NOV-1995; 95AU-0006751.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Boyce T, Brownlie JC, Campbell PM, Claudianos C;
XX Newcomb RD, Oakeshott JG, Roblin GC, Russell RJ, Smyth K;
XX WPI: 1997-298113/27.
XX P-PSDB; AAM17765.
XX
XX DNA encoding enzyme that degrades organophosphate pesticides -
XX useful for decontamination of soil, water, food etc
XX
XX Claim 4; Fig 1; 52pp; English.
XX
XX DNA molecule Lc743 (AAT68596) codes for an esterase (AAM17765) from
XX a malathion susceptible strain of *Lucilia cuprina*. Comparison
XX with a consensus sequence from derived from clones of the
XX Lc-alpha-E7 resistant allele (see also AAM17768) indicated only one
XX replacement site difference, a Trp to Leu substitution at amino
XX acid position 251 (nucleotide position 752). This mutation is an
XX excellent candidate for the malathion resistance mutation. The
XX resistant enzyme acts as a malathion carboxylesterase and can be
XX formulated for use in degrading environmental carboxylester or
XX dimethyl general organophosphates.
XX
XX Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other:
Query Match 100.0%; Score 1713; DB 18; Length 1713;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATTCACACGTTAGTTGATGAGAAATTAAATGAGATTAATGCATTGAAAT 60
DB 1 ATGAATTCACACGTTAGTTGATGAGAAATTAAATGAGATTAATGCATTGAAAT 60
QY 61 AAGTTTAAACTATACGTTTAACATCAATGAAACGGGTGAGTGAACATGATATGAC 120
DB 61 AAGTTTAAACTATACGTTTAACATCAATGAAACGGGTGAGTGAACATGATATGAC 120
QY 121 AAGTGAAGCGTTAAACGTTAACTGTACGATGATCTTACTACAGTTTGAAGGT 180
DB 121 AAGTGAAGCGTTAAACGTTAACTGTACGATGATCTTACTACAGTTTGAAGGT 180
QY 181 ATACCGTACGCCCAACCCCGAGTGGTGAAGATTTAAAGCCACCCAGGACCAACA 240
DB 181 ATACCGTACGCCCAACCCCGAGTGGTGAAGATTTAAAGCCACCCAGGACCAACA 240
QY 241 CCTGGATGTGTGCGGATGTTGCAATCATAAAGATTAAGTGCACAGTTGATTTT 300
DB 241 CCTGGATGTGTGCGGATGTTGCAATCATAAAGATTAAGTGCACAGTTGATTTT 300
QY 301 ATACGGGCAAAAGTGTGTGCTCAGAGAGATGTCTATACCTAAGTCTATACGAATAT 360
DB 301 ATACGGGCAAAAGTGTGTGCTCAGAGAGATGTCTATACCTAAGTCTATACGAATAT 360
QY 361 CTAATATCCCGAAACTAAACGTCGCCGTTTACTATATCATATGATGGTGTGTTTATTC 420
DB 361 CTAATATCCCGAAACTAAACGTCGCCGTTTACTATATCATATGATGGTGTGTTTATTC 420
QY 421 GGTGAATATCATGCGATATGATGATGTCCTGATTTTCATTAATAAAGATGTGTGTTG 480
DB 421 GGTGAATATCATGCGATATGATGATGTCCTGATTTTCATTAATAAAGATGTGTGTTG 480
QY 481 ATTAACATATACATATATCGTTGGAGCTCTAGATTTTCTAAGTTTAAATTCAGAACCTT 540
DB 481 ATTAACATATACATATATCGTTGGAGCTCTAGATTTTCTAAGTTTAAATTCAGAACCTT 540
QY 541 AATGCGCCGGTAAATGCGCGCTTAAGATCAAGTCATGCGCTTGATTTAAAT 600
DB 541 AATGCGCCGGTAAATGCGCGCTTAAGATCAAGTCATGCGCTTGATTTAAAT 600
QY 601 AATGCGCCGGTAAATGCGCGCTTAAGATCAAGTCATGCGCTTGATTTAAAT 660
DB 601 AATGCGCCGGTAAATGCGCGCTTAAGATCAAGTCATGCGCTTGATTTAAAT 660
QY 661 GCTGCTCTACCCACTATGATGATTTAAACGAAACATCGCGCTTTCCATGCTGT 720
DB 661 GCTGCTCTACCCACTATGATGATTTAAACGAAACATCGCGCTTTCCATGCTGT 720
QY 721 ATACTAATGTGGGTATGCTATTTGTCCATGCGCTAATACCAATGTCACATGCTGCC 780
DB 721 ATACTAATGTGGGTATGCTATTTGTCCATGCGCTAATACCAATGTCACATGCTGCC 780
QY 781 TTCACTTAGCCCAATTTGCGCGCTATTAAGGTGAGATTAATGATTAAGATGTTTGA 840
DB 781 TTCACTTAGCCCAATTTGCGCGCTATTAAGGTGAGATTAATGATTAAGATGTTTGA 840
QY 841 TTTCTATGAAGCCACAGCATTTAATAAACTTGAAGAAAAGTTTAACTGTA 900
DB 841 TTTCTATGAAGCCACAGCATTTAATAAACTTGAAGAAAAGTTTAACTGTA 900
QY 901 GAAGAGCGTACAAATTAAGTATGTTTCTTTGTCCTGACCTGTTGACCATATAGACC 960
DB 901 GAAGAGCGTACAAATTAAGTATGTTTCTTTGTCCTGACCTGTTGACCATATAGACC 960
QY 961 GGTGATTTGTCTTACCAAAACATCTCGGGAAGATTTAAACGCTGGGGTAATTCG 1020
DB 961 GGTGATTTGTCTTACCAAAACATCTCGGGAAGATTTAAACGCTGGGGTAATTCG 1020
QY 1021 ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 ATACCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080

OY 1081 CAATGCTATGCTTGTAAAGAAATGGAACCTGTTGTCATTTTGTGCCAAGTGAATG 1140
 |||||||
 DB 1081 CAATGCTATGCTTGTAAAGAAATGGAACCTGTTGTCATTTTGTGCCAAGTGAATG 1140
 OY 1141 GGTGATGCTGAACGACCGCCCGACAGACCTTGGAAATGGTGTAAATTAATAAAGCT 1200
 |||||||
 DB 1141 GGTGATGCTGAACGACCGCCCGACAGACCTTGGAAATGGTGTAAATTAATAAAGCT 1200
 OY 1201 CATGTTACAGGAAACACACACAGCTGATATTTATGATCTTTGCTGCATCTAT 1260
 |||||||
 DB 1201 CATGTTACAGGAAACACACACAGCTGATATTTATGATCTTTGCTGCATCTAT 1260
 OY 1261 TTCTGTTTCCCATGACGCTTTGTTGCAATTAACCTTCAATCACACCGCGGTACACC 1320
 |||||||
 DB 1261 TTCTGTTTCCCATGACGCTTTGTTGCAATTAACCTTCAATCACACCGCGGTACACC 1320
 OY 1321 GTCTACTGTATGCTTGCAGCTTTGATTCGGAAGATCTTATTAATCCCTATGCTATG 1380
 |||||||
 DB 1321 GTCTACTGTATGCTTGCAGCTTTGATTCGGAAGATCTTATTAATCCCTATGCTATG 1380
 OY 1381 CGTAGTGACGCTGTGTTAAGGCTGTAGTACATGCTGATGAATTAACCTATTTCTCTG 1440
 |||||||
 DB 1381 CGTAGTGACGCTGTGTTAAGGCTGTAGTACATGCTGATGAATTAACCTATTTCTCTG 1440
 OY 1441 AATCAATTGGCCAAACGATGCTTAAGAAATCGCGTGAATACAAACCAATTTGAAGCT 1500
 |||||||
 DB 1441 AATCAATTGGCCAAACGATGCTTAAGAAATCGCGTGAATACAAACCAATTTGAAGCT 1500
 OY 1501 ACTGATATGATGATCAATTTTCCACACCTGCTGTAATCTTATAGCATGAATTTGAAGCT 1560
 |||||||
 DB 1501 ACTGATATGATGATCAATTTTCCACACCTGCTGTAATCTTATAGCATGAATTTGAAGCT 1560
 OY 1561 ATGGAATAATGTTCTCGGATCCATTAAGAAATCCGACGAATACAGATTTGAAT 1620
 |||||||
 DB 1561 ATGGAATAATGTTCTCGGATCCATTAAGAAATCCGACGAATACAGATTTGAAT 1620
 OY 1621 ATTAGTACGAATTTGAATTAATGATGCTGCTGAATTAAGATTAACATGCGAA 1680
 |||||||
 DB 1621 ATTAGTACGAATTTGAATTAATGATGCTGCTGAATTAAGATTAACATGCGAA 1680
 OY 1681 TCGATGTTGAAACATAGAGATTTATTAG 1713
 |||||||
 DB 1681 TCGATGTTGAAACATAGAGATTTATTAG 1713
 |||||||
 RESULT 3
 ID AA091566 standard; cDNA; 1713 BP.
 XX AA091566;
 AC
 XX 22-DEC-1995 (first entry)
 DT
 XX OP-resistant esterase Lc/L103con.
 DE
 XX Esterase: E3; bioremediation: organophosphate; carbamate;
 KW insecticide; pesticide; water decontamination; meat decontamination;
 KM ss.
 XX
 OS Lucilia cuprina.
 XX
 XX Key Location/Qualifiers
 FH 1.1713
 FT CDS /*tag= a
 XX
 XX WO9519440-A1.
 XX
 XX 20-JUL-1995.
 XX
 XX 13-JAN-1995; 95WO-AU00016.
 PF
 XX 13-JAN-1994; 94AU-000347.
 PR

XX (CSTR) COMMONWEALTH SCI & IND RES ORG.
 PA Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 XX Parker AG, Robin GC, Russell RJ, Smyth K;
 PI WPI: 1995-263870/34.
 DR
 XX Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 PS Example 4: Page 12-17: 38pp; English.
 XX
 XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
 CC OP-susceptible esterase E3 of *L. cuprina*) from a diazinon
 CC resistant strain, Llandillo 103. 4 isolated clones were
 CC sequenced (UC/L103 A-D, AA091562-65) that encoded diazinon-resistant
 CC esterases; a consensus sequence is given in AA091566.
 CC
 XX
 SO Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other:
 Query Match 98.2%; Score 1682.6; DB 16; Length 1713;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 1694; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 OY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAAGTAAATGCAATTTGAAT 60
 DB 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAAGTAAATGCAATTTGAAT 60
 OY 61 AAGTTTAACTATGCTTTAATCAATGAACCGGTGCTAGCTGAATGATTTGCG 120
 DB 61 AAGTTTAACTATGCTTTAATCAATGAACCGGTGCTAGCTGAATGATTTGCG 120
 OY 121 AAGTGAAGGCGTTAAACGTTTAACTGCTGATGATGATTTAAAGCAACCCGACGACACA 240
 DB 121 AAGTGAAGGCGTTAAACGTTTAACTGCTGATGATGATTTAAAGCAACCCGACGACACA 240
 OY 181 ATACGCTAGCCCAACCGCCAGTGGTGAAGTAAAGCAACCCGACGACACA 240
 DB 181 ATACGCTAGCCCAACCGCCAGTGGTGAAGTAAAGCAACCCGACGACACA 240
 OY 241 CCCTGGATGCTGCTGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 241 CCCTGGATGCTGCTGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 300
 OY 301 ATACGCTAGCCCAACCGCCAGTGGTGAAGTAAAGCAACCCGACGACACA 360
 DB 301 ATACGCTAGCCCAACCGCCAGTGGTGAAGTAAAGCAACCCGACGACACA 360
 OY 361 CTAAATCCCGAAACTAAACGCTGCTTTATGATACATGATGATGATGATGATGATGATGATGAT 420
 DB 361 CTAAATCCCGAAACTAAACGCTGCTTTATGATACATGATGATGATGATGATGATGATGATGAT 420
 OY 421 GGTGAATATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 421 GGTGAATATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 OY 481 ATTAACATACATATGCTGTTGGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 481 ATTAACATACATATGCTGTTGGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 540
 OY 541 AATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 541 AATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 OY 601 AATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 601 AATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 OY 661 GCTGCTTACCCACTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 DB 661 GCTGCTTACCCACTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720


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Oy 721 ATACTAATGTGGGGAATGCTATTGTCATGGGCTATACCAATGCAACATGTCGCC 780
Db 721 ATACTAATGTGGGGAATGCTATTGTCATGGGCTATACCAATGCAACATGTCGCC 780
Oy 781 TTCACCTTAGCCAAATTTGGCGGCTATAGGCTGAGCATTAATGATAGCATTTTGGAA 840
Db 781 TTCACCTTAGCCAAATTTGGCGGCTATAGGCTGAGCATTAATGATAGCATTTTGGAG 840
Oy 841 TTTCTTATGAAGCCCAAGCCACAGATTTAATAAACTTGAGGAAAAAGTTTAACTCTA 900
Db 841 TTTCTTATGAAGCCCAAGCCACAGATTTAATAAACTTGAGGAAAAAGTTTAACTCTA 900
Oy 901 GAAGAGCTACAAATAAAGTATGTTTCCCTTTGGTCCCACTGTTGACCCATACAGACC 960
Db 901 GAAGAGCTACAAATAAAGTATGTTTCCCTTTGGTCCCACTGTTGACCCATACAGACC 960
Oy 961 GCTGATTTGCTTACCCAAACATCTCGGAAATGTTAAACCTGTTGGGGTAATTCG 1020
Db 961 GCTGATTTGCTTACCCAAACATCTCGGAAATGTTAAACATGCTTGGGGTAATTCG 1020
Oy 1021 ATACCCTATGATGGGTAAACCTTCAATGAGGGTCTATTTTCACTTCAATTTCTTAAG 1080
Db 1021 ATACCCTATGATGGGTAAACCTTCAATGAGGGTCTATTTTCACTTCTTCTTAAG 1080
Oy 1081 CAAATGGCTATGCTTGAAGGAATTTGAACCTTGTCTCATTTTGTGCCAAGTCAATTCG 1140
Db 1081 CAAATGGCTATGCTTGAAGGAATTTGAACCTTGTCTCATTTTGTGCCAAGTCAATTCG 1140
Oy 1141 GCTGATGCTGAAGCAGCCGCCAGAGACCTTGAATGGGTGCTAAATTTAAAGAGCT 1200
Db 1141 GCTGATGCTGAAGCAGCCGCCAGAGACCTTGAATGGGTGCTAAATTTAAAGAGCT 1200
Oy 1201 CATGTTACAGAGAAACACCAACACAGCTGATTAATTTATGATCTTGTCTCACATCTAT 1260
Db 1201 CATGTTACAGAGAAACACCAACACAGCTGATTAATTTATGATCTTGTCTCACATCTAT 1260
Oy 1261 TTCTGGTCCCAATGATGCTTGTGCAATTTAGCTTTCATTCATCCACCTCGGTACACC 1320
Db 1261 TTCTGGTCCCAATGATGCTTGTGCAATTTAGCTTTCATTCATCCACCTCGGTACACC 1320
Oy 1321 GTCTACTTGTATCGCTTGCCTTGCATTCGAGAGATCTTATTAATCCCTATCGTATTAAG 1380
Db 1321 GTCTACTTGTATCGCTTGCCTTGCATTCGAGAGATCTTATTAATCCCTATCGTATTAAG 1380
Oy 1381 CGTACTGACAGTGGTGTAAAGGGTGTAGTCTGATGATGAATTAACCTATTTCTTCTGG 1440
Db 1381 CGTACTGACAGTGGTGTAAAGGGTGTAGTCTGATGATGAATTAACCTATTTCTTCTGG 1440
Oy 1441 AATCAATTTGGCCAAACGTAATGCTTAAGAAATCGGTAATCAAAACAAATGAAGCTAAG 1500
Db 1441 AATCAATTTGGCCAAACGTAATGCTTAAGAAATCGGTAATCAAAACAAATGAAGCTAAG 1500
Oy 1501 ACTGCTATATGATGATCAATTTTGCACCACTGGTAAATCCCTTATAGCAATGAATTTGAAGT 1560
Db 1501 ACTGCTATATGATGATCAATTTTGCACCACTGGTAAATCCCTTATAGCAATTTGAAGT 1560
Oy 1561 ATGCAAAATGTTTCTCTGGGATCCAAATTAAGAAATCCGACGAGATTAACAAGTGTGAAAT 1620
Db 1561 ATGCAAAATGTTTCTCTGGGATCCAAATTAAGAAATCCGACGAGATTAACAAGTGTGAAAT 1620
Oy 1621 ATTACTGAGATTAAGAAATGATGATGCTGAATGATGAATGAATTAACCAATGGGAA 1680
Db 1621 ATTACTGAGATTAAGAAATGATGATGCTGAATGATGAATGAATTAACCAATGGGAA 1680
Oy 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713
Db 1681 TCGATGTTTGAAGAAACATAGAGATTTATTTAG 1713

```

RESULT 4
-AA091564
ID AA091564 standard; cDNA: 1713 BP.

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XX AA091564;
AC 22-DEC-1995 (first entry)
DT 22-DEC-1995 (first entry)
XX OP-resistant esterase Lc7Li03c allele.
DE Esterase; E3; bioremediation; organophosphate; carbamate;
XX Insecticide; pesticide; water decontamination; meat decontamination;
XX ss.
OS Lucilia cuprina.
XX
XX Key Location/Qualifiers
XX CDS 1..1713
XX F1 /*tag= a
XX
XX W09519440-A1.
XX 20-JUL-1995.
XX
XX 13-JAN-1995; 95WO-A000016.
XX
XX 13-JAN-1994; 94AU-0003347.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX Parker AG, Robin GC, Russell RJ, Smyth K;
XX WPI: 1995-263870/34.
XX
XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX eliminate residues of organo:phosphate and carbamate pesticides from
XX water, meat etc.
XX
XX Example 4: Page 12-17; 38pp; English.
XX
XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX OP-susceptible esterase E3 of L. cuprina) from a diazinon
XX resistant strain, Llandillo 103. 4 Isolated clones were
XX sequenced (Lc7Li03 A-D, AA091562-65) that encoded diazinon-resistant
XX esterases. The esterases, or cells expressing them, are used
XX in bioremediation.
XX
XX Sequence 1713 BP; 512 A; 308 C; 368 G; 525 T; 0 other:
XX
XX Query Match 98.0%; Score 1679.4; DB 16; Length 1713;
XX Best Local Similarity 98.8%; Pred. No. 0;
XX Matches 1692; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Oy 1 ATGAATTTCAACGTTAGTTTGAAGGAGAAATTAATGAATTAATGCAATTAATTAAT 60
Db 1 ATGAATTTCAACGTTAGTTTGAAGGAGAAATTAATGAATTAATGCAATTAATTAAT 60
Oy 61 AAGTTTAACTATGCTTAACTACCAATGAAGGAGGAGTGAAGTGAATATATGCG 120
Db 61 AAGTTTAACTATGCTTAACTACCAATGAAGGAGGAGTGAAGTGAATATATGCG 120
Oy 121 AAAGTGAAGGCGTTAAAGCTTTAACTGCTGATGATGATTTCTTACTACAGTTTGAAGGT 180
Db 121 AAAGTGAAGGCGTTAAAGCTTTAACTGCTGATGATGATTTCTTACTACAGTTTGAAGGT 180
Oy 181 ATACCGTAGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCGAGCACACA 240
Db 181 ATACCGTAGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCGAGCACACA 240
Oy 241 CCCTGGAGTGGTGGCTGATGCTGCAATCAATTAAGATTAACCTGCTGAATGATTTT 300
Db 241 CCCTGGAGTGGTGGCTGATGCTGCAATCAATTAAGATTAACCTGCTGAATGATTTT 300
Oy 301 ATACGGGCAAGGTGGCTCAGAGATTTGCTATACCTTAAGTGTATACGAATAT 360
Db 301 ATACGGGCAAGGTGGCTCAGAGATTTGCTATACCTTAAGTGTATACGAATAT 360

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Db 301 ATACAGGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGCTCTATACGAATAT 360
 QY 361 CTAATCCCGCAAACTAAACGTCGCCGTTTGTATATACATACATGAGGGGTTTATATAC 420
 Db 361 CTAATCCCGCAAACTAAACGTCGCCGTTTGTATATACATACATGAGGGGTTTATATAC 420
 QY 421 GGTGAAAATCATGCTGATATGATATGTCCTGATTATTTCAATTAAGAGATGCTGTG 480
 Db 421 GGTGAAAATCATGCTGATATGATATGTCCTGATTATTTCAATTAAGAGATGCTGTG 480
 QY 481 ATTAACATACAAATATGCTTTGGGAGCTCTAGCTTTTCTAGTTTAAATTCGAAGACCTT 540
 Db 481 ATTAACATACAAATATGCTTTGGGAGCTCTAGCTTTTCTAGTTTAAATTCGAAGACCTT 540
 QY 541 AATGTCGCCGCTAATGCGCGCTTAAGATCAATGATGCGCTTGCCTGATTAATAAT 600
 Db 541 AATGTCGCCGCTAATGCGCGCTTAAGATCAATGATGCGCTTGCCTGATTAATAAT 600
 QY 601 AATTGCGCCCAACTTGGTGGCAATCCGATTAATTTACAGTCTTTGGTGAAGTCCGGT 660
 Db 601 AATTGCGCCCAACTTGGTGGCAATCCGATTAATTTACAGTCTTTGGTGAAGTCCGGT 660
 QY 661 GCTGCTCTACCCACATGATGATTTAACGCAACAACTGCGGCTTTCCATCGTGT 720
 Db 661 GCTGCTCTACCCACATGATGATTTAACGCAACAACTGCGGCTTTCCATCGTGT 720
 QY 721 ATACTAATGTGGGTAATGCTATTTGTCTCATGGGCTAATACCAATGCTCAACATCGTGC 780
 Db 721 ATACTAATGTGGGTAATGCTATTTGTCTCATGGGCTAATACCAATGCTCAACATCGTGC 780
 QY 781 TTGACCTTACCAAAATTTGGCGGCTAATAGGAGATTAATGATTAAGATGTTTGGAA 840
 Db 781 TTGACCTTACCAAAATTTGGCGGCTAATAGGAGATTAATGATTAAGATGTTTGGAG 840
 QY 841 TTTCTTATGAAGCAAGCAGCAGATTAATTAATAAATTGAGAAAAAGTTTAACTCTA 900
 Db 841 TTTCTTATGAAGCAAGCAGCAGATTAATTAATAAATTGAGAAAAAGTTTAACTCTA 900
 QY 901 GAAGAGCTGTCAAAATAGTCAATGTTCTTTTGTCCCACTGTGAGCCATATCAGACC 960
 Db 901 GAAGAGCTGTCAAAATAGTCAATGTTCTTTTGTCCCACTGTGAGCCATATCAGACC 960
 QY 961 GCTGATTTGTCTTACCAAACTCCTCGGAAATGTTTAAACTGCTTGGGTAATTCG 1020
 Db 961 GCTGATTTGTCTTACCAAACTCCTCGGAAATGTTTAAACTGCTTGGGTAATTCG 1020
 QY 1021 ATACCCATATGATGGTAAACACTTCAATGAGGCTCTATTTTCACTCAATCTTAAG 1080
 Db 1021 ATACCCATATGATGGTAAACACTTCAATGAGGCTCTATTTTCACTCAATCTTAAG 1080
 QY 1081 CAATGCTCTATGCTTTTAAAGAACTGTGTCAATTTTGTCCCAAGTGAATG 1140
 Db 1081 CAATGCTCTATGCTTTTAAAGAACTGTGTCAATTTTGTCCCAAGTGAATG 1140
 QY 1141 GGTGATGTGAAGCAGCCGCCAGAGACCTTGAATGGGCTTAATAAATTAAGAGCT 1200
 Db 1141 GGTGATGTGAAGCAGCCGCCAGAGACCTTGAATGGGCTTAATAAATTAAGAGCT 1200
 QY 1201 CATGTTACAGGAAACACCAACAGCTGTAATTTTATGATCTTGTCTCAGATCTAT 1260
 Db 1201 CATGTTACAGGAAACACCAACAGCTGTAATTTTATGATCTTGTCTCAGATCTAT 1260
 QY 1261 TTTCTGTTCCCATGATGATGTTTGAATTAACGTTTAAATCACACCTCCGCTACACC 1320
 Db 1261 TTTCTGTTCCCATGATGATGTTTGAATTAACGTTTAAATCACACCTCCGCTACACC 1320
 QY 1321 GTCTACTGTTATCGCTTGCATTTTGAATGGAAGATCTTATTAATCCCTATGATTAAG 1380
 Db 1321 GTCTACTGTTATCGCTTGCATTTTGAATGGAAGATCTTATTAATCCCTATGATTAAG 1380
 QY 1381 GGTAGTGACGCTGTGTTAAGGCTGTACTCATGCTGATGAATTAACCTATTTCTTGG 1440
 Db 1381 GGTAGTGACGCTGTGTTAAGGCTGTACTCATGCTGATGAATTAACCTATTTCTTGG 1440

QY 1441 AATCAATTTGCCCAACGATATGCTTAAGAAATCCGCTGAATACAAACATTTGAACGTATG 1500
 Db 1441 AATCAATTTGCCCAACGATATGCTTAAGAAATCCGCTGAATACAAACATTTGAACGTATG 1500
 QY 1501 ACTGATATGATGATACATTTTGGCCACCATGTAATCCTTATGCAATGAATTTGAAGT 1560
 Db 1501 ACTGATATGATGATACATTTTGGCCACCATGTAATCCTTATGCAATGAATTTGAAGT 1560
 QY 1561 ATGGAATAATGTTTCTGGGATTCGAATTTAGAAAATCCGACGAGTATACAGTGTGAAT 1620
 Db 1561 ATGGAATAATGTTTCTGGGATTCGAATTTAGAAAATCCGATGAGTATACAGTGTGAAT 1620
 QY 1621 ATTAGTGACGATTTGAATAATGATTTAGTCCCTGAATTTGATTAAGATTAACATGGAA 1680
 Db 1621 ATTAGTGACGATTTGAATAATGATTTAGTCCCTGAATTTGATTAAGATTAACATGGAA 1680
 QY 1681 TCGATGTTTGAATAACATAGATTAATTTAG 1713
 Db 1681 TCGATGTTTGAATAACATAGATTAATTTAG 1713
 RESULT 5
 AAQ91565
 ID AAQ91565 standard; cDNA; 1713 BP.
 XX
 AC AAQ91565;
 XX
 DT 22-DEC-1995 (first entry)
 XX
 DE OP-resistant esterase Lc7L103D allele.
 XX
 KM Esterase; E3: bioremediation; organophosphate; carbamate;
 KW insecticide; pesticide; water decontamination; meat decontamination;
 SS.
 XX
 OS Lucilia cuprina.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1713
 FT /tag- a
 XX
 PN W09519440-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 13-JAN-1995; 95MO-AU00016.
 XX
 PR 13-JAN-1994; 94AU-0003347.
 XX
 PA (CSTR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
 PI Parker AG, Robin GC, Russell RJ, Smyth K;
 XX
 DR WPI; 1995-263870/34.
 XX
 PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
 PT eliminate residues of organo:phosphate and carbamate pesticides from
 PT water, meat etc.
 XX
 PS Example 4; Page 12-17; 38pp; English.
 XX
 CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
 CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
 CC resistant strain, Llandillo 103. 4 isolated clones were
 CC sequenced (Lc7L103 A-D, AAQ91562-65) that encoded diazinon-resistant
 CC esterases. The esterases, or cells expressing them, are used
 CC in bioremediation.
 XX
 SQ Sequence 1713 BP; 513 A; 307 C; 369 G; 524 T; 0 other;
 Query Match 98.0%; Score 1679.4; DB 16; Length 1713;

Best Local Similarity 98.8%; Pred. No. 0;
Matches 1692; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACGTTAGTTGATGGAGAAATTAATAAGAGATTAATGATTTGAAT 60
 Db 1 ATGAATTTCAACGTTAGTTGATGGAGAAATTAATAAGAGATTAATGATTTGAAT 60
 QY 61 AAGTTTTAACTATCGTTTAACTAACATGAACGGGTGATGAAGCAATGATGGC 120
 Db 61 AAGTTTTAACTATCGTTTAACTAACATGAACGGGTGATGAAGCAATGATGGC 120
 QY 121 AAAGTGAAGCGCTTAAACGTTTAACTAGTATGATGATTCCTACAGTTTGAAGGT 180
 Db 121 AAAGTGAAGCGCTTAAACGTTTAACTAGTATGATGATTCCTACAGTTTGAAGGT 180
 QY 181 ATACCGTACGCGCAACCGCGGTGAGCTGAGATTTAAAGCAACCCGACGACAAACA 240
 Db 181 ATACCGTACGCGCAACCGCGGTGAGCTGAGATTTAAAGCAACCCGACGACAAACA 240
 QY 241 CCTGGGATGGTGGCGGATTTGGCAATCATTAAGATTAAGTACAGTACGATTTT 300
 Db 241 CCTGGGATGGTGGCGGATTTGGCAATCATTAAGATTAAGTACAGTACGATTTT 300
 QY 301 ATAAAGGCAAGGTGTGCTCAGAGATTTCTATACCTAAGTCTATACCAATAT 360
 Db 301 ATAAAGGCAAGGTGTGCTCAGAGATTTCTATACCTAAGTCTATACCAATAT 360
 QY 361 CTAAATCCCGAACTAAACGTCGCCGTTTATGATATACATACATGCTGCTTTATATC 420
 Db 361 CTAAATCCCGAACTAAACGTCGCCGTTTATGATATACATACATGCTGCTTTATATC 420
 QY 421 GGTAAATATCATGATATGATGTCCTGATTTATTCATTAATAAGAGATGCTGTG 480
 Db 421 GGTAAATATCATGATATGATGTCCTGATTTATTCATTAATAAGAGATGCTGTG 480
 QY 481 ATTAACATACAAATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAACCTT 540
 Db 481 ATTAACATACAAATATCGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAACCTT 540
 QY 541 AATGTCGCCGTAATGGCGGCTTAAAGATCAATCAATGCGCTTGGATTTAAAT 600
 Db 541 AATGTCGCCGTAATGGCGGCTTAAAGATCAATCAATGCGCTTGGATTTAAAT 600
 QY 601 AATTGCCCACTTTGGTGGCAATCCGATATATTAACAGTCTTTGGGAAGTCCGCT 660
 Db 601 AATTGCCCACTTTGGTGGCAATCCGATATATTAACAGTCTTTGGGAAGTCCGCT 660
 QY 661 GCTGCTCTACCCACTACATGATGTTAACGCAAACTCGCGTCTTTCCATCGTGGT 720
 Db 661 GCTGCTCTACCCACTACATGATGTTAACGCAAACTCGCGTCTTTCCATCGTGGT 720
 QY 721 ATACTAATGTGGGTAATGCTATTTGTCATGGCTTAATACCAATGTCAACATGTCGC 780
 Db 721 ATACTAATGTGGGTAATGCTATTTGTCATGGCTTAATACCAATGTCAACATGTCGC 780
 QY 781 TTACACTTAGCCAAATTTGGCGGCTATAGGGTGGATATGATAGGATTTTGGAA 840
 Db 781 TTACACTTAGCCAAATTTGGCGGCTATAGGGTGGATATGATAGGATTTTGGAA 840
 QY 841 TTTCTTATGAAGCAAGCCACAGATTTTAAACTTGAAGAAAAGTTTAACTCTA 900
 Db 841 TTTCTTATGAAGCAAGCCACAGATTTTAAACTTGAAGAAAAGTTTAACTCTA 900
 QY 901 GAAGAGGTACAAATTAAGGTATGTTTCTTTGCTCCACTGTTGAGCCATATCAGACC 960
 Db 901 GAAGAGGTACAAATTAAGGTATGTTTCTTTGCTCCACTGTTGAGCCATATCAGACC 960
 QY 961 GCTGATTTGCTTACCCAAATCCTCGGAAATGGTAAACATGCTTGGGTAATTCG 1020
 Db 961 GCTGATTTGCTTACCCAAATCCTCGGAAATGGTAAACATGCTTGGGTAATTCG 1020
 QY 1021 ATACCACATATGATGGTAAACACTTCAATGAGGGTCTATTTTCACTCAATTTTAAG 1080
 Db 1021 ATACCACATATGATGGTAAACACTTCAATGAGGGTCTATTTTCACTCAATTTTAAG 1080

Db 1021 ATACCACATATGATGGTAAACACTTCAATGAGGGTCTATTTTCACTCAATTTTAAG 1080
 QY 1081 CAATGGCTATGCTTTGTTAAGAAATTTGAAACTGTGTGCAATTTTGTGCCAAGTGAATG 1140
 Db 1081 CAATGGCTATGCTTTGTTAAGAAATTTGAAACTGTGTGCAATTTTGTGCCAAGTGAATG 1140
 QY 1141 GCTGATGCTGAACGACCGCCCGAGACCTTTGGAATGGGTGCTTAAATTTAAAGAGCT 1200
 Db 1141 GCTGATGCTGAACGACCGCCCGAGACCTTTGGAATGGGTGCTTAAATTTAAAGAGCT 1200
 QY 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTATATGATCTTTGCTCACAATCTAT 1260
 Db 1201 CATGTTACAGAGAAACACCAACAGCTGATATTTATGATCTTTGCTCACAATCTAT 1260
 QY 1261 TTTGCGTTCCCATATGATGCTTTGTTGCAATTTACGTTTCAATTCACACTCCGGTACACC 1320
 Db 1261 TTTGCGTTCCCATATGATGCTTTGTTGCAATTTACGTTTCAATTCACACTCCGGTACACC 1320
 QY 1321 GTCTACTTGTATCGCTTGCATTTGATTCGGAAGATCTTATTAATCCCTATCGTATTATG 1380
 Db 1321 GTCTACTTGTATCGCTTGCATTTGATTCGGAAGATCTTATTAATCCCTATCGTATTATG 1380
 QY 1381 GGTAGTGACGTGGTGTAAAGGGTGTATGTCATGCTGATGAATTAACCTATTTCTTGG 1440
 Db 1381 GGTAGTGACGTGGTGTAAAGGGTGTATGTCATGCTGATGAATTAACCTATTTCTTGG 1440
 QY 1441 AATCAATTTGGCCAAACGATATGCTTAAGAAATCCGCTGATACCAAAACATTTGAAGCTATG 1500
 Db 1441 AATCAATTTGGCCAAACGATATGCTTAAGAAATCCGCTGATACCAAAACATTTGAAGCTATG 1500
 QY 1501 ACTGATATGATGATACATTTGGCCACGCTGATATCTTTTAAAGAAATTTGAAGT 1560
 Db 1501 ACTGATATGATGATACATTTGGCCACGCTGATATCTTTTAAAGAAATTTGAAGT 1560
 QY 1561 ATGGAATATGTTTCTGGGATCCATTAAGAATCCGAGATATACAGTGTGTAAT 1620
 Db 1561 ATGGAATATGTTTCTGGGATCCATTAAGAATCCGAGATATACAGTGTGTAAT 1620
 QY 1621 ATTAGTGACGAATTTGAATATGATGATGCTGCTGAATAGATTAAGATTAACAAATGGGAA 1680
 Db 1621 ATTAGTGACGAATTTGAATATGATGATGCTGCTGAATAGATTAAGATTAACAAATGGGAA 1680
 QY 1681 TCGATGTTTGAATAAATCATGAGATTTATTTAG 1713
 Db 1681 TCGATGTTTGAATAAATCATGAGATTTATTTAG 1713

RESULT 6
 AA091563
 ID AA091563 standard; cDNA; 1713 bp.
 XX
 AC AA091563;
 XX
 DT 22-DEC-1995 (first entry)
 XX
 DE OP-resistant esterase Lc7L103B allele.
 XX
 KW Esterase; E3; bioremediation; organophosphate; carbamate;
 KW insecticide; pesticide; water decontamination; meat decontamination;
 KW ss.
 XX
 OS Lucilia cuprina.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1713
 FT /*tag= a
 PN W091519440-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 13-JAN-1995; 95WO-AU00016.
 XX

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FR 13-JAN-1994: 94AU-0003347.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX WPI, 1995-263870/34.
XX
XX Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
PT eliminate residues of organo-phosphate and carbamate pesticides from
PT water, meat etc.
XX
XX Example 4; Page 12-17; 38pp; English.
XX
XX RT-PCR was used to clone a cDNA allele of *lc-alpha-E7* (encoding
CC Op-susceptible esterase E3 of *L. cuprina*) from a diazinon
CC resistant strain, *landlillo 103*. 4 isolated clones were
CC sequenced (*lc7L103 A-D*, *AAQ1562-65*) that encoded diazinon-resistant
CC esterases. The esterases, or cells expressing them, are used
CC in bioremediation.
XX
XX Sequence 1713 BP; 513 A; 308 C; 368 G; 524 T; 0 other:
SQ
Query Match 97.9%; Score 1677.8; DB 16; Length 1713;
Best Local Similarly 98.7%; Pred. No. 0;
Matches 1691; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
OY 1 ATGATTTTCAACGTTAGTTGATGAGAAATTTAAATGGAATTAATGATTTGAAAT 60
DB 1 ATGATTTTCAACGTTAGTTGATGAGAAATTTAAATGGAATTAATGATTTGAAAT 60
OY 61 AAGTTTAACTATGCTTTAACTCAATGAACGGGTGAGTGAATGCTGAATATGCG 120
DB 61 AAGTTTAACTATGCTTTAACTCAATGAACGGGTGAGTGAATGCTGAATATGCG 120
OY 121 AAGTGAAGGGGTTAAACGTTAACTGTGACGATGATCTCTCACTCACTTGAAGGT 180
DB 121 AAGTGAAGGGGTTAAACGTTAACTGTGACGATGATCTCTCACTCACTTGAAGGT 180
OY 181 ATACCGTAGCCCAACCGCCAGTGGGTGAGATTTAAAGCACCCGACGACCAACA 240
DB 181 ATACCGTAGCCCAACCGCCAGTGGGTGAGATTTAAAGCACCCGACGACCAACA 240
OY 241 CCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 CCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
OY 301 ATACGGGCAAAAGTGTGCTCAGAGATTTCTATACCTAAGTCTCTATACGAATAT 360
DB 301 ATACGGGCAAAAGTGTGCTCAGAGATTTCTATACCTAAGTCTCTATACGAATAT 360
OY 361 CTAAATCCCGAACTAAACGTCCTGTTTATGATATACATACATGCTGCTGCTGCT 420
DB 361 CTAAATCCCGAACTAAACGTCCTGTTTATGATATACATACATGCTGCTGCTGCT 420
OY 421 GGTGAATATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GGTGAATATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
OY 481 ATTAACATACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 ATTAACATACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
OY 541 AATGCGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 AATGCGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
OY 601 AATGCGCGCAACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 AATGCGCGCAACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
OY 661 GCTGCGCTACCGCACTGATGATTTAACGAAACAACCTGCGGCTTTTCCATGCTGT 720

DB 661 GCTGCGCTACCGCACTGATGATTTAACGAAACAACCTGCGGCTTTTCCATGCTGT 720
OY 721 ATACTAATGTCGGTAATGCTATTTTCCATGAGGGCTAAATACCAATGCTCAATGCTGCC 780
DB 721 ATACTAATGTCGGTAATGCTATTTTCCATGAGGGCTAAATACCAATGCTCAATGCTGCC 780
OY 781 TTCACCTTAGCCAAATGTCGGCTATAGGCTGAGGATATGATATGATATGATTTGGAG 840
DB 781 TTCACCTTAGCCAAATGTCGGCTATAGGCTGAGGATATGATATGATATGATTTGGAG 840
OY 841 TTTCTTATGAAGCCAAACGACGATTTAATTAACCTGAGGAAACCTTTTAACTCTTA 900
DB 841 TTTCTTATGAAGCCAAACGACGATTTAATTAACCTGAGGAAACCTTTTAACTCTTA 900
OY 901 GAAGAGCGTACAAATTAATGCTATGCTTTTGGTCCACTGTTAGCCATATGACGACC 960
DB 901 GAAGAGCGTACAAATTAATGCTATGCTTTTGGTCCACTGTTAGCCATATGACGACC 960
OY 961 GCTGATTTGCTTACCCAAACATCTCGGAAATGTTAAACATGCTGCGGTAATTCG 1020
DB 961 GCTGATTTGCTTACCCAAACATCTCGGAAATGTTAAACATGCTGCGGTAATTCG 1020
OY 1021 ATACCCACTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 ATACCCACTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
OY 1081 CAATGCGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 CAATGCGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
OY 1141 GCTATGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1200
DB 1141 GCTATGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1200
OY 1201 CATGTTACGAGGAAACCAACAGCTGATATTTATGATCTTTGCTCTCACTAT 1260
DB 1201 CATGTTACGAGGAAACCAACAGCTGATATTTATGATCTTTGCTCTCACTAT 1260
OY 1261 TTTGCTGCTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 TTTGCTGCTCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
OY 1321 GTCTACTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
DB 1321 GTCTACTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
OY 1381 CGTAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB 1381 CGTAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
OY 1441 AATCAATTTGCCAAACGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 AATCAATTTGCCAAACGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
OY 1501 ACTGCTATGATGATACAAATTTGCCACACTGCTGATATCTTATAGCAATGAAATGAG 1560
DB 1501 ACTGCTATGATGATACAAATTTGCCACACTGCTGATATCTTATAGCAATGAAATGAG 1560
OY 1561 ATGGAATTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 ATGGAATTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
OY 1621 ATTTAGTGAAGTGAAGAAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 ATTTAGTGAAGTGAAGAAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
OY 1681 TCGATGTTTGAAGAAACATAGATTTATTTAG 1713
DB 1681 TCGATGTTTGAAGAAACATAGATTTATTTAG 1713
RESULT 7

AA091562
ID AA091562 standard; cDNA: 1713 BP.
XX
AC AA091562;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103a allele.
XX
KW Esterase; E3; bioremediation; organophosphate; carbamate;
KW Insecticide; pesticide; water decontamination; meat decontamination;
XX ss.
XX Lucilia cuprina.
XX
FH key Location/Qualifiers
FT CDS 1..1713
FT /*tag= a
XX
PN MO9519440-A1.
XX
PD 20-JUL-1995.
XX
PF 13-JAN-1995; 95WO-AU00016.
XX
PR 13-JAN-1994; 94AU-000347.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
PI Parker AG, Robin GC, Russell RJ, Smyth K;
XX
DR WPI: 1995-263870/34.
XX
PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
PT eliminate residues of organo:phosphate and carbamate pesticides from
XX water, meat etc.
XX
PS Example 4; Page 12-17; 38pp; English.
XX
CC RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
CC resistant strain, Ilandillo 103. 4 Isolated clones were
CC sequenced (Lc7L103 A-D. AA091562-65) that encoded diazinon-resistant
CC esterases. The esterases, or cells expressing them, are used
XX in bioremediation.
XX
SQ Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;
Query Match 97.9%; Score 1676.2; DB 16; Length 1713;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1690; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 301 ATACGGCGAAAGTGTGGCTCAGAGATTGCTATACCTAAGTCTATACGATAAT 360
DB 301 ATTACAGCGAAAGTGTGGCTCAGAGATTGCTATACCTAAGTCTATACGATAAT 360
QY 361 CTAAATCCCGAAACCTAAACGTCCTTTAGTATACATACAGTGTGGTTTATATC 420
DB 361 CTAAATCCCGAAACCTAAACGTCCTTTAGTATACATACAGTGTGGTTTATATC 420
QY 421 GGTGAAATCATCGTATATGATGTGCTCTGATTTTCATTAAAGATGTGTTG 480
DB 421 GGTGAAATCATCGTATATGATGTGCTCTGATTTTCATTAAAGATGTGTTG 480
QY 481 ATTACATACAAATATGTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT 540
DB 481 ATTACATACAAATATGTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAACCTT 540
QY 541 AATGTGCCCGGTAAATGCCGCTTAAAGATCAAGTCATGCGCTTGTGATTAATAAT 600
DB 541 AATGTGCCCGGTAAATGCCGCTTAAAGATCAAGTCATGCGCTTGTGATTAATAAT 600
QY 601 AATGCGCCCACTTTGTGGGCAATCCCGATATATTACAGTCTTTGTGTAAGTCCGCT 660
DB 601 AATGCGCCCACTTTGTGGGCAATCCCGATATATTACAGTCTTTGTGTAAGTCCGCT 660
QY 661 GCTGCTCTACCCACTACATGATGTTAAACCGAAACAACTCGGGCTTTTCCATGCTGT 720
DB 661 GCTGCTCTACCCACTACATGATGTTAAACCGAAACAACTCGGGCTTTTCCATGCTGT 720
QY 721 ATACTAATGTGCGGTAATGCTATTTGTCCATGCGGCTAATACCAATGTCACATGCTGC 780
DB 721 ATACTAATGTGCGGTAATGCTATTTGTCCATGCGGCTAATACCAATGTCACATGCTGC 780
QY 781 TTCACCTTAGCCAAATTTGGCGGCTATTAAGGTGAGGATATGATTAAGATTTTGGAA 840
DB 781 TTCACCTTAGCCAAATTTGGCGGCTATTAAGGTGAGGATATGATTAAGATTTTGGAA 840
QY 841 TTTCTTTTGAAGCCAGACGACAGATTTAATAAACTTGAGAAAAGTTTAACTCTA 900
DB 841 TTTCTTTTGAAGCCAGACGACAGATTTAATAAACTTGAGAAAAGTTTAACTCTA 900
QY 901 GAAGAGCGTCAAAATTAAGTCAATGTTTCCCTTTGTCACATGTTGAGCCATATCAGAC 960
DB 901 GAAGAGCGTCAAAATTAAGTCAATGTTTCCCTTTGTCACATGTTGAGCCATATCAGAC 960
QY 961 GCTGATTTGTCTTACCAACATCTCTGGGAAATGTTAAACTGCTTTGGGTAATTCG 1020
DB 961 GCTGATTTGTCTTACCAACATCTCTGGGAAATGTTAAACTGCTTTGGGTAATTCG 1020
QY 1021 ATACCACCTATGATGGTATACCTCATATGAGGGCTATTTTCACTTCAATTCCTTAG 1080
DB 1021 ATACCACCTATGATGGTATACCTCATATGAGGGCTATTTTCACTTCAATTCCTTAG 1080
QY 1081 CAATATGCTATGCTTTTAAGGAATTTGAACTTGTGCAATTTTGTGCAAGTGAATG 1140
DB 1081 CAATATGCTATGCTTTTAAGGAATTTGAACTTGTGCAATTTTGTGCAAGTGAATG 1140
QY 1141 GCTGATGCTGAAGCGACCGCCCAAGACCTTTGAAATGGTGTCTTAATTTAAAGGCT 1200
DB 1141 GCTGATGCTGAAGCGACCGCCCAAGACCTTTGAAATGGTGTCTTAATTTAAAGGCT 1200
QY 1201 CATGTTACAGGAAACCAACACAGCTGATATTTATGATCTTGTCTCACATCTAT 1260
DB 1201 CATGTTACAGGAAACCAACACAGCTGATATTTATGATCTTGTCTCACATCTAT 1260
QY 1261 TTCTGTTTCCCGATCATGTTTGTGCAATTTACCTTTCAACACACCTCCGCTACACC 1320
DB 1261 TTCTGTTTCCCGATCATGTTTGTGCAATTTACCTTTCAACACACCTCCGCTACACC 1320
QY 1321 GTTACTGTTATGCTTGTGACTTTGATTCGGAAGATCTTATTAATCCCTATGATATG 1380
DB 1321 GTTACTGTTATGCTTGTGACTTTGATTCGGAAGATCTTATTAATCCCTATGATATG 1380
QY 1381 CTTAGTGAACGCTGTGTTAAGGCTGTACTCATGCTGATGAATTAACCTATTTCTTCTG 1440


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|||||
Db 1381 CCTAGGAGACGTGTGTAAAGGCTGTAGCATGCTGATGAATTAACCTATTCTCTGG 1440
Qy 1441 AATCAATTTGGCCAAACGTAATGCTTAAGAATGCCGTAATACAAAACATTAAGCTATG 1500
Db 1441 AATCAATTTGGCCAAACGTAATGCTTAAGAATGCCGTAATACAAAACATTAAGCTATG 1500
Qy 1501 ACTGATATATGATACAAATTTGGCCACCTGTAATCCTTATGCAATGAATGAAGCT 1560
Db 1501 ACTGATATATGATACAAATTTGGCCACCTGTAATCCTTATGCAATGAATGAAGCT 1560
Qy 1561 ATGGAATAATGTTCTCGGATCCAAATTAAGAATCCGACGAGTATACAACTTTGAAT 1620
Db 1561 ATGGAATAATGTTCTCGGATCCAAATTAAGAATCCGACGAGTATACAACTTTGAAT 1620
Qy 1621 ATTAGTACGAATTTGAATAATGATGATGCTGCAATGATGAATTAACAATGGGA 1680
Db 1621 ATTAGTACGAATTTGAATAATGATGATGCTGCAATGATGAATTAACAATGGGA 1680
Qy 1681 TCGATGTTGAAAAACATAGAGATTATTTAG 1713
Db 1681 TCGATGTTGAAAAACATAGAGATTATTTAG 1713

```

RESULT 8

AA168597 standard; DNA; 1710 BP.

AA168597:

08-AUG-1997 (first entry)

Md-alpha-E7 gene.

Malathion carboxylesterase; organophosphate; insecticide; pesticide; remediation; bioremediation; decontamination; ds.

Musca domestica Rutgers strain.

Key Location/Qualifiers
752 mutation

FT /tag= a
FT /note= "Trp-251 TGC codon is altered to a Ser
codon in resistant mutants"

WO9719176-A1.

29-MAY-1997.

22-NOV-1996; 96WO-AU00746.

23-NOV-1995; 95AU-0006751.

(CSIR) COMMONWEALTH SCI & IND RES ORG.

Boyce T, Brownlie JC, Campbell PM, Claudianos C,
Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

WPI; 1997-298113/27.

P-PSDB: AAW17767.

DNA encoding enzyme that degrades organophosphate pesticides -
useful for decontamination of soil, water, food etc

Claim 6; Fig 3; 52pp: English.

A 1710 bp DNA molecule (AA168597) comprises the Md-alpha-E7
coding sequence of the Musca domestica Rutgers strain. It was
isolated by amplification of genomic DNA using alpha-esterase
consensus primers (see also AA168598-99) and use of a 534 bp
amplicon to screen a genomic library of M. domestica. A
mutation of the gene, resulting in substn. of serine for tryptophan
at amino acid position 251 (see also AAW1767), confers malathion

CC resistance. The resistant enzyme acts as a malathion
CC carboxylesterase and can be formulated for use in degrading
CC environmental carboxylester or dimethyl general organophosphates.

XX Sequence 1710 BP; 498 A; 369 C; 394 G; 449 T; 0 other;

Query Match 55.8%; Score 956.6; DB 18; Length 1710;
Best Local Similarity 73.4%; Pred. No. 5e-254;
Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;

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Qy 44 TTAAATGATTAATAATTAATGTTTAACTATGTTTAACTACCAATGAACGGGTGAG 103
Db 44 TTAAATGATTAATAATTAATGTTTAACTATGTTTAACTACCAATGAACGGGTGAG 103
Qy 104 CTGAATGATTAATGCAAAAGTGAAGGCTTAAGCTTAACCTGATGATGATGATTTCT 163
Db 104 TCGATACTGATTAATGCAAAATTAAGGCTTAAAGCAATGACCGTCTACAGATGATTTCT 163
Qy 164 ACTACAGTTTGAAGGTATACCGTACGACCCACGCGCAGTGGGTGAGTGAATTAAG 223
Db 164 ACTACAGTTTGAAGGTATACCGTACGACCCACGCGCAGTGGGTGAGTGAATTAAG 223
Qy 224 CACCCGAGCGACCAACACCCCTGGGATGCTGGGATGCTGATGCTGATGCTGATGCT 283
Db 224 CACCCGAGCGCGCTGACCAAGGAGGTGTACGTATGCTGTGGGCGACGCCAACAGAT 283
Qy 284 CAGTGAAGTTGATTTTATACGCGCAAGTGTGTGCTCAGAGATGCTATACCTAA 343
Db 284 CAGTGAAGTTGATTTTATACGCGCAAGTGTGTGCTCAGAGATGCTATACCTAA 343
Qy 344 GTGCTATACGAATTAATCTAATCCGAACTAAGCTCCGTTTAACTATACATACATG 403
Db 344 GTGCTATACGAATTAATCTAATCCGAACTAAGCTCCGTTTAACTATACATACATG 403
Qy 404 GTGGTGGTTTATTAATCGGGAATAATCATGCTATATGATGCTGATTTATTCATTA 463
Db 404 GTGGTGGTTTATTAATCGGGAATAATCATGCTATATGATGCTGATTTATTCATTA 463
Qy 464 AAAAGATGCTGTGTTGATTAACTAATCAATATGTTGGAGCTCTAGGTTTCTAAGTT 523
Db 464 AAAAGATGCTGTGTTGATTAACTAATCAATATGTTGGAGCTCTAGGTTTCTAAGTT 523
Qy 524 TAAATTCAGAGACCTTAATATGTCGCGGTATATCCGCGCTTAAAGATCAAGTATGCGCT 583
Db 524 TAAATTCAGAGACCTTAATATGTCGCGGTATATCCGCGCTTAAAGATCAAGTATGCGCT 583
Qy 584 TGGCTGATTAAATAATTAATGCGCAACTTGTGCGCAATCCGCAATATATTAAGTCT 643
Db 584 TGGCTGATTAAATAATTAATGCGCAACTTGTGCGCAATCCGCAATATATTAAGTCT 643
Qy 644 TTGGTGAAGTGGCGGTGCTGCTTACCCATACATGATGTTAAACCGAACAACCTCGCG 703
Db 644 TTGGTGAAGTGGCGGTGCTGCTTACCCATACATGATGTTAAACCGAACAACCTCGCG 703
Qy 704 GTCTTTCCATGCTGCTGATATATGTCGCGGTATATGCTATATTTGTCATGGGCTAATCC 763
Db 704 GTCTTTCCATGCTGCTGATATATGTCGCGGTATATGCTATATTTGTCATGGGCTAATCC 763
Qy 764 AATGTCACATCGTGCCTTACCTTAAGCAATTTGGCGCGCTTAAGGCTGAGATTAATG 823
Db 764 AATGTCACATCGTGCCTTACCTTAAGCAATTTGGCGCGCTTAAGGCTGAGATTAATG 823
Qy 824 ATAGGATGTTTGAATTTCTTATGAAGCCACAGCCACAGATTAATTAATTAATCTTGA 883
Db 824 ATAGGATGTTTGAATTTCTTATGAAGCCACAGCCACAGATTAATTAATTAATCTTGA 883
Qy 884 AAAAGTTTAACTCTAGAAAGACGTTAAGTATGTTCTTTTGGTCCACTG 943
Db 884 AAAAGTTTAACTCTAGAAAGACGTTAAGTATGTTCTTTTGGTCCACTG 943
Qy 944 TTGAGCATATCAGACCGCTGATGCTGCTTACCAAACTCTCGGGAAATGCTTAANA 1003
Db 944 TTGAGCATATCAGACCGCTGATGCTGCTTACCAAACTCTCGGGAAATGCTTAANA 1003

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QY	1004	CTGCTGGGTAAATTCGATATCCACATATATAGGGTAACACTCATATAGAGGCTCATTTT	1063
Db	1004	GCCTCTGGGAAATTGCATACCCACTTATATAGCATACCTCTACGAGGTTTGCTTT	1063
QY	1064	TCACCTTCATATCTTAAAGCAAAATCCCTATCTGTTAAGGAATTTGMAACTGTGTGCATTT	1123
Db	1064	CCAAATCAATATTCGCAAAACATATTCGGAGAGTTGTAAAGAGTTGGAATTCGTGTGAATT	1123
QY	1124	TTGTGCCAAGTGAATTGGCTGATGCTGAAACGACGCCCCAGACACTTTGGAAATGGGTG	1183
Db	1124	ATGTGCTTGGGAGTTGGCTGACAGTGAACGCGAGTCCCGGMAAACCTTGAGAGGGCTG	1183
QY	1184	CTAAATTAATAAAGGCGATGTTACGGGAAAGCAACACACGTATATTTATAGATC	1243
Db	1184	CCATTTGAAAAAGGCCCATGTGTGATGGGAAACCTTACTGTGATATTTTATGAGGC	1243
QY	1244	TTTCTCTCACATCATATTTCTGGTTCCTCCCATCATCGTTGTGGAATATAGCTTTCATC	1303
Db	1244	TTTCTCTCTATTTCTATTTCTTCTTCCCATGATGCTCTCTACAAATTTGGCTTTCAAAC	1303
QY	1304	ACACCTTCGGGTACACCCGTCCTACTTGTATCGCTTCGACTTTGATTCGGAAGATCTATTA	1363
Db	1304	ACACAGCTGGACCCCATTTATTTGTATGTCGTTGATTTGCAATTCGAGAAATATATA	1363
QY	1364	ATCCCTATCGATATTATGCGTAGTGACGCTGCTTAAGGGTTATGTCATGCTGATGAT	1423
Db	1364	ACCCCTATCGATATTATGCGTTGGCCCTGGGGGCTTAAAGGTATAGCATGGCCATGAGC	1423
QY	1424	TAACTATTCTTCTGGAATCATTTGGCCAAACGTAATGCTTAAGAAATTCGGTGAATCA	1483
Db	1424	TAACTATCTCTTCTGGAACATTTTGTGGAAGGCCCTGCCAAAGGAAGCCGCGCATATCA	1483
QY	1484	AAACAATTGAACGATATGCTGATATGTAATGTAACATTTGCCACACTGCTATATCCTTTA	1543
Db	1484	AAACCATTTGAACGATGCTGTTGGCATTTTGGACGGAATTTGCCACCCACGGAACCATCATCA	1543
QY	1544	GCAATGAATTTGAAGATGTAGGAAAAATGTTCTCGTGAGATCCAAATTAAAGAAATCCGACAG	1603
Db	1544	GCAATGATATAGCCGCGCATGGAAACCTCACCTGGGATCCCATATAAAAAATCCGATGATG	1603
QY	1604	TATCAAGTGTTTGAATATTATAGTACGAAATTTGAAATGATATATGCTCGTAATGATTA	1663
Db	1604	TCTATTAATGTTTAAATATCGGGAGATGATGAACCTTTGGAATTTGGCCAGAAATGATTA	1663
QY	1664	AGATTAACAACGGGATGCAATGTTTGAAGAAACATGACATTTATTT	1710
Db	1664	AAATTAACAATGGGCAAGTATATTCGATTAATAAGAGGAATTTGTT	1710

	RESULT 9
ABLO2067	
ID	ABLO2067 standard; cDNA; 2001 BP.
XX	
AC	ABLO2067;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 683.
XX	
KW	Drosophila; developmental biology; cell signalling; insecticide;
KW	pharmaceutical; gene; ss.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO200171042-A2.
PD	
XX	
PD	27-SEP-2001.
XX	
PF	23-MAR-2001; 2001WO-US09231.
XX	
PR	23-MAR-2000; 2000US-191637P.
PR	11-JUL-2000; 2000US-0614150.

[illegible]


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Db 695 AATTTGGCTAGTTTGGCGGAGATCCCACTGCATCTGTTTGTGAGAGTGGTGA 754
Qy 661 GCTGCCCTACCCAGTACATGATGTTAACGAAACAACGGCGTCTTTCCATCGTGT 720
Db 755 GGGCGCTCCACTACTACTATGATGATGATCCGATACAGACCAGGCGCTTTTCGGCG 814
Qy 721 ATACTAATGTGGGTATGCTATTTGTCCATGGGC--TAAATACCCCAATGTCACATCGT 777
Db 815 ATCTGACAGTGGGCAATGGCATTTGTCTTGGGCTACAGAGGCGCATTAACCCATAT 874
Qy 778 GCTTACACCTTACCAAAATTTGGCGGCTATAGGGTGAAGATATGATTAAGATGTTTG 837
Db 875 CCTACAGAGTATACCAAGCTGGTGGCTACAGGGGAGACACAGCATGATGCTG 934
Qy 838 GAATTTCTTATGAAAGCCAGACAGGATTTAATAAATTAGGAAAGAAATTTAACT 897
Db 935 GATTTCTTGACAGACGTAAGGCAAGATCTTATTCGGCTGAGGAAATGTCCTGACA 994
Qy 898 CTAGAGAGCGGTACAATAAGTCAATGTTTCTTTGGTCCACTGTGAGCCATATCAG 957
Db 995 CTGAGAGAAAGCATGAAGAAATATGTTTCTTTGGCCATCCCTGGAACATCTCTC 1054
Qy 958 ACCGCTGATTTGCTTACCCAAACATCCCGGGAATGTTAAACTGTTGGGTAAT 1017
Db 1055 ACCGCCGAATGTGTATATCAAGCTCCAAAGAGATGATGAAGACCGCTTGAGTAC 1114
Qy 1018 TCGATACCCACTATGATGGGTAACTTCAATATGAGGGTCTATTTTCACTTCAATCTT 1077
Db 1115 TCCATCCCATGTTTATAGAAACACTTGTGTAGAGGGCTGCTGGGTCCAGAGTA 1174
Qy 1078 AAGCAATGCTTGTGTTGTAAGAAATGGAACCTGTCTCAATTTTGTGCCAAGTGA 1137
Db 1175 AAGCTTATCCCGAGGTGTGTGACAGCTGATGATGCGACACCTTTCATTTCCCAAGAA 1234
Qy 1138 TTGGCTGATGCTGAAGCAGCCGCCAGAGACCTTGAATGGGTACTAAATTAAGA 1197
Db 1235 TTGCTGGCCAGGAGGCCAGTAAAGAAACCTGATTCGTGGAGTGCACAGATTCAGAT 1294
Qy 1198 GCTCATGTTACAGAGAAACACCACAGCTGATTAATTTATGAGCTTTGCTCAATC 1257
Db 1295 GTTCATGCGACTGGTCTCAGAAAGCACCAGATTAATTAATGATGCTGTGTGATTAAC 1354
Qy 1258 TATTTGTGTTCCCATGATGCTTTGTGTGCAATTAAGTTTCAATACACCTCCGTA 1317
Db 1355 TACTTGTGTTTCCCGCTCGAGGGGTGTCATTTCCCGACGCGCTGAGAGCT 1414
Qy 1318 CCCGTTACTTGTATGCTTGCATTTGATGTCGAGATCTTATTAATCCCTATGCTATT 1377
Db 1415 CCAGTATATTTCTATGATATGATCTTGCACCTCCGAGAGCTATTTTCCGTACCCGATT 1474
Qy 1378 ATGCGTAGTGAAGTGTGTTAAGGTGTTAAGTCAATGATGATTAACCTATTTCTTC 1437
Db 1475 ATGCGGTGAGACGGGTGTCAAGGGGTGAGCATGCGGAGATTGAGCTAACCAATTC 1534
Qy 1438 TGAATCAATTTGGCCAAACGATATGCTAAAGAAATCGCTGAATACAAACATTTGAC 1497
Db 1535 ACCAGCTCTGCTGCTGCGGTTGCGGAAGAAAGTCGAGATCGAAGATCGAACA 1594
Qy 1498 ATGACTGTATATGATATCAATTTGGCACCATGTAATCTTATGCAANTGAATTTGA 1557
Db 1595 ACCGTGGCATCTGACACCAAGTTTGTGCGCAGGGTAATCCCTACAGCAGAGATCAAC 1654
Qy 1558 GGTATGAAATATGTTCTGAGGATCCAAATTAAGAAATCCGAGAGATTAACAAGTTTG 1617
Db 1655 GGTATGACACTGTCGACATGATTCAGTTTCGAAATCGAGAGGTATCAATCAAGTCC 1714
Qy 1618 AATATTAGTGAAGATTTGAATTAATGATGATGCTGGAATGATTAAGATTAACAAATG 1677
Db 1715 AACATCAGTACCTGAGTGAAGTTTCAATGATCTGCTGAGTGGCCCAATTTGAAGGTG 1774
Qy 1678 GAATGATGTTTGAAGAAACATAGATTTATTTT 1711

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Db 1775 GAGAGCCTTATGACGACAAACAAGATTTATTTCT 1808
RESULT 10
ID ABL02081 standard; cDNA; 1704 BP.
XX
AC ABL02081;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide seq ID NO 725.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmacological; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PMD, Myers EW;
XX
DR WPI: 2001-656860/75.
XX
DR P-PSDB: ABB57978.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 725; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 1704 BP; 417 A; 445 C; 460 G; 382 T; 0 other;
XX
Query Match 22.2%; Score 380.2; DB 23; Length 1704;
Best Local Similarity 54.0%; Pred. No. 1.1e-94;
Matches 878; Conservative 0; Mismatches 728; Indels 21; Gaps 4;
Qy 85 ACCAATGAAGAGCTGTACTGTAATGCAATGCAAGTGAAGGCGTTAAAGCTTTA 144
Db 64 AGCAATGACAAAGTCTATCCCGACACGGTCTACGAAAGGTAAAGGGGTGAAGTGGCAG 123
Qy 145 ACTGTGTACGATGATCTTACTACAGTTTGAAGGTATACCTGACGCCCAACCGCATG 204
Db 124 TCCATCTAGGCAACAACACTACTAGCTTGAAGGGATCCGTTGGCAAGCGCGGGT 183
Qy 205 GGTGACCTGAGATTTAAAGCACCCAGCAGCAACCTGGAGTGTGCGTATTTCT 264
Db 184 GCGAGGCTCTCCCTTCAAGGCGCCGCGAGCCAGACACTGTGATGATCAAGCGGTGC 243
Qy 265 TGCATCATAAAGATTAAGTCAATGCAAGTGTATTTATTAACGGGCAAGTGTGGCTCA 324
Db 244 ACACATGTTTGGCGCAAGCCGTGCAAGTCAATGCTTGTGAAGCAGGTGCAAGGACG 303

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OY	325	GAGGATGTCGTATACCTAAAGTGTCTTACGAGTAATCTAAATCCCGGAACCTAAAGTCCC	384
Db	304	GAGGACTGTCTGTACCTCAATGTCTACACGAGGAGTTACATCCACACAGACTTTGGCG	363
OY	385	GTTTATAGTATACATACATGCTGGTGGTTTATTCGTGTAAGAAATCATCTGATATGAT	444
Db	364	GTTCTGTGTGGATCTATGCGCGGTGGATTCCAAATGGGGAAAGCATTCGGGATCTGTAC	423
OY	445	GGTCCATATTTTCATTAAGAAAGGATGTGGTGTGATTACATACATATTCGTTGGGA	504
Db	424	AGCCCGGACTACATTTATGATGGAACATGTCTACGTGCTGTAAATCTCATCGTTAGGA	483
OY	505	GCTTAGGTTTCTCAAGTTTAAATTCAGAAAGCCTTAATGTGCCGGTAATGCCGGCTT	564
Db	484	GCCCTGGGATTCCTTACTGTCTGACACGAAAGATGATGTTCCTGGAAGACGGCGACTA	543
OY	565	AAAGATCAAGTCATGGCTTGCCTGGTGAATTAATAATGTGGCCACCTTGTGGGCAT	624
Db	544	AAGATCAAGTTATGGCTTGCCTGGTGGTCAACAGGAATTTGCCAGTCTTGTGGGCAT	603
OY	625	CCCGATTAATTTACAGCTTTGGTGAAGTGGCCGTGCTGCTCTACCCACTACATGATG	684
Db	604	CCCATATATTAACCGTTTGTGTGAGAGTGTGGAGGTGATCCACACATTATATATG	663
OY	685	TTAACCCAAACAACTGCGCGTCTTTCCATCTGTGTAATCTATGTCGGTAATAGCTTT	744
Db	664	CTGACGGATCAGGCGCAAGGCGCTATTTTCACAGACATATTATATGTGGGATCCGACTG	723
OY	745	TGTCCATGGGCTAATACCCAATGTCA--ACATCTGCTTCACCTTAGCCAAATTGGCC	801
Db	724	GCACCCCTGGCGCGACAGCCCAACCCACATTAATTTGGCCCTATGCGCTGGCAGCGCACT	783
OY	802	GGCTATTAAGGGTGAAGTAATGATTAAGATGTTTGGAAATTTCTATGAAGCCAGCA	861
Db	784	GGCTACACAGGAGATGCTAACGATCGGAGCATTTTGGCCCATCTCAAGAAATGTAAAGCC	843
OY	862	CAGGATTTAATTAACCTTGAGGAAAAAGTTTAACTTGAAGAGCCGTACAAATTAAGT-	920
Db	844	AGTAGCATGTGTAAGGTGGCCGAGGATATCATCACATGGAAGACGACACAGCGGTTG	903
OY	921	--CATGTTTCCCTTTGGTGTCCACCTGTGTTGAGCAATTAACACGCGTATGTGTCTAAC	978
Db	904	ACCATGTTCAGCTTTGGACCCACACATCGAGCCCTATTATGACTCTCATTTGTGTCTCC	963
OY	979	AAACATCCTCGGGAATGTTTAAACTGCTTGGGGTAATTCGATCCCACTATGATGGGT	1038
Db	964	AAGTCCCACTGGAATAATGATGCGGACTGTGGGGCAACAGCATTTCCATGGTATCGGA	1023
OY	1039	AACACTCATATGAGGTCATATTTTTCACCTTCATTTCTTAAGCAAAATGCTATGCTTGT	1098
Db	1024	GGAAGCTCTTCGAAGTCTCCCAATGTTTCCGAAATGAAACAACTGGCCGGAATGCTT	1083
OY	1099	AAGAAATTTGAAACTTGTGTCAATTTTGTGCCAAGATTTGGGTGATGTGATGACGACACC	1158
Db	1084	TGCCAGCTGGGTACTCTCGAAGACCTGCGCCCTCAAGATGTGCCACGTATGATGACGACAA	1143
OY	1159	GCCCCAGAGACCTTGGAAATGSGTGCTAAATTTAAAAAGGCTCATGTTTACAGGAGAAACA	1218
Db	1144	AGAAAGAGGTTTGGAAAGAAAGTACAGAGACTATATTTGGCGATGAGACCTCTGGCGAG	1203
OY	1219	CCAACAGCTGATTAATTTATGATGACTTGTCTGTCTGCACATCTATTTCTGGTGTCCCATGAT	1278
Db	1204	AAGACCATTTGGAGTACACGATCTCTTCTGTACAAATATTTCTGGCATGTGCATTTAT	1263
OY	1279	CGTTTGTGCATTTACGTTTCAATCAACACCTCGGATACACCCGCTACTGTGATGCTTC	1338
Db	1264	AGGACTTGTGCTCGCGCTGTCTACACAGCCCACTTGGCCCCAACATTCCTGTACAGCAATTC	1323
OY	1339	GACTTATATTCGAAAGATCTTATTATNCCCTATCGATATATGCGATGAGAGACGTGTGT	1398
Db	1324	GATTTGCACTG--AAGCACTTCAATATATACGGAATATATACCTGTGGCCGCAAGGTG	1380

OY	1399	AAGGGGTGATGACATGCTGATGAATTAACCTATTCTCTGGAAATTAATGGCAACGCT	1458
OY	1381	CGCGGACACCTGTACACGCGGATGATCTGTCTGATTCTTACATGCGCGTCCCAAAAG	1440
OY	1459	ATGCCTAAAGAATTCGGTGAATACAAACAATTTGAACGTATGACTGGTATGATGATCA	1518
Db	1441	CTGAACACGCGGACACGACAGCTTCAAGACATTAACCGTTTGGTATCCATGTCGTTAC	1500
OY	1519	TTTGGCCACCATGTGTATTCCTTATA-----GCATGAATTAAGGTATGAGAA	1566
Db	1501	TTTGGCATTTCCGGGGATCTCCCAACATACCGATGCTGCCAGATGAGAAGAACACGCC	1560
OY	1567	AATGTTTCTCGGATCCATTTAAGAATCCGACGAGTATACAAAGTGTGATATTAGT	1626
Db	1561	CGTGGCGCTGCGCTGCCATTTTCGAAGGACGATTAAGGTGTCCAGTCCGATATATTCG	1620
OY	1627	GACGATTAAGAATGATGTATGTCCTGAATGATGAATGATTAACAATGGGAATGATG	1686
Db	1621	CACGATGTGTCATGTGATTTATTTGCCGGAAGCCGAAAAGCTGACACTTTGGACTGCATC	1680
OY	1687	TTTGGAA 1693	
Db	1681	TACGACA 1687	
RESULT	11		
ABL02066			
ID	ABL02066	standard; cDNA; 6175 BP.	
XX	ABL02066;		
AC			
DT	26-MAR-2002	(first entry)	
XX			
DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 680.		
XX			
KW	Drosophila: developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.		
XX			
OS	Drosophila melanogaster.		
PN	WO2001/1042-A2.		
XX			
PD	27-SEP-2001.		
XX			
PF	23-MAR-2001; 2001WO-US09231.		
XX			
PR	23-MAR-2000; 2000US-191637P.		
PR	11-JUL-2000; 2000US-0614150.		
XX			
PA	(PEKE) PE CORP NY.		
XX			
PI	Venter JC, Adams M, Li PWD, Myers EW;		
XX			
DR	WPI: 2001-656860/75.		
XX	P-PSDB; ABB57963.		
PT	New isolated nucleic acid detection reagent for detecting 1000 or more		
PT	genes from Drosophila and for elucidating cell signalling and cell-cell		
XX	interactions -		
PS	Claim 1; SEQ ID NO 680; 21pp + Sequence Listing; English.		
XX			
CC	The invention relates to an isolated nucleic acid detection reagent		
CC	capable of detecting 1000 or more genes from Drosophila. The invention is		
CC	useful in developmental biology and in elucidating cell signalling and		
CC	cell-cell interactions in higher eukaryotes for the development of		
CC	insecticides, therapeutics and pharmaceutical drugs. The invention		
CC	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA		
CC	(ABB57737-ABB72072).		
CC	The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences.		

XX Sequence 6175 BP: 1732 A; 1242 C; 1350 G; 1851 T; 0 other:
 Query Match 21.6%; Score 370.6; DB 23; Length 6175;
 Best Local Similarity 54.5%; Pred. No. 8,76-92;
 Matches 1052; Conservative 0; Mismatches 614; Indels 263; Gaps 5;

46 AATGATGAAATTAAGTTTAACTATGCTTAACTACCAATGAAGCGGTGAGCT 105
 3054 AGACCATGAGCATTAAGTCCACAGCATGCGACCAATGAACAGTGTGCTAC 3113
 106 GAACTGATATGCAAGTGAAGCGCTTAAACGTTAAGCTGATGATTCCTAC 165
 3114 GACACGAGTACGCGCAAGTGAAGGATGACAGCGTCTATCTCTACAGATGTCCTAC 3173
 166 TACAGTTTGAAGGTTAAGCTACGCGCAACCGCAGTGGGTGAGCTGATTTAAACA 225
 3174 TTGAGCTTCGAGGTTATCCGTACGCGCCAGCTCCGCTGGGGAGTGGGTTTAAAGCC 3233
 226 CCCCAGCAGCAACACCTGGGATGCTGCTGATGTTGCAATCATTAAGATGCA 285
 3234 CCTGAGAGCCCATCCCTGGGACGAGTTCGACTGACAGCGCAAGGATTAAGGCC 3293
 286 GTGCAAGTTGATTTATTAACGCGCAAGTGTGGCTCAGAGGATGCTATACCTAAGT 345
 3294 GTCCAGGTGACGCTGCTTTCGATTAAGGTAGAGGGCTCCAGAGACTCCCTATCTCAAT 3353
 346 GTCTATAGCAATTAAT-----CTAATCCGCAACTAAGC 3413
 3354 GTGTACCAACCAATGATGATTAATCTATTAACCTGTTGATTAACCTGTTAAAC 3413
 361 -----CTAATCCGCAACTAAGC 380
 3414 GTAATACCTTAAACATTTTATTTGTTGATACATTTAGGTGAAGCCGCAAGCTCG 3473
 381 TCCCGTTTATGATACATGATGCTGCTTATTAACGTTGAATCACTGATAT 440
 3474 CCGGTTATGTTGATTCACGAGAGGCTTCATTAATCGCGCAAGGCAATCGGATG 3533
 441 GTATGCTGCTGATTTATTTCTTAAAGAGTGTGTTGATTAACATACATTAATCTTT 500
 3534 GTATGCGCCGATTAATTTATTAAGAGATGTTGTTCTGCTACAGATACAGTACGACT 3593
 501 GGGAGCTCT----- 509
 3594 TGGGCTTTGGGTAATCTACTGTGCGATGCGCAATATTTGACTAATATTAATGA 3653
 510 -----AGTTTCTAAGTTTAAATTCAGAGACCTTAATGTCGCGGTATGCGCGGC 562
 3654 CCTACACAGATTTATGATCTTAAGTCCCGAGCTAAATGATCAAGAGAAATGCTGGCC 3713
 563 TTAAGATCAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 622
 3714 TCAAGGATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3773
 623 ATCCGATTAATTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 682
 3774 ATCCCACTGATCACTGTTTGGAGAGAGTGTGAGGCGCTGCTGCTGCTGCTGCTGCTG 3833
 683 TGTTAACGCAAACTGCGGCTCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 742
 3834 TGTCAACGATCAAGCCCAAGGCTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3893
 743 TTTGCTCATGAGGCT-----TAATACCAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTG 799
 3894 TTTGCTCATGAGGCTCAACAGCGGCAATTAATCCATTAATCCATCAAGGATTAAGCTG 3953
 800 CCGGCTTAAGGCTGAGGATTAATGATTAAGGATTTTGGATTTTGAATTTGAAGCCAAAG 859
 3954 TTGCTCAAGAGGCGAGCAACGACAGATGCTGAGGATTTCTGCAAGACGTTAAAG 4013
 860 CACAGGATTAATTAACCTGAGGAAAGTTTAACTGAGAGAGCTTAACAAATTAAG 919

4014 CCAAGATCTTATTCGCGTGAAGAAATGCTCTGACACTGAGGAGCAATGAACAGA 4073
 920 TCAGTTTCCCTTTTGTGCTCCACTGTTGAGCCATATCAGACCGCTGATGCTTACCA 979
 4074 TATGTTTGCCTTTGGCCCATCCCTGGAACATTTCTCCACGCGCCGAATGTTGATATCA 4133
 980 AACATCCCTGGGAATGTTTAAACTGCTTGGGTAATTTGATACCATATGATAGGGTA 1039
 4134 ACCCTCAAAAGAGATGATGTAAGACCGCTGAGTACTCATCCCATGTTTATAGGA 4193
 1040 ACACCTTATGAGGCTCT-----ATTTTCACTCAATTTTACGAATGCTGCTGCTG 1058
 4194 ACACCTTATGAGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1097
 1059 -----ATTTTCACTCAATTTTACGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4313
 4254 TTTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4253
 1098 TAAGAAATGGAATCTTGTGCTCAATTTTGTGCAAGTATGCTGATGCTGCAAGCCAC 1157
 4314 GCAGAGCTTGAATGCTGCGACACCTTTCATTTCCCAAGAAATTTGCTGGCCAGGAGCCAG 4373
 1158 CCGCCAGAGACCTTGAAGTGGTCTAAATTAATAAGCTCATGTTACAGGAGAAAC 1217
 4374 TAAAGAAACTGATTCGTTGAGTGCACAGATTCGAGATGTTCAATGCTGCTGCTGCTG 1242
 1218 ACCAAGCTGATTAATTTATGAT----- 1242
 4434 AAGCAGCCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4493
 1243 -----CTTTGCTCAGATTAATTTATGAT----- 1282
 4494 AAGCTGATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1342
 1283 TGTTCGAATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4613
 4554 TGTTCATTTCCCGACACCGCTGAGCGCTGAGCTGAGTCCGATTAATTTATTAATTAATTA 1402
 1343 TTTGATGGAAGATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4673
 4614 TCGACTCCGAGAGCTCAATTTTCCGTTACCGCATTAATTAATTAATTAATTAATTAATTA 1462
 1403 GTTATGATCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4733
 4674 GGTTCAGCCATCCGACGATTTGACCTACCAATTAATTAATTAATTAATTAATTAATTA 1522
 1463 CTAAAGATCGGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4793
 4734 CGAAGGAATGCGGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1582
 1523 CCACCTGATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4853
 4794 CTGCGACGGGTAATTTCCCTACAGGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTA 4913
 1583 CAATTAAGATCGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1642
 4854 CAGTTCCGAATTCGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4913
 1643 TTTGATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1702
 4914 TCGATCTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4973
 1703 ATTTATTTT 1711
 4974 ATTTATTTG 4982

RESULT 12
 ID ABL02099
 standard: cdna: 1665 BP.
 ABL02099;
 AC
 XX

Db	144	TTGGCCACAAAGGTGCAACAGTACCGGCTCTCCAGGGTCCACACAGTATTTTGGACACCA	203
QY	113	AATATGCAAAAGTGAAGGCGTTAAACGTTAACTGTGTACG---ATGATTTCTACTACA	169
Db	204	AGTACGGACAGGTGCGCGGACTCCAAAGGAAACAGGTCTCTACAGACAGAGGCCGCTTTTG	263
QY	170	GTTTGAAGGATTAACCGTACGCCCCAACCCGACAGTGGGTGAGTGAATTTAAACACCCC	229
Db	264	CTTTGAGGGGATTCCTGTACGCCAACCCCCGGTGGGTACCTCCGATTTACAGGGCTCTC	323
QY	230	AGCGACCAACCCCTGGGATGTGTGCGTGAATTTGTCAATCATTAAGTACGTGC	289
Db	324	AGCCACCGGAACCCCTGGCAGAGAGTGTCTCAACTGCACACTACCAATGATCCAAAGCCATGC	383
QY	290	AAGTTGATTTTATAACGGGCAAGGTGTGTGGCTCAAGAGATTTGTATACCTAAATGTCT	349
Db	384	ACAGGAAACATGCTCTGTGGATTTCTGAGGGCAGTGAAGATTTGTTTGCAATTTGAACGCTT	443
QY	350	ATPACGATTAATTAATCCGAACCTAAAGCTGCCGTTTATGATATACATACATGTGTGTG	409
Db	444	ATGTCAAAAGCTTTGAAGTCGAAAACCCGCTGCCGTAATTTGTGTGATTTACGAGGTG	503
QY	410	GTTTATTAATTCGGTGAATAATCATGTGTATGTGTCTCGTATTTATTCATTAATAAG	469
Db	504	GTTTCCAAAGAGGTGAGGCTCCAGAGGATTAATTTACGTCCGATTAATTCATTAATAAG	563
QY	470	ATGTGTGTGATTAATCAATCAATTCGTTTGGGAGCTTAAGTTTCTAAGTTTAAT	529
Db	564	CAGTGTATTCGTCGCTATCACTACAGTGTGCGACGCTAGAGTTTCTCAGTCTAAAG	623
QY	530	CAGAAAGCTTAATGTGTGCGCGTAAATGCGGCTTTAAAGATCAAGTCAATGCGCTGTG	589
Db	624	ACCCGAAGCTGTGATTTCTCGGCAATGCGGAGCTTAAGACCAAGTATGTCTGTG	683
QY	590	GGATTAATAAATTAATGCGCCCACTTGTGGGGAATCCCGATTAATTAACGTCTTTGTG	649
Db	684	GGATTAAGCAGAAACATGCGCCACTTAATGTGCGAAGCCCAACATTCACATTTGATGGAG	743
QY	650	AAAGTCCGCGTGTGCTGCTTACCACACTCATGTATTAAACGCAACAAATCGCGCTCTT	709
Db	744	AAAGTCCGCGTGTGCTGCTTACCACACTCATGTATTAAACGCAACAAATCGCGCTCTT	803
QY	710	TCCATGTGTGATTAATGTGCGGCTTAATGCTTTTGTCCATGGGCTAATACCAATGTC	769
Db	804	TCCATTAAGGCTATCAATGCAATGGGATGTGCTCCAGCCGAATGGGTGAGACTCCGGATA	863
QY	770	AACATGCTGCTTACCTTACCTTAAGCAATTTGGCCGCTTAATTAAGGATGATGATTAAG	829
Db	864	ACATATGGCATTTGCGCTGCGCCAGAAATCTGGCTTCAAGGGCGACGAAAGATGCGG	923
QY	830	ATGTTTGAATTTCTTAATGAAGCCAGCCACAGATTTAATTAACCTTGAAGAAAAAG	889
Db	924	ATGCTTAAGCTTTCTTAAGTTTGGCGACGCCAGATAGGGGCTATTTGATCAAGAGG	983
QY	890	TTTTTAAGTGAAGAGCGTAAATTAAGTCAATTTGCTTTTGGTCCACATGTTGAGC	949
Db	984	TTATCAATTTGGACGAGGTGTCACAACTTCTCAATTTGCAATTTGGTCTGTGATGAAC	1043
QY	950	CATATCAGACCGCTGATTTGTGCTTAACCAACATCTCTCGGAAATGTTAAATCTGTT	1009
Db	1044	CTTACGAAACCGACACTGTGTGTGTCGCCAAAGGCAACAGAGATCTGTGTCCGAACGT	1103
QY	1010	GGGGAATTCGATACCCACTATGATGGGTAAACATTTATGAGAGGTGTATTTTCACTT	1069
Db	1104	GGGGAACGACATTTCCGCTTATTTGTGCGTGAATTTCTTTCCAGGGCTTTGTTTCTAC	1163
QY	1070	CAATTTTAAGCAATATGCTATGCTTTTGAAGATTTGAATTTGAACCTGTGTCAATTTGTG	1129
Db	1164	AACATGAAGAAAGATCTTGTGGCTTTGAATACTTTACAAACATCTGCGCAAGGGAGG	1223
QY	1130	CAAGTGAATTTGGCTGATGCTGAACGCAAGCCGCCAGAGACCTTGAATTTGGTGTATAA	1189
Db	1224	TTAGGAAGACGACGTGTGGAAGGAGAGATCTACTGTGTGCGCGCATTAAGC---AAC	1280

OY	1190	TTTAAAGGCTCATGTTATACAGGAAACCAACAGCTGATATATTTTATGATCTTGCT	1249
Db	1281	TTCTACTTCAACCAACAGAGATCGAGGAATTCATGAGATGTTTCGAGGCCCTGATATATTTT	1340
OY	1250	CTCACATCTATTTCTGGTTTCCCATCATGTTTGTTCGAATTAAGCTTTCATCACACT	1309
Db	1341	CGCATGCCAGATTTTGGCAGATAGCAATCGGCTTATTTCTGCCCGTCGAATCTATGCC	1400
OY	1310	CCGGTACACCCGCTCTACTGTATATCCGTGTGACTTTTGAGAGATCTTATATCCCT	1369
Db	1401	CCAAAGGCCCACTATCATCTATTCGTTTTGACTGTGCACG-----CCCGACATTCATCAT	1457
OY	1370	ATCGTATATTATCGTAGTGCAGCGGTGTAAAGGTTGTATGTCATGATTAATACCT	1429
Db	1458	TTGCCGCACGTGTGTGGGGGATCGGATTTCCGGGATACCCATCGGATGACATCATAT	1517
OY	1430	ATTTCTTCTGGAATCAATTGGCCAAAGCTATGCTTAAGAGATCGCGTATACAAACA	1489
Db	1518	ACCTGTTCTACAAACATCATATGCCCTCCAAACCTGGATTAAGCATCGATGAAATACAAACA	1577
OY	1490	TTGACGCTATGACGTGATATATGATACAAATTTGGCCACGCTGTATGCTTATAGCAATG	1549
Db	1578	TTTGAGAAATATGTGGCATATGACGTGCTTTGCCCTCCAGTGGGAATCCAAATTTGCCAG	1637
OY	1550	AAATTTGAAGGTATGAAAAATGTTTCTCGGGATCCAAATTAAGAAATCCAGACGAATATACA	1609
Db	1638	AACGTGGATCTGCCAAATATGGGAAGCCGTCAGCTTAAAGAAATATGCC-----GTGGAGA	1691
OY	1610	AGCTTTGGATATTTAGTACGAATTTGAAATATGATATGTGCTTCAATATGAT	1662
Db	1692	AGTCTTCAACATTATGGCACGATCTTTGAGATGGGAATTTTGGCGGAGTCCGAT	1744

RESULT 14	
ABL01859	
ID	ABL01859 standard; cDNA; 1863 BP.
XX	
AC	ABL01859;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 59.
XX	
KW	Drosophila; developmental biology; cell signalling; insecticide;
KW	pharmaceutical; gene; ss.
XX	
OS	Drosophila melanogaster.
XX	
FN	WO200171042-A2.
XX	
PD	27-SEP-2001.
XX	
PE	23-MAR-2001; 2001WO-US09231.
XX	
FR	23-MAR-2000; 2000US-191637P.
PR	11-JUL-2000; 2000US-0614150.
XX	
PA	(PEKE) PE CORP NY.
XX	
PI	Venter JC, Adams M, Li PWD, Myers EW;
XX	
DR	WPI; 2001-656860/75.
DR	P-PSDB; ABB57756.
XX	
PT	New isolated nucleic acid detection reagent for detecting 1000 or more
PT	genes from Drosophila and for elucidating cell signalling and cell-cell
PT	interactions -
XX	
PS	Claim 1; SEQ ID NO 59; 21pp + Sequence listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent
CC	capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABJ161716-ABJ30511), expressed DNA
CC sequences (ABJ01840-ABJ16175) and the encoded proteins
CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/publ/published_pat_sequences](http://wipo.int/pub/publ/published_pat_sequences).

XX
CC
XX Sequence 1863 BP; 425 A; 493 C; 523 G; 422 T; 0 other;
SQ

Query Match	18.9%	Score 323;	DB 23;	Length 1863;
Best Local Similarity	51.5%;	Pred. No. 7.5e-79;		
Matches 796;	Conservative	0;	Mismatches 745;	Indels 6;
				Gaps 2;

QY	1	ANGAATTTCAACGTTAGTTTGATGAGAAATTAATAATGSAACATTAATAATGCATTTGAAAT	60.
Db	166	ATGGAGATCCAGTGGAGTGGGCAATTCCTGCTAAATAATGGCCACCAAGCTATGGCCAC	225
QY	61	AAGTTTTAAACTATGTTTTAACTACCAATGAAAGCGTGTAGCTGAAACTAATAATGAC	120
Db	226	AAGATCGTCACATATCGCTTGGCCAAAGCAGACGAAGTGTGCTGCACAGGGATGGC	285
QY	121	AAAGTAAAGCGGTTAAACGTTAACTGTGT---ACGATGATTTCTACTACAGTTTGG	177
Db	286	CAGGTGCGGGACATCGCCGAGAGACACTTACGACGAGAGAAATGATCTTCCTTCGAG	345
QY	178	GCTATACGGCTACGCCCAACCGCCACTGGGTGAGTGTAGATTTTAAAGCACCCGAGGACA	237
Db	346	GGAATTCCTTTGCAAGCGCCGGTGGGGAGCTGTGCTTCGAGCCCCCGACGACCA	405
QY	238	ACACCCCTGGAGTGTGTGCTGATTTGTTGCAATCAATAAGATAAGTCAAGTTGAT	297
Db	406	CATCCCTGTTGGGGGTGGGGATTCACACTTATCCGCGGCCACCGATGCAAAAAGCAC	465
QY	298	TTTATACGGCGCAAAAGTGTGTGCTCAGAGATGTGCTTACCTAAGTATCTATACGAAT	357
Db	466	TTTCGTGCTCAGCATGTGTCGAAGGACGCGAGATTTGCTCTACCTGACGTAATTTCCAA	525
QY	358	AATCTAATCCCGAAATAAACGTCCTGTTTTAGTATACATACANGTGTGTTTTAT	417
Db	526	CGCTGAGATCGGAGCAAGCGCGCTGCCGCTGATGTGTGATCTATGCGCGGTGATTCAG	585
QY	418	ATCGGTGAAATATCATGCGATATGATGTGCTGATTTATTTATTTAAAGATGGG	477
Db	586	TTTCGCGAGCGCTGTGTGAGATTTTCTACACTCCAGACTACTTTTATCGCAACAGCTAG	645
QY	478	TTGATTTAATCATATATGCTTTGGAGCTCTAGAGTTTCTAAGTTTAATTCAGAAAC	537
Db	646	GTTCACATTCATTAATATAGGSGTGGGCGATTTGGGCTTCTCAGCCTCCGGATCGCAC	705
QY	538	CTTAAATGTGCCCGGTATCCGGGCTTAAAGATCAAGTCATGGCCTTGCCTTGATTA	597
Db	706	TTGGATGTGTCCCGGAAATGTGCTGTCAAGGACCAAGATGATGGCCTTCGCTGATCACT	765
QY	598	AATTAATGGGCAACTTTGGTGGCAATCCCGAATTAATTAACGCTTTGGTAAAGTGC	657
Db	766	CAGAACATATGCCCAATTCATATGAGATCCCAAAATTAATACGCTGATGGCGAGATGG	825
QY	658	GGTGTGCTTACCCACTACATGATGTTTAACCGAACAACACTCGCGGCTTTTTCATCTCT	717
Db	826	GGAGCAGCTCGCTTACAGCGCTTTGATGACACCGAGCAACCCGAGGGCTGTTCCACAG	885
QY	718	GGTATACATATGTGGGATATGCTATTTGTCCATGGGCTAATACCAATGTCAACATGCT	777
Db	886	GCCATCATGCAATCGGATCCATGTTTCTCGAGTGGGCCCAATGAGCCCAAGTGGCAGGTG	945
QY	778	GCCTTCACCTTATGCCAAATTTGGCGGCTTAAAGTGAGGATGAATGATTAAGATGTTTTG	837
Db	946	GCATGCCAGCTGGCTGCCAATTTGGGATATCTGGGCGACGTGAACAGAGAGAAGATGTTT	1005
QY	838	GAAATTTCTTATGAAGCCAGCCACAGATTTTAAATAAATCTTGAGGAAAAATTTTAAC	897

Oy	771	ACATCGGCGCTAACCTTACCACAAATTTGGCGCGCTATTAAGGCTGGATTAATGATTAAGA	830
Oy	772	TTATTTGGCTTATBGGCTGGCCCCAAAATTTGGATBACCGGTGACATTAAGACAAAGCC	725
Oy	831	TGTTTTGGAAATTTCTTATGAAAGCCCAAGCCACAGATTTTAAATTAACCTTAGAGAAAAGT	890
Db	726	GATCTTTGAGTTCTGGGATCATTGAGTGGCGGGAGATTTGCAMGGCCACCACCAAGT	785
Oy	891	TTTAACTCTAGAGAGCGCTACAAATBAGTCATGTTTCTTTGGTCCCACTGTTGAGCC	950
Db	786	TCTCAGACAGATGAAAAGCATCATCGATTCCTTTTCCGCTTCGGACCTGTGTGAGAAC	845
Oy	951	ATATCAGACCGGTGATGTGCTCTTACCACAAACCTCTCGGGAAATAGTTAAACCTGCTG	1010
Db	846	ATATACTACCGAGACACACTGTGTGCTTAAACCAACCGCATGATGACAGAAATAGCTG	905
Oy	1011	GGGTAAATTCGATACCCCACTATGATGGGTAAACATTCATATGAGGGTCAATTTTCATTC	1070
Db	906	GAGTCACAGATTAACCATGATGTTTGGAGGACAGACTTCAGAGGATTTGATTTCTATCC	965
Oy	1071	AATTTTAAAGCAATGCCATATGCTTGTAAAGAAATGGAACCTTGTCMAATTTTGTGCC	1130
Db	966	AGAGGTTTCAAGGGCGCCACACACCTCGATGAGGTGGTAACTCAAGAAATCTGCTACC	1025
Oy	1131	AAGTGATTTGGCTGATCTCTAAGCACACCGCCACAGACCTTGGAAATGGTGTCTAAAT	1190
Db	1026	GAGGATCTGGT---CTTAACTCTGATGCCCAAACTGGGTAGAGACATGAGCTTGCAAC	1081
Oy	1191	TAAAGAGCTCATCTTACAGAGAAACACCAACAGCTGATAT-----TTTAAAG	1240
Db	1082	TGAAGAGGCTATTTGGGGAGACAACTCTTACAGGCAACATGATGAAGTTTCTCG	1141
Oy	1241	ATCTTGCTCTCACATCTATTTCTGTTGCCCAATGCAATGTTTGAATTAACCTTCA	1300
Db	1142	AGCTATGCTCATATCGAGAGTTCTGGCACCCCTATATACAGGCACTTTGAACCGTGCC	1201
Oy	1301	ATCACACCTCCGATACACCCGCTACTGTATGTCGCTTGCACTTTGATTTGGAAATCTTA	1360
Db	1202	GGCATCTCAGG---CACCCAGCTATCTGATGATGATGATCAGCATTTCCAAA---CTGT	1255
Oy	1361	TTAATCCCTATCGATTTATCGTATGAGACAGTGGTTTAAAGGTTTATGATCGCTGATG	1420
Db	1256	GCAACGCCATTAGATTTGACTTTGGGGCCATCAGATGGGAGGTGTTGTATGTTGACG	1315
Oy	1421	AATTACCTATTTCTCTGGAATCAATTGGCCAAACGTATGCTTAAAGAAATCGCTGAT	1480
Db	1316	ATCTGTGCTATATTTTCCACAGCATGTGTGCGATCAATCCGCTCCGATCTCCGAGAC	1375
Oy	1481	ACAAACAACTTGAACGTATACGTGATATGATATACAAATTTGCCACCACTGTATCTT	1540
Db	1376	ACAAAGTTTATACCGGAATGGTCGAGTTTGGACGATTTCCGACCCACAGAGATCCCA	1435
Oy	1541	ATATCAATGAATTTGAGGTATGAGAAATGTTTCCGGGATGCCATTTAAGAAATCCGACG	1600
Db	1436	ACTCGGAAAGATATAATCACTCAAGTTTGCACCCATGCAAAACGTAAACAA-----	1487
Oy	1601	AAGTATACAAAGTGTGATATTTAGTGACGAATTGAATGATTTGATGTGCTCGAATGG	1660
Db	1488	-----CTTAAAGTGTCAATATTTGGGATACAGTTTAACTCATGCGCTTCCAGAAATTC	1543
Oy	1661	ATAAGATTTAAAC	1672
Db	1544	AGAAATCGAAC	1555

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:24:12 ; Search time 1663.49 Seconds
(without alignments)
16677.553 Million cell updates/sec

Title: US-09-776-910-7

Sequence: 1 atgaattcaacgttagttt.....aacatagagattattttag 1713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estda:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_estl3:*
13: gb_estl4:*
14: gb_estl5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inu:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	313.6	18.3	778	9	AI062034 GH01076.5
2	284	15.6	649	9	AI388926 GH19977.5
3	265.2	15.5	688	9	AI403569 GH23036.5
4	236.6	15.0	671	9	AI517692 GH28740.5
5	234.4	14.9	569	13	BI609541 RH14337.5
6	250.2	14.6	660	13	BI639486 SD22067.5

7	250	14.6	674	13	BI628316	BI628316 RH56682.5
8	249.4	14.6	676	13	BI635372	BI635372 SP16705.5
9	248.4	14.5	673	13	BI614181	BI614181 RH43493.5
10	246.8	14.4	672	13	BI614443	BI614443 RH43812.5
11	246.4	14.4	670	13	BI233202	BI233202 RH29491.5
12	245	14.3	648	9	AI113763	AI113763 GH10213.5
13	245	14.3	648	9	AI403098	AI403098 GH22464.5
14	243.4	14.2	646	9	AI109901	AI109901 GH09292.5
15	243.4	14.2	646	9	AI293416	AI293416 LP06524.5
16	241	14.1	526	9	AI108080	AI108080 GH06811.5
17	239.8	14.0	516	9	AI108156	AI108156 GH06911.5
18	239.2	13.9	658	13	BI564586	BI564586 RH61888.5
19	238.4	13.9	656	13	BI619037	BI619037 RH49995.5
20	236.8	13.8	656	13	BI614821	BI614821 RH44286.5
21	236.6	13.8	659	13	BI588370	BI588370 RH29681.5
22	236.2	13.8	656	13	BI621302	BI621302 RH52624.5
23	233.8	13.6	630	9	AI403830	AI403830 GH23353.5
24	233.2	13.6	628	9	AI109573	AI109573 GH08808.5
25	231.4	13.5	619	9	AI516869	AI516869 GH27454.5
26	231	13.5	638	13	BI564361	BI564361 RH37254.5
27	230.8	13.5	628	9	AI513346	AI513346 GH26524.5
28	230	13.4	614	12	BG641228	BG641228 SD12519.5
29	230	13.4	647	13	BI575862	BI575862 RH32195.5
30	229.6	13.4	614	9	AI107729	AI107729 GH05557.5
31	229.6	13.4	614	9	AI134360	AI134360 GH11805.5
32	229.2	13.4	622	9	AI134524	AI134524 GH12012.5
33	228	13.3	633	13	BI370683	BI370683 RH57386.5
34	222.6	13.0	670	9	AI389766	AI389766 GH21022.5
35	219.8	12.8	614	13	BI617897	BI617897 RH48369.5
36	219.2	12.8	615	13	BI588504	BI588504 RH29849.5
37	218.6	12.8	587	9	AI517539	AI517539 GH28541.5
38	218.6	12.8	588	13	BI638519	BI638519 SP20822.5
39	218.6	12.8	607	13	BI624437	BI624437 RH63994.5
40	218.6	12.8	609	13	BI567389	BI567389 RH37771.5
41	218.6	12.8	609	13	BI607309	BI607309 RH74350.5
42	218.6	12.8	609	13	BI622392	BI622392 RH54254.5
43	218.6	12.8	609	13	BI630054	BI630054 RH59016.5
44	218.6	12.8	611	13	BI572606	BI572606 RH08182.5
45	217.8	12.7	612	13	BI631806	BI631806 RH61455.5

ALIGNMENTS

RESULT 1
AI062034 778 bp mRNA linear EST 19-APR-2001
LOCUS
DEFINITION
GH01076.5prime GH Drosophila melanogaster head pot2 Drosophila melanogaster cDNA clone GH01076 5prime similar to U51050:
Drosophila melanogaster alpha esterase (aet) gene, partial cds,
mRNA sequence.

ACCESSION
AI062034
VERSION
AI062034.1 GI:3337873
KEYWORDS
EST.
SOURCE
fruit fly.
ORGANISM
Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 778)

REFERENCE
Harvey,D., Broksstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.

BDGP/RHMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP

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Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Plate: 10 row: G column: 4
High quality sequence stop: 363.
Location/Qualifiers

FEATURES

QY	908	GTACAAATTAAGTCATGTTCCCTTTGGTCCACATGTTGAGCATATACAGACCCGCTGAT	967
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[illegible]

Matches 376: Conservative 0; Mismatches 199; Indels 0; Gaps 0;

1 ATGAATTCACGTTAGTTCATGAGAAATTAATGAAGATTAAATGCAATGAAAT 60
 95 ATGAATTAAGAACCTCGCTTGTGTGAGCGCTCGCGCTCAAAACCATCGAGCAT 154
 61 AAGTTTAACTATCGTTTAACTACCAATGAAGGTGTGAGTCAATGAATGCG 120
 155 AAGTCCACAGTATCGCCAGTGCACCAATGAACAGTTGCGCCGACGAGTACG 214
 121 AAGTAAAGGGGCTTAAGCTTAACTGTACATGATTCCTACAGTTTGAAGGT 180
 215 CAAGTAAAGGGGCTTAACTGTATCTCTACATGATTCCTACAGTTTGAAGGT 274
 181 ATACCGTACCCACACCCAGTGTGAGTGAATTTAAAGCCACCCACGACACA 240
 275 ATCCCGTACCCACACCCAGTGTGAGTGAATTTAAAGCCACCCACGACATT 334
 241 CCCGAGTGTGAGTGTGATTCATTAATGAATGAATGATGATGATTTT 300
 335 CCGTGAAGGAGTGTGAGTGTGATTCATTAATGAATGAATGATGATTTT 394
 301 ATACGGGCAAGTGTGAGTGTGATTCATTAATGAATGAATGATGATTTT 360
 395 GTCTTGAATGAAGGAGTGTGATTCATTAATGAATGAATGATGATTTT 420
 361 GTAAATCCGCAAGTGTGAGTGTGATTCATTAATGAATGAATGATGATTTT 454
 455 GTGAAGCCGCAAGTGTGAGTGTGATTCATTAATGAATGAATGATGATTTT 514
 421 GGTGAATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 515 GCGAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 574
 481 ATTAACATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 540
 575 GTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 634
 541 AATGTGCGGCTTAAGTGTGATGATGATGATGATGATGATGATGATGATG 575
 635 AATGTGCGGCTTAAGTGTGATGATGATGATGATGATGATGATGATGATG 669

RESULT 5
 B1609541 569 bp mRNA linear EST 07-SEP-2001
 LOCUS RH14337, Sprime RH Drosophila melanogaster normalized Head p1c-1
 DEFINITION Drosophila melanogaster cDNA clone RH14337 5 similar to alpha-Est7:
 (GO:0004091) located on: 3R 84D5-84D5; 08/17/2001, mRNA sequence.
 (GO:0004091) located on: 3R 84D5-84D5; 08/17/2001, mRNA sequence.

ACCESSION B1609541
 VERSION B1609541
 SOURCE EST
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 569)
 J. Stemple, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
 Stemple, M., Chavez, C., Dorsett, V., Farfan, D., Fiske, E., George
 R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, S., Mista, S.,
 Munall, C. J., Nuno, J., Paclet, J., Paragas, V., Park, S.,
 Phanavong, S., Wan, K., Yu, C., Lewis, S. E., Celisner, S., and Rubin
 G. M.
 BDGP/HMI RH Drosophila EST Project
 Unpublished (2001)
 Contact: Stemple, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu

Plate: RH.143 row: D column: 1
 High quality sequence stop: 447.
 Location/Qualifiers
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 /db_xref="taxon:7227"
 /clone_lib="RH14337"
 /clone_lib="RH Drosophila melanogaster normalized Head
 p1c-1"
 /sex="male and female"
 /dev_stage="Adult"
 /lab_host="DH5-alpha Tona"
 /note="Organ: head; Vector: p1c1; Site: 1; XhoI: Site: 2;
 BamHI: Library was kindly generated by Piero Garinai at
 the RIKEN. The library was normalized and excised using
 Cre recombinase. Plasmid cDNA library."

BASE COUNT 126 a 147 c 167 g 129 t
 ORIGIN

Query Match 14.9%; Score 254.4; DB 13; Length 569;
 Best Local Similarity 65.5%; Pred. No. 1.9e-58; Indels 0; Gaps 0;
 Matches 372: Conservative 0; Mismatches 196;

17 GTTGTGAGAGAAATTAATGAAGATTAAATGCAATGAAATGCAATGAAAT 60
 1 GCTTTGTGAGAGCGCTTGTGTGAGCGCTCGCGCTCAAAACCATCGAGCAT 76
 77 GTTGTGAGAGAAATTAATGAAGATTAAATGCAATGAAATGCAATGAAAT 136
 61 GCCAGTGCACATGAACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 120
 137 AAGCTTAACTGTGATGATGATGATGATGATGATGATGATGATGATGATG 196
 121 AGCTTATCTCTCTACAGTGTGATGATGATGATGATGATGATGATGATG 180
 197 CGCAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 240
 181 CTCGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 316
 257 GTGATGTTGCAATCAATGAATGAATGAATGAATGAATGAATGAATGAAT 300
 241 GCGAGTGCACAGCGCAAGAGTGAAGCGCTTCAAGTGTGATGATGATGATG 376
 317 GTGAGTGCACAGCGCTTCAATGAATGAATGAATGAATGAATGAATGAAT 360
 301 AGGAGTGCACAGCGCTTCAATGAATGAATGAATGAATGAATGAATGAAT 436
 377 AAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 361 CTCGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 496
 437 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 421 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
 497 GTTGTGAGAGCTTGAAGTTTCAATGAATGAATGAATGAATGAATGAATG 556
 481 GACTTGTGAGCGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 540
 557 CCGGCTTAAAGATCAATGATGATGATGATGATGATGATGATGATGATGATG 584
 541 CTGGCTTAAAGATCAATGATGATGATGATGATGATGATGATGATGATGATG 568

RESULT 6
 B1639486 660 bp mRNA linear EST 10-SEP-2001
 LOCUS SD22067, Sprime SD Drosophila melanogaster Schneider L2 cell culture
 DEFINITION SD22067 Sprime SD Drosophila melanogaster cDNA clone SD22067 5 similar to
 alpha-Est7: Fban0001112 GO: [carboxylesterase (GO:0004091):
 carboxylesterase (GO:0004091) located on: 3R 84D5-84D5; 05/19/2001
 , mRNA sequence.

ACCESSION B1639486

VERSION	BIT639486.1	GI:15541696
KEYWORDS	EST.	
SOURCE	Fruit fly.	
ORGANISM	Drosophila melanogaster	
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridioidea; Drosophilidae; Drosophila.	
AUTHORS	1 (bases 1 to 660)	
TITLE	Lawley, D., Brokstein, P., Hong, L., Evans-Hoim, M., Su, C., Tsang, G., Lewis, S., and Rubin, G.M.	
JOURNAL	BDGP/HMI Drosophila EST Project	
COMMENT	Unpublished (2001)	
	Contact: Stapleton, M.	
	BDGP	
	Lawrence Berkeley National Lab	
	One Cyclotron Rd., Berkeley, CA 94720, USA	
	Fax: 510 486 6798	
	Email: http://www.fruitfly.org/EST , estfruitfly.berkeley.edu	
	Plate: SD 220 row: F column: 7	
	High quality sequence stop: 346.	
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	/clone="SD22067"	
	/clone_lib="SD Drosophila melanogaster Schneider L2 cell culture port2"	
	/lab_host="DH5-alpha"	
	/note="Vector: port2; Site1: EcoRI; Site2: XhoI; Sized fractionated cDNAs were directly ligated into port2. Plasmid cDNA library."	
BASE COUNT	169 a 170 c 176 g 145 t	
ORIGIN		
Query Match	14.6%; Score 250.2; DB 13; Length 660;	
Best Local Similarity	64.4%; Pred. No. 2.8e-57;	
Matches	391: Conservative 0; Mismatches 213; Indels 3; Gaps 1.	
535	GACCTTAATGTGCGCGGTAATCGCGGCTTAAAGATCAAGTCATGCGCTTGGTGATT	594
Db		
9	GAGCTAAATGTATCCAGGAATATGCTGGCTTCAGAGATAGTGCTGGCCCTCAAGTGGATC	68
555	AAAAATTAATGCGCCAACTTTGGTGGCAATCCCGATTAATATTACAGTCTTGGTGAAGT	654
Db		
69	AAGAACAATTTGCGGTAGTTTCCGGCGAGATCCCAACTGCATCATCTTTTGGAGAGAGT	128
655	GCGGCTGCGCCTCAACCACTACATACATGATGTTAACCAGAACATCGCGGCTTTTCCAT	714
Db		
129	GCTGAGGCGCTCCACTCACTACATGATGATTAACCGATCAACCCAGGCTCTTTCT	188
715	CGTGTATTAATCTCGGTAATCTGATTTTTCATGAGGC--TAAATACCAATGTCAA	771
Db		
189	CGCGGATCTTTCAGATCGGGGAGTGCCATTTTCTTGGGCTTACACGCGGCACTTACC	248
772	CATGTCGCTTCACTTAAACCAATTTGGCGGCTATAAGGTGAGATTAATGATAAGAT	831
Db		
249	CATTAATCCCTACAGATAGCCCAAGCTGGTGGCTCAAGGCGAGACAAACGAAGAT	308
832	GTTTGGAAATTTCTATGAGAACCAAGCACAGAGATTAAATAACTTGAGGAAAAAGTT	891
Db		
309	GTCGTGAGTCTTTCAGAGACGTAAAGGCGCAAGGATCTTATTCGCGTGAAGAAATGTG	368
892	TTAATCTTAAGAGACGTACAATAAGGTCATGTTTCTTGGTCCACTTTGAGCCA	951
Db		
369	CTGACACTGAGAGAACGATGAACAAGATTAATGTTTGGCTTTGGCCCACTCGAGACA	428
952	TATCAGACCGCTGATTTGTCTTACCCAAACACTCTCGGGAATGTTAAACTGCTTGG	1011
Db		
429	TTCCTACAGCCCGAATGTGTGATATTCCAAGCTCCCAAGAGATGATGAAGACCGCTGG	488
1012	GCTAATTCGATACCACTATGATGGTAACTTCAATGAGAGGCTATTTTTCACCTTA	1071
Db		
489	ATAATCTCATCCCATGTTTATAGAAACCTTGTAAGAGGCGCTGCTGGGTCCA	548

[illegible]

Db 231 CAAGTGGAGGGATGATCAGCGTCTATCTCTACAGATGTGCCTACTCAGTTGAGGGT 290
 QY 181 ATACCGTACGCCCAACCCGCTAGTGTGAGTATTAAGCACCCAGGACCAACA 240
 Db 291 ATCCGTCAGCGCCACCTCCGGTGGGGAGTTCGGTTTAAGCCCTCAGAGGCCATT 350
 QY 241 CCCCTGGGATGTGCTCGTATGTTGCAATCATTAAGATAGTCAAGTGCATGTTATTT 300
 Db 351 CCCCTGGAGGAGTTCGGGACTGCAAGCCAGGAGATTAAGCCGCTCAGTGCAGTTTC 410
 QY 301 ATACCGGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTGTCTATACGAATAT 360
 Db 411 GCTCTCGATAGAGTGTAGAGGCTCCGAGACTGCTCTATCTAATCAAGTGTACCAACAT 470
 QY 361 CTAATATCCGGAATCAACGTCCTGTTTATGATATCATGATGATGTTGTTTATATTC 420
 Db 471 GTGAGAGCCGCAAGAGCTGCGCCGGTTATGTTGATTCACGAGAGAGGCTTCATATTC 530
 QY 421 GGTGAATATCATGATATGATGTGCTGATTTATTTTCAATTAAGAGATGTGTGTTG 480
 Db 531 GCGGAGGCCAATCGGGAAATGATGCGCCGATTAATCTATGAAAGAGATGTGTCTTC 590
 QY 481 ATTAACATCAATATGCTTTGGAGCTCTAGTCTTCTAAGTTTAATTCAGAAACCTT 540
 Db 591 GTCAGGATACAGTACCTGCTGGGCTGTGGATTATGAGCTTAAGTCCCGCCAGCTA 650
 QY 541 AATGTGCGCGGTAAATGCGCGCT 563
 Db 651 AATGTACCAAGAAATGCTGCT 673

RESULT 8
 BI635372
 LOCUS SD16705.5prine SD Drosophila melanogaster Schneider L2 cell culture
 DEFINITION
 BI635372 676 bp mRNA linear EST 10-SEP-2001
 SD16705.5prine SD Drosophila melanogaster Schneider L2 cell culture
 port2 Drosophila melanogaster cDNA clone SD16705 5 similar to
 alpha-EST: Fban0001112 GO: [carboxylesterase (GO:0004091)],
 carboxylesterase (GO:0004091) located on: 3R 84D5-84D5; 05/18/2001
 , mRNA sequence.

ACCESSION BI635372
 VERSION BI635372.1 GI:15537582
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 676)
 AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S., and Rubin, G.M.
 TITLE BDGP/HMI Drosophila EST Project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDCP

Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
 Plate: SD 167 row: A column: 5
 High quality sequence stop: 641.

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 /clone_11b="SD Drosophila melanogaster Schneider L2 cell
 culture port2"
 /lab_host="DH5-alpha"
 /note="Vector: port2; Site 1: EcoRI; Site 2: XhoI; Sized
 fractionated cDNAs were directly ligated into port2.
 Plasmid cDNA library."

BASE COUNT 155 a 173 c 194 g 154 t
 ORIGIN

Query Match 14.6%; Score 249.4; DB 13; Length 676;
 Best Local Similarity 65.2%; Pred. No. 4.7e-57;
 Matches 367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 1 ATGAATTCACAGTTAGTTGATGAGAAATTAATGAAGATTAATGCATTGAAT 60
 Db 114 ATGAATTAAGAACCTCGGCTTTGTGTGGAGCGTTCGCGTCCGCTCAAAACATCGAGCAT 173
 QY 61 AGCTTTTAACATATCTGTTTAACTACCAATGAAGAGGTGTGTAAGTGAATATATGATGC 120
 Db 174 AAGATCCAGCATATGCGCAGTCGACCAATGAAGATGTTGCGGACAGAGATGACGC 233
 QY 121 AAGATGAAGGCGTTAAAGCTTTAACTGTGATGATGATTCCTACTACAGTTTGAAGGT 180
 Db 234 CAAGTGGAGGGATCAAGGCTCTATCTCTACAGATGTGCTACTTACAGTTGAGGGT 293
 QY 181 ATACCGTACGCCCAACCCGCTAGTGTGAGCTGAGATTTTAAGCACCCAGGACCAACA 240
 Db 294 ATCCGTCAGCGCCACCTCCGGTGGGGAGTTCGGTTTAAGCCCTCAGAGGCCATT 353
 QY 241 CCCCTGGGATGTGCTCGTATGTTGCAATCATTAAGATAGTCAAGTGCATGTTATTT 300
 Db 354 CCTGGAGGAGGATTCGCGACTGCAAGCCAGGAGATTAAGCCGCTCAGTGCAGTTTC 413
 QY 301 ATACCGGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTGTCTATACGAATAT 360
 Db 414 GCTCTCGATAGAGTGTAGAGGCTCCGAGACTGCTCTATCTAATCAAGTGTACCAACAT 473
 QY 361 CTAATATCCGGAATCAACGTCCTGTTTATGATATCATGATGATGTTGTTTATATTC 420
 Db 474 GTGAGAGCCGCAAGAGCTGCGCCGGTTATGTTGATTCACGAGAGAGGCTTCATATTC 533
 QY 421 GGTGAATATCATGATATGATGTGCTGATTTATTTTCAATTAAGAGATGTGTGTTG 480
 Db 534 GCGGAGGCCAATCGGGAAATGATGCGCCGATTAATCTATGAAAGAGATGTGTCTTC 593
 QY 481 ATTAACATCAATATGCTTTGGAGCTCTAGTCTTCTAAGTTTAATTCAGAAACCTT 540
 Db 594 GTCAGGATACAGTACCTGCTGGGCTGTGGATTATGAGCTTAAGTCCCGCCAGCTA 653
 QY 541 AATGTGCGCGGTAAATGCGCGCT 563
 Db 654 AATGTACCAAGAAATGCTGCT 676

RESULT 9
 BI614181
 LOCUS RH43493.5prine RH Drosophila melanogaster normalized Head p1c-1
 DEFINITION
 BI614181 673 bp mRNA linear EST 07-SEP-2001
 RH43493.5prine RH Drosophila melanogaster normalized Head p1c-1
 Drosophila melanogaster cDNA clone RH43493 5 similar to alpha-EST:
 Fban0001112 GO: [carboxylesterase (GO:0004091)]; carboxylesterase
 (GO:0004091) located on: 3R 84D5-84D5; 08/18/2001, mRNA sequence.

ACCESSION BI614181
 VERSION BI614181.1 GI:15509706
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 673)
 AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
 J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Fritse, E., George
 R., Gonzalez, M., Guerin, H., Harris, N., Li, P., Lio, G., Misra, S.,
 Mungall, C.J., Nunoo, J., Pacleb, J., Parasas, V., Park, S.,
 Phananaavong, S., Wan, K., Yu, C., Lewis, S.E., Celisner, S., and Rubin
 G.M.

TITLE BDGP/HMI RH Drosophila EST Project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDCP

Lawrence Berkeley National Lab


```

Db 471 GTGAAGCCGACAGAGCTCCCGGTTATGTTGGATTACAGGAGAGCTTCATTATC 530
OY 421 GGTGAATATCATGTGATATGATGCTGCTGATTATTTATTAAGAGATGCTGTTG 480
Db 531 GCGAGAGCCAAATCGGGAATGATGCGCGGATTTACTTATGAAAGATGTTGTTTC 590
OY 481 ATTAACATACATATTCGTTTGGAGCTAGTCTTCTTAAGTTTAATTCAGAAACCTT 540
Db 591 CTCAGATACATACGACTTGGGCTTTGGGATTATGACTTAAAGTCCCGAGCTA 650
OY 541 AATGTCCCGGTATGCGGCC 562
Db 651 AATGTACCAAGAAATGCTGGCC 672

RESULT 11
Bi233202 670 bp mRNA linear EST 11-JUL-2001
LOCUS RE29491.5prlme RE Drosophila melanogaster normalized Embryo, pR1c-1
DEFINITION Drosophila melanogaster cDNA clone RE29491.5 similar to alpha-Est7:
Pban001112 located on: 3R 84D5-84D5.; 04/12/2001, mRNA sequence.
ACCESSION Bi233202
VERSION Bi233202.1 GI:14700784
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 670)
Stapleton,M., Brokslein,P., Hong,L., Tyler,D., Berman,B., Carlson
,J., Chame,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George
,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Mista,S.,
Mungall,C.J., Nuno,J., Pacled,J., Paragas,V., Park,S.,
Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celinker,S. and Rubin
,G.M.
BDBP/HMMI RE Drosophila EST Project
Unpublished (2001)
JOURNAL Contact: Stapleton, M.
COMMENT BDBP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: RE.294 row: H column: 7
High quality sequence stop: 534.
Location/Qualifiers
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/db_xref="taxon:7227"
/clone="RE29491"
/clone_lib="RE Drosophila melanogaster normalized Embryo
pR1c-1"
/sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DHS-alpha Tona"
/note="Organ: embryo; Vector: pR1c1, Site_1: XhoI; Site_2:
BamHI. Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
BASE COUNT 152 a 168 c 194 g 155 t 1 others
ORIGIN
Query Match 14.4% Score 246.4; DB 13; Length 670;
Best Local Similarity 64.9% Pred. No. 3,1e-56;
Matches 364; Conservative 0; Mismatches 197; Indels 0; Gaps 0;
OY 1 ATGAATTTCAAGCTTATGATGAGAAATTAATGAAGAGATTAAATGATGAAT 60
Db 110 ATGAATTAAGAACTCGCTTGTGAGCGCTTGCGGCGCCCTCAAAACATGAGCAT 169
OY 61 AAGTTTAAACTATCGTTTAACATGAAGAAAGCGTGTAGCTGAAGTGAATATGCC 120

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Db 170 AAGTCCACAGATATCCAGCCAGTGCAGCAATGAAGACAGTTGTGCCGACAGGATACGC 229
OY 121 AAGTGAAGAGCGTTAAAGCTTAACTGTAAGATGATTCCTACTACAGTTTAAAGGT 180
Db 230 CAAGTAGGGGATCAAGGCTATCTCTACGATGTCCTACTTACGCTTCAGAGGT 289
OY 181 ATACGTTACGCCCAACCCGACAGTGGTACGATGAATTAAGCAACCCAGCAGCAACA 240
Db 290 ATCCGTACGCCACAGCTCCGAGTGGGGAGTTGCGGTTTAAAGCCCTCAGAGGCCAT 349
OY 241 CCCTGGATGCTGTGCTGATATTTGCAATCATTAAGATAGTCAGTCAAGTATTT 300
Db 350 CCCTGGAGCGAGTTGCGACATGCGACCGCAGCGAAGATGAAGCCGCTCAGGTGACGTT 409
OY 301 ATACGCGCAAGTGTGTGCTCAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
Db 410 GTCTTCGATTAAGGTAGAGGCTCCGAGAGCTCCTATCTAATGTGACCAACAT 469
OY 361 GTAAATCCCGAAACTAAACGTCCTGTTTATATACATACATAGTGTGTTTATATC 420
Db 470 GTGAAGCCCGACAGAGCTCCCGGTTATGTTGATTCACGAGAGAGGCTTCATTATC 529
OY 421 GGTGAATATCATGATATGATGCTGCTGATATTTATTTAATAAAGATGCTGTG 480
Db 530 GCGAGGCCAATCGGGAATGATGCGCGGATTTACTTATGAAGAAATGTTGTTCTC 589
OY 481 ATTAACATACATATTCGTTTGGAGCTGAGCTTCTTAAGTTTAATTCAGAAACCTT 540
Db 590 CTCAGATACATACGACTTGGGCTTTGGGATTATGAGCTTAAGTCCCGCAGCTA 649
OY 541 AATGTCCCGGTATGCGGCC 561
Db 650 AATGTACCAAGAAATGCTGGC 670

RESULT 12
A1113763 648 bp mRNA linear EST 19-APR-2001
LOCUS GH10213.5prlme GH Drosophila melanogaster head pot2 Drosophila
DEFINITION melanogaster cDNA clone GH10213 5prlme similar to us1050:
Drosophila melanogaster alpha esterase (aer) gene, partial cds,
mRNA sequence.
ACCESSION A1113763
VERSION A1113763.1 GI:3514566
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 648)
Harvey,D., Brokslein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDBP/HMMI Drosophila EST Project
Unpublished (2001)
JOURNAL Contact: Stapleton, M.
COMMENT BDBP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
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High quality sequence stop: 435.
Location/Qualifiers
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              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 646)
AUTHORS      Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
              Lewis,S. and Rubin,G.M.
TITLE        BDGP/HMII Drosophila EST Project
JOURNAL      Unpublished (2001)
COMMENT      Contact: Stapleton, M.
              BDGP
              Lawrence Berkeley National Lab
              One Cyclotron Rd
              Berkeley, CA 94720, USA
              Fax: 510 486 6798
              Email: http://www.fruitfly.org/EST, estfruitfly.berkeley.edu
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                pot2. Plasmid cDNA library."

BASE COUNT   152 a      163 c      182 g      149 t

ORIGIN
Query Match      14.2%; Score 243.4; DB 9; Length 646;
Best Local Similarity 64.8%; Pred. No. 2e-55;
Matches 361; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

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ACCESSION  A1293416
VERSION     A1293416.1  GI:3942823
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SOURCE      fruit fly,
ORGANISM    Drosophila melanogaster
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              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 646)
AUTHORS      Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
              Lewis,S. and Rubin,G.M.
TITLE        BDGP/HMII Drosophila EST Project
JOURNAL      Unpublished (2001)
COMMENT      Contact: Stapleton, M.
              BDGP
              Lawrence Berkeley National Lab
              One Cyclotron Rd, Berkeley, CA 94720, USA
              Fax: 510 486 6798
              Email: http://www.fruitfly.org/EST, estfruitfly.berkeley.edu
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                ligated into pot2. Plasmid cDNA library."

BASE COUNT   151 a      163 c      184 g      148 t

ORIGIN
Query Match      14.2%; Score 243.4; DB 9; Length 646;
Best Local Similarity 64.8%; Pred. No. 2e-55;
Matches 361; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 1 ATGAATTTCAAGCTTGGTTGATGAGAAATTAATGAAGCAATTAATGCAATGAAAT 60
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1713	100.0	1713	4	US-09-068-960-7 Sequence 7, Appl
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6	1698.6	99.2	1713	4	US-09-068-960-5 Sequence 5, Appl
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ALIGNMENTS

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Sequence 1, Application US/08669524
Patent No. 5843758
GENERAL INFORMATION:
APPLICANT: RUSSELL, Robyn J.
APPLICANT: NEWCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPBELL, Peter M.
APPLICANT: PARKER, Anthony G.
APPLICANT: OAKESHOTT, John G.
APPLICANT: SMYTH, Kerrie A.
TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe Price Leblanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,524
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-669-524-1
Query Match 100.0%; Score 1713; DB 2; Length 1713;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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; Patent No. 6235515
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; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
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US-09-068-960-7

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Db 241 CCTGGAGTGTGTGCTGATGTTGTCATCATTAAGATTAAGTCAAGTCAAGTCAAGT 300
Oy 301 ATACGGGCAAGGTTGTGGCTCAGAGATTTGCTATACCTAAGTGTATACGATATAT 360
Db 301 ATACGGGCAAGGTTGTGGCTCAGAGATTTGCTATACCTAAGTGTATACGATATAT 360
Oy 361 CTAAATCCGAAAGTAAAGCTCCGTTTATGATACATACATGTTGTTTATATC 420
Db 361 CTAAATCCGAAAGTAAAGCTCCGTTTATGATACATACATGTTGTTTATATC 420
Oy 421 GGTGAATATCATGATATGATGTCCTGATTTATTCATTAAGATGATGTTG 480
Db 421 GGTGAATATCATGATATGATGTCCTGATTTATTCATTAAGATGATGTTG 480
Oy 481 ATTAACATATCATATGTTGGAGCTAGGTTTCTAAGTTTAAATCAGAACCTT 540
Db 481 ATTAACATATCATATGTTGGAGCTAGGTTTCTAAGTTTAAATCAGAACCTT 540
Oy 541 AATGTCGCCGTTAATGCGGCTTAAAGATCAAGTCATGCTGTTGATTTAAAT 600
Db 541 AATGTCGCCGTTAATGCGGCTTAAAGATCAAGTCATGCTGTTGATTTAAAT 600
Oy 601 AATGTCGCCGTTAATGCGGCTTAAAGATCAAGTCATGCTGTTGATTTAAAT 660
Db 601 AATGTCGCCGTTAATGCGGCTTAAAGATCAAGTCATGCTGTTGATTTAAAT 660
Oy 661 GCTGCTCTACCCAGTATGATTTAACGAAACATCGCGGCTTTTCCATGCTGCT 720
Db 661 GCTGCTCTACCCAGTATGATTTAACGAAACATCGCGGCTTTTCCATGCTGCT 720
Oy 721 ATACTAATGTCGGTATGCTATTTGTCATGCTGCTAATACCAATGTCATGCTGCT 780
Db 721 ATACTAATGTCGGTATGCTATTTGTCATGCTGCTAATACCAATGTCATGCTGCT 780
Oy 781 TTCACCTTAGCCAAATGTCGGCTAATAGGTTAGGATTAATAGATGTTTGGAA 840
Db 781 TTCACCTTAGCCAAATGTCGGCTAATAGGTTAGGATTAATAGATGTTTGGAA 840
Oy 841 TTTCTTATGAAGCCAGCCAGATTTAATTAACCTGAGGAAATTTTAACTTA 900
Db 841 TTTCTTATGAAGCCAGCCAGATTTAATTAACCTGAGGAAATTTTAACTTA 900
Oy 901 GAAGAGCGTCAAAATAGATGATTTTCTTTGTCCTGCTGCTGAGCCATATGACAC 960
Db 901 GAAGAGCGTCAAAATAGATGATTTTCTTTGTCCTGCTGCTGAGCCATATGACAC 960
Oy 961 GGTGATGTCGTTACCCAAATCATCTCGGGAATGTTAAACCTGCGGTAATTCG 1020
Db 961 GGTGATGTCGTTACCCAAATCATCTCGGGAATGTTAAACCTGCGGTAATTCG 1020
Oy 1021 ATACCCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 ATACCCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Oy 1081 CAAATGCTATGCTTTAAGGAATGGAATGCTGTCATTAATTTTGTGCAAGTGAATG 1140
Db 1081 CAAATGCTATGCTTTAAGGAATGGAATGCTGTCATTAATTTTGTGCAAGTGAATG 1140

Oy 1141 GCTGATGCTGAGACGACCGCCCGCCAGACCTTGAATGCTGCTAAATTAAGAGCT 1200
Db 1141 GCTGATGCTGAGACGACCGCCCGCCAGACCTTGAATGCTGCTAAATTAAGAGCT 1200
Oy 1201 CATGTTACAGAGAAACCAACACAGCTGATTAATTTATGATGATGATGATGATGAT 1260
Db 1201 CATGTTACAGAGAAACCAACACAGCTGATTAATTTATGATGATGATGATGATGAT 1260
Oy 1261 TTTGCTGTTCCCATGATGCTGTTTGTGCAATTAAGTTTCAATCAACCTCGGTAACCC 1320
Db 1261 TTTGCTGTTCCCATGATGCTGTTTGTGCAATTAAGTTTCAATCAACCTCGGTAACCC 1320
Oy 1321 GTCCTGTTGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 1321 GTCCTGTTGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Oy 1381 CGTATGAGACGTCGTTAAGGTTAGTCAATGCTGATGATTAACCTATTTCTGTCG 1440
Db 1381 CGTATGAGACGTCGTTAAGGTTAGTCAATGCTGATGATTAACCTATTTCTGTCG 1440
Oy 1441 AATCAATTTGCCAAACGTAATGCTTAAGATGCTGATACCAACCAATTAAGCTATG 1500
Db 1441 AATCAATTTGCCAAACGTAATGCTTAAGATGCTGATACCAACCAATTAAGCTATG 1500
Oy 1501 ACTGATATGATGATCAATTTGCCACACTGTAATCCTTAAGCAATGAATTAAGT 1560
Db 1501 ACTGATATGATGATCAATTTGCCACACTGTAATCCTTAAGCAATGAATTAAGT 1560
Oy 1561 ATGAAATGTTTCTGCGATCAATTAAGATGCTGATGATTAACCTATTTCTGTCG 1620
Db 1561 ATGAAATGTTTCTGCGATCAATTAAGATGCTGATGATTAACCTATTTCTGTCG 1620
Oy 1621 ATTAGTACGAAATGGAATGATGATGCTGCTGAATGATGATTAACCAATGGA 1680
Db 1621 ATTAGTACGAAATGGAATGATGATGCTGCTGAATGATGATTAACCAATGGA 1680
Oy 1681 TCGATGTTGAAGAAACATGAGATTTATTTAG 1713
Db 1681 TCGATGTTGAAGAAACATGAGATTTATTTAG 1713

RESULT 3
US-09-068-960-9
; Sequence 9, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patenclin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-9

Query Match 99.4%; Score 1703.4; DB 4; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ATGAATTTCAACGTTAGTTTGTATGGAGAAATTTAAATGGAAGATTAAATGATGAAAT 60
Db 1 ATGAATTTCAACGTTAGTTTGTATGGAGAAATTTAAATGGAAGATTAAATGATGAAAT 60
Oy 61 AAGTTTTAACTATCGTTTAACTACCAATGAAAGGTTGTCGAAACCTGAATATGTC 120
Db 61 AAGTTTTAACTATCGTTTAACTACCAATGAAAGGTTGTCGAAACCTGAATATGTC 120

Db	61	AAAGTTTAAACTATACGTTTAACTACCAATGAACGGGTAGCTGAACCTGAATATGGC	120
QY	121	AAAGTGAAGGGCGTTAAACGTTTAACTGTGTACATGATTTCTACTACGATTTTGAGGGT	180
Db	121	AAAGTGAAGGGCGTTAAACGTTTAACTGTGTACATGATTTCTACTACGATTTTGAGGGT	180
QY	181	ATAACGCTACGCCCAACCCGCAAGTGGGTAGCTGTGAATTTAAAGACCCCGGCAACCA	240
Db	181	ATAACGCTACGCCCAACCCGCAAGTGGGTAGCTGTGAATTTAAAGACCCCGGCAACCA	240
QY	241	CCCTGGGATGGTGTGCGGTGATTTGGCAATCAATAAAGATAAGTCAGTCAAGTTGATTT	300
Db	241	CCCTGGGATGGTGTGCGGTGATTTGGCAATCAATAAAGATAAGTCAGTCAAGTTGATTT	300
QY	301	ATAACGGGGCAAGTGTGTGGCTGACAGAGATTTGTCTATACCTAAGTGTCTATACGAATAT	360
Db	301	ATAACGGGGCAAGTGTGTGGCTGACAGAGATTTGTCTATACCTAAGTGTCTATACGAATAT	360
QY	361	CTAAATCCCGAAACATAACGTCGCCGTTTATAGTATACATACATGCTGTGTTTATATAC	420
Db	361	CTAAATCCCGAAACATAACGTCGCCGTTTATAGTATACATACATGCTGTGTTTATATAC	420
QY	421	GGTGAATTCATTCGTGATATGTATGTGTCTGATTTATTTCAATAAAGAGATGTGTTTG	480
Db	421	GGTGAATTCATTCGTGATATGTATGTGTCTGATTTATTTCAATAAAGAGATGTGTTTG	480
QY	481	ATTAAACATACAAATATCGTTTGGAGGCTCTAGTGGTTTCTAAGTTTAAATTCACAGACCTT	540
Db	481	ATTAAACATACAAATATCGTTTGGAGGCTCTAGTGGTTTCTAAGTTTAAATTCACAGACCTT	540
QY	541	AATGGCCCCGTTATGCGGCGCTTAAAGATCAAGTCATGGCCTTGCTGGATTAATAAT	600
Db	541	AATGGCCCCGTTATGCGGCGCTTAAAGATCAAGTCATGGCCTTGCTGGATTAATAAT	600
QY	601	AATTGGCCCACTTGGTGGCAATCCCGATAATATACAGTCTTTGGGTGAAGTCCCGGT	660
Db	601	AATTGGCCCACTTGGTGGCAATCCCGATAATATATACAGTCTTTGGGTGAAGTCCCGGT	660
QY	661	GCTGCTCTACCCCACTACATGATGTTAACCGAACAAACTCGGCGCTTTCCATGATGT	720
Db	661	GCTGCTCTCTACCCCACTACATGATGTTAACCGAACAAACTCGGCGCTTTCCATGATGT	720
QY	721	ATACATAATGCGGGTATGCTATTTGTCATAGGGCTAATACCAGTGTCAACATGCTGCC	780
Db	721	ATACATAATGCGGGTATGCTATTTGTCATAGGGCTAATACCAGTGTCAACATGCTGCC	780
QY	781	TTACCTTTAGCCAAATTTGGCCGCTTAAGAGGTGAAGATAATGATTAAGATGTTTGGAA	840
Db	781	TTACCTTTAGCCAAATTTGGCCGCTTAAGAGGTGAAGATAATGATTAAGATGTTTGGAA	840
QY	841	TTTCTTTGTAAGAACCAAGCACAGGATTTAATTAACCTTGAGGAAAAAGTTTAACTCTA	900
Db	841	TTTCTTTGTAAGAACCAAGCACAGGATTTAATTAACCTTGAGGAAAAAGTTTAACTCTA	900
QY	901	GAAAGCGGTACAATAAGGTCAATGTTCTTTTGGTCCACAGTGTGAGCCATATCAGACC	960
Db	901	GAAAGCGGTACAATAAGGTCAATGTTCTTTTGGTCCACAGTGTGAGCCATATCAGACC	960
QY	961	GGTGATTTGTCTTACCCCAACATCTCGGGAATGGTTAAACCTGTTGGGGTAATTTCG	1020
Db	961	GGTGATTTGTCTTACCCCAACATCTCGGGAATGGTTAAACCTGTTGGGGTAATTTCG	1020
QY	1021	ATTACCCACTGTATGGGTGAACACTTCATATGAGGGTCAATTTTTCACATCAATCTTAAG	1080
Db	1021	ATTACCCACTGTATGGGTGAACACTTCATATGAGGGTCAATTTTTCACATCAATCTTAAG	1080
QY	1081	CAATGCGCTATGCTGTTAAGGAATTTGGAACCTGTGTCAATTTTGTGCCAAGGAATTG	1140
Db	1081	CAATGCGCTATGCTGTTAAGGAATTTGGAACCTGTGTCAATTTTGTGCCAAGGAATTG	1140
QY	1141	GGTGATGCTGAACGACCGCCCAAGACCTTGGAAATGGGTGCTAAATTTAAAAAGCT	1200
Db	1141	GGTGATGCTGAACGACCGCCCAAGACCTTGGAAATGGGTGCTAAATTTAAAAAGCT	1200

QY	1201	CATGTTACAGAGAAAACACCACAGCTGATTAATTTATGATGCTTTGCTCACATCTAT	1260
Db	1201	CATGTTACAGAGAAAACACCACAGCTGATTAATTTATGATGCTTTGCTCACATCTAT	1260
QY	1261	TTCTGGTCCCAATGCATGCTTTGTTGCAATTAACGTTTCAACACACCTCCGGTACACC	1320
Db	1261	TTCTGGTCCCAATGCATGCTTTGTTGCAATTAACGTTTCAACACACCTCCGGTACACC	1320
QY	1321	GTCATCTGATGATGCTTCGACTTTGATTTGCGAAGATCTTATTAATCCCTATGCTATATG	1380
Db	1321	GTCATCTGATGATGCTTCGACTTTGATTTGCGAAGATCTTATTAATCCCTATGCTATATG	1380
QY	1381	CGTAGTGGACGTGTGTGTTAAGGGTGTATTGATCAATGCTGATGAATTAACCATTTCTTGG	1440
Db	1381	CGTAGTGGACGTGTGTGTTAAGGGTGTATTGATCAATGCTGATGAATTAACCATTTCTTGG	1440
QY	1441	AATCAATTTGGCCAAACGTAATGCTTAAGAATGCGGTGAATACAAAACAATTGAACGATG	1500
Db	1441	AATCAATTTGGCCAAACGTAATGCTTAAGAATGCGGTGAATACAAAACAATTGAACGATG	1500
QY	1501	ACTGATATTTGATGATTCACAAATTTGCGACACACTGTATTCCTTATAGAATGAATTAAGCT	1560
Db	1501	ACTGATATTTGATGATTCACAAATTTGCGACACACTGTATTCCTTATAGAATGAATTAAGCT	1560
QY	1561	ATGGAATAATGTTTCTGGGATCAATTAAGAAATCCGACGAAGTATACAGTGTGTTGAAT	1620
Db	1561	ATGGAATAATGTTTCTGGGATCAATTAAGAAATCCGACGAAGTATACAGTGTGTTGAAT	1620
QY	1621	ATTAGTACGATTAAGAAATGATGTGCTGTAAGATGAATGAATTAAGATTAAGCAATGGGAA	1680
Db	1621	ATTAGTACGATTAAGAAATGATGTGCTGTAAGATGAATGAATTAAGATTAAGCAATGGGAA	1680
QY	1681	TCGATGTTTGAAGAAACATAGAGATTTATTTTAA	1713
Db	1681	TCGATGTTTGAAGAAACATAGAGATTTATTTTAA	1713
RESULT 4			
US-09-068-960-1			
: Sequence 1, Application US/09068960A			
: Patent No. 6235515			
: GENERAL INFORMATION:			
: TITLE OF INVENTION: Commonwealth Scientific and Industrial Rsrch. Org.			
: FILE REFERENCE: Aotorney Docket No. 6235515 50179-051			
: CURRENT FILING DATE: 1998-05-20			
: EARLIER APPLICATION NUMBER: PCT/AU96/00746			
: EARLIER FILING DATE: 1996-11-22			
: EARLIER APPLICATION NUMBER: AU 6751			
: NUMBER OF SEQ ID NOS: 43			
: SOFTWARE: PatentIn Ver. 2.0			
: SEQ ID NO 1			
: LENGTH: 1713			
: TYPE: DNA			
: ORGANISM: Lucilia cuprina			
US-09-068-960-1			
Query Match 99.3%; Score 1701.8; DB 4; Length 1713;			
Best Local Similarity 99.6%; Pred. No. 0;			
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
QY	1	ATGAATTTCAACGTTAGTTGATGAGAGAAATTAATGAGATTAATGCAATGAAAAT	60
Db	1	ATGAATTTCAACGTTAGTTGATGAGAGAAATTAATGAGATTAATGCAATGAAAAT	60
QY	61	AAGTTTAAACATATGCTTTAACTACCAATGAAGACGGTGTACTGAAATGAAATGGC	120
Db	61	AAGTTTAAACATATGCTTTAACTACCAATGAAGACGGTGTACTGAAATGAAATGGC	120

QY 121 AAAGTGAAGGCGTTAAACGTTTAACGTGTACGATGATTCCTACTACAGTTTGGAGGT 180
DB 121 AAAGTGAAGGCGTTAAACGTTTAACGTGTACGATGATTCCTACTACAGTTTGGAGGT 180
QY 181 ATACCGTACGCCCAACGCCGACGTGAGCTGAGATTTAAAGCACCAGGACCAACA 240
DB 181 ATACCGTACGCCCAACGCCGACGTGAGCTGAGATTTAAAGCACCAGGACCAACA 240
QY 241 CCTGGATGGTGGCTGTGATTTGTGCAATCAATGAAGTGCAGTCCAGTTGATTTT 300
DB 241 CCTGGATGGTGGCTGTGATTTGTGCAATCAATGAAGTGCAGTCCAGTTGATTTT 300
QY 301 ATAAAGGCGCAAGTGTGAGCTCAGAGATTTGTATCTAAGTGTGTATACGAATAT 360
DB 301 ATAAAGGCGCAAGTGTGAGCTCAGAGATTTGTATCTAAGTGTGTATACGAATAT 360
QY 361 CTAAATCCCGAACTAAACGTCCTTTTACTATACATACATAGTGTGTATATATAT 420
DB 361 CTAAATCCCGAACTAAACGTCCTTTTACTATACATACATAGTGTGTATATATAT 420
QY 421 GGTGAATATCANTCGTATGTATGTATGATTTATTCATTAATAAGATGTGTGTG 480
DB 421 GGTGAATATCANTCGTATGTATGTATGATTTATTCATTAATAAGATGTGTGTG 480
QY 481 ATTAACATACATATATGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAACCTT 540
DB 481 ATTAACATACATATATGTTTGGAGCTCTAGGTTTCTAAGTTTAAATTCAGAAACCTT 540
QY 541 AATGTCGCGGTAATGCGGCTTAAGATCAATGATGCGCTTGGTGGATTAATAAT 600
DB 541 AATGTCGCGGTAATGCGGCTTAAGATCAATGATGCGCTTGGTGGATTAATAAT 600
QY 601 AATGTCGCGGTAATGCGGCTTAAGATCAATGATGCGCTTGGTGGATTAATAAT 660
DB 601 AATGTCGCGGTAATGCGGCTTAAGATCAATGATGCGCTTGGTGGATTAATAAT 660
QY 661 GCTGCTCTACCCACTACATGATGTTAACGAAACAACTCGCGCTTTTCCATGCTGT 720
DB 661 GCTGCTCTACCCACTACATGATGTTAACGAAACAACTCGCGCTTTTCCATGCTGT 720
QY 721 ATACTAATGTGGGTAATGCTATTTTGTCCATGAGCTAATACCAATGTCACATGCTGC 780
DB 721 ATACTAATGTGGGTAATGCTATTTTGTCCATGAGCTAATACCAATGTCACATGCTGC 780
QY 781 TTCACCTTAGCAAAATTTGGCGGCTATAAGGTTGAGATTAAGATGTTTGGAA 840
DB 781 TTCACCTTAGCAAAATTTGGCGGCTATAAGGTTGAGATTAAGATGTTTGGAA 840
QY 841 TTTCTTATGAAGCCCAACGACAGATTTAATAAACTTGAGGAAAGTTTAACTGTA 900
DB 841 TTTCTTATGAAGCCCAACGACAGATTTAATAAACTTGAGGAAAGTTTAACTGTA 900
QY 901 GAAGAGCGTACAAATTAAGTCAATGTTTCTTTGCTCCACTGTTGAGCCATATCAGAC 960
DB 901 GAAGAGCGTACAAATTAAGTCAATGTTTCTTTGCTCCACTGTTGAGCCATATCAGAC 960
QY 961 GCTGATTTGTCTTACCCAAACATCTCGGGAATGTTTAAACGCTTGGGTAATTCG 1020
DB 961 GCTGATTTGTCTTACCCAAACATCTCGGGAATGTTTAAACGCTTGGGTAATTCG 1020
QY 1021 ATACCATATGATGAGTACACTATGAGGCTATTTTCTACCTTCAATTTCTTAAG 1080
DB 1021 ATACCATATGATGAGTACACTATGAGGCTATTTTCTACCTTCAATTTCTTAAG 1080
QY 1081 CAATGCTATGCTTGTAAAGAAATGGAACCTTGCTCAATTTTGTCCAAATGTAATG 1140
DB 1081 CAATGCTATGCTTGTAAAGAAATGGAACCTTGCTCAATTTTGTCCAAATGTAATG 1140
QY 1141 GCTGATGCTGAAGCAGCCGCCAGAGACCTTGGAATGAGGCTGAATTAATAAGGCT 1200
DB 1141 GCTGATGCTGAAGCAGCCGCCAGAGACCTTGGAATGAGGCTGAATTAATAAGGCT 1200
QY 1201 CATGTTACAGAGAAACCAACAGCTGATTAATTTATGATCTTTGCTCACAATCAT 1260

DB 1201 CATGTTACAGAGAAACCAACAGCTGATTAATTTATGATCTTTGCTCACAATCAT 1260
QY 1261 TTTCTGTTCCCATGATGATGCTTTTGTGCAATTTAGCTTTCAATCACACTCCGGTACACC 1320
DB 1261 TTTCTGTTCCCATGATGATGCTTTTGTGCAATTTAGCTTTCAATCACACTCCGGTACACC 1320
QY 1321 GTCATCTGTATGCTGCTGACCTTGTGGAAGATCTTATTAATCCCTATGCTATTAG 1380
DB 1321 GTCATCTGTATGCTGCTGACCTTGTGGAAGATCTTATTAATCCCTATGCTATTAG 1380
QY 1381 CGTAGTGAAGCTGTGTTAAGGCTGTTATGCTATGCTGATGATTAATTAATTTCTTCTG 1440
DB 1381 CGTAGTGAAGCTGTGTTAAGGCTGTTATGCTATGCTGATGATTAATTAATTTCTTCTG 1440
QY 1441 AATCAATTTGCCAAACGTAATGCTTAAGAATGCGGTGAATCAAAACATTTGACGTATG 1500
DB 1441 AATCAATTTGCCAAACGTAATGCTTAAGAATGCGGTGAATCAAAACATTTGACGTATG 1500
QY 1501 ACTGATATGATGATCAATTTTCCACCTGATATCTTATAGCAATGAATGAAGT 1560
DB 1501 ACTGATATGATGATCAATTTTCCACCTGATATCTTATAGCAATGAATGAAGT 1560
QY 1561 ATGGAATATGTTTCTCGGATCCAAATTAAGAAATCCGACGAAGTATACAGTGTGAT 1620
DB 1561 ATGGAATATGTTTCTCGGATCCAAATTAAGAAATCCGATGAAGTATACAGTGTGAT 1620
QY 1621 ATTAGTCAATTTGAATAATGATGCTGCTGAATAGATTAAGATTAACATGAGGA 1680
DB 1621 ATTAGTCAATTTGAATAATGATGCTGCTGAATAGATTAAGATTAACATGAGGA 1680
QY 1681 TCGATGTTTGAATAACATAGAGATTTATTTAG 1713
DB 1681 TCGATGTTTGAATAACATAGAGATTTATTTAG 1713

RESULT 5
US-09-068-960-3
; Sequence 3, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rarch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patenlin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia cuprina
US-09-068-960-3

Query Match 99.3%; Score 1701.8; DB 4; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1706; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACGTTAGTTTGTGAGAAATTTAAATGAGATTAATGCAATTAAT 60
DB 1 ATGAATTTCAACGTTAGTTTGTGAGAAATTTAAATGAGATTAATGCAATTAAT 60
QY 61 AAGTTTAAACTATGCTTTAATCAATGCAATGAAGGCTGTAAGTGAATGTAATG 120
DB 61 AAGTTTAAACTATGCTTTAATCAATGCAATGAAGGCTGTAAGTGAATGTAATG 120
QY 121 AAAGTGAAGGCGTTAAACGTTTAACTGTACGATGATTCCTACTACAGTTTGGAGGT 180
DB 121 AAAGTGAAGGCGTTAAACGTTTAACTGTACGATGATTCCTACTACAGTTTGGAGGT 180

181 ATACGGTACGCCCAACCCAGCTGGTACGTGAGATTAAAGCCACCAGCCAGCACA 240
181 ATACGGTACGCCCAACCCAGCTGGTACGTGAGATTAAAGCCACCAGCCAGCACA 240
241 CCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
241 CCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
301 ATACGGGCAAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
301 ATACGGGCAAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
361 CTAAATCCGCAAACTAAAGCTCCGCTTTAGTATACATACATGCTGTGTGTGTGTGT 420
361 CTAAATCCGCAAACTAAAGCTCCGCTTTAGTATACATACATGCTGTGTGTGTGTGT 420
421 GGTGAAATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
421 GGTGAAATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
481 ATTAACATACATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
481 ATTAACATACATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
541 AATGTCGCCGCTAATGCCGCTTAAGATCAATGATGATGATGATGATGATGATGATGAT 600
541 AATGTCGCCGCTAATGCCGCTTAAGATCAATGATGATGATGATGATGATGATGATGAT 600
601 AATGTCGCCGCTAATGCCGCTTAAGATCAATGATGATGATGATGATGATGATGATGAT 660
601 AATGTCGCCGCTAATGCCGCTTAAGATCAATGATGATGATGATGATGATGATGATGAT 660
661 GGTGCTCTACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
661 GGTGCTCTACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
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721 ATACTATGTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
781 TTTACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
781 TTTACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
841 TTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
841 TTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
901 GAAGAGCGTACAAATTAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
901 GAAGAGCGTACAAATTAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
961 GGTGATGTCGCTTACCCAAATCTCGGGAATGATGATGATGATGATGATGATGATGATGAT 1020
961 GGTGATGTCGCTTACCCAAATCTCGGGAATGATGATGATGATGATGATGATGATGATGAT 1020
1021 ATACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
1021 ATACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
1081 CAATGCTATGCTGTGTAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
1081 CAATGCTATGCTGTGTAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
1141 GCTGATGCTAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1200
1141 GCTGATGCTAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1200
1201 CATGTTACAGAGAAACCAACAGCAGTATATTTATGATGATGATGATGATGATGATGAT 1260
1201 CATGTTACAGAGAAACCAACAGCAGTATATTTATGATGATGATGATGATGATGATGAT 1260

1261 TTTCTGTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
1261 TTTCTGTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
1321 GTCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
1321 GTCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
1381 GCTAGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
1381 GCTAGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
1441 ATTCATGTCGCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1441 ATTCATGTCGCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1501 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1561 ATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
1561 ATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
1621 ATAGTACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
1621 ATAGTACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
1681 TCGATGTTGAAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
1681 TCGATGTTGAAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740

RESULT 6
US-09-068-960-5
Sequence 5, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 1713
TYPE: DNA
ORGANISM: Lucilia cuprina
US-09-068-960-5

Query Match 99.2%; Score 1698.6; DB 4; Length 1713;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 ATGATTTCAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
1 ATGATTTCAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
61 AGTTTAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
61 AGTTTAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
121 AAAGTGAAGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 180
121 AAAGTGAAGGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 180
181 ATACGTTACAGAGAAACCAACAGCAGTATATTTATGATGATGATGATGATGATGATGATGAT 240
181 ATACGTTACAGAGAAACCAACAGCAGTATATTTATGATGATGATGATGATGATGATGATGAT 240

Db 181 ATACCGTACGCCAACCCGACGGGTGAGCTGAGATTTAAAGCACCCGACGCCAACACA 240
Qy 241 CCTGGGATGCTGCGGTGATTTGTGCAATCATTAAGATTAATCTGTCAGATTTATTTT 300
Db 241 CCTGGGATGCTGCGGTGATTTGTGCAATCATTAAGATTAATCTGTCAGATTTATTTT 300
Qy 301 ATAAAGGCGCAAGTGTGCGTACAGAGATTGCTATACCTTAAGTGTATATCAATAT 360
Db 301 ATAAAGGCGCAAGTGTGCGTACAGAGATTGCTATACCTTAAGTGTATATCAATAT 360
Qy 361 CTAAATCCCGAAACCTAAAGCTCCCTTTTAAATACATACATAGTGTGTTTATATC 420
Db 361 CTAAATCCCGAAACCTAAAGCTCCCTTTTAAATACATACATAGTGTGTTTATATC 420
Qy 421 GGTGAAATCATGCTGATATGATGCTGCTGATTTTTCATTAAAAAGATGTGTTG 480
Db 421 GGTGAAATCATGCTGATATGATGCTGCTGATTTTTCATTAAAAAGATGTGTTG 480
Qy 481 ATTAACATACATATGCTTTTGGAGCTTAAAGTCTTAAATCAATACATAGTGTGTTTAT 540
Db 481 ATTAACATACATATGCTTTTGGAGCTTAAAGTCTTAAATCAATACATAGTGTGTTTAT 540
Qy 541 AATGTCGCCGATATGCGCGCTTAAAGATCAATGCGCTTGCCTGATTAATAAT 600
Db 541 AATGTCGCCGATATGCGCGCTTAAAGATCAATGCGCTTGCCTGATTAATAAT 600
Qy 601 AATGTCGCCGATATGCGCGCTTAAAGATCAATGCGCTTGCCTGATTAATAAT 660
Db 601 AATGTCGCCGATATGCGCGCTTAAAGATCAATGCGCTTGCCTGATTAATAAT 660
Qy 661 GGTGCTTACCCACATACATGATGTTAAACGAAACCTGCGGCTTTTCCATGCTG 720
Db 661 GGTGCTTACCCACATACATGATGTTAAACGAAACCTGCGGCTTTTCCATGCTG 720
Qy 721 ATACTAATGTCGGGTAAATGCTATTTGTCATGCGCTTAAATACCAATGTCACATGCTG 780
Db 721 ATACTAATGTCGGGTAAATGCTATTTGTCATGCGCTTAAATACCAATGTCACATGCTG 780
Qy 781 TTCACCTTAGCCAAATGTCGGGTAAAGGCTAGAGATTAATGATAGATGTTTGGAA 840
Db 781 TTCACCTTAGCCAAATGTCGGGTAAAGGCTAGAGATTAATGATAGATGTTTGGAA 840
Qy 841 TTTCTTATAAAGCCAGGACAGATTAATAAACCTGAGAAATTTTAACTCTCA 900
Db 841 TTTCTTATAAAGCCAGGACAGATTAATAAACCTGAGAAATTTTAACTCTCA 900
Qy 901 GAAGAGCCTAAATTAAGTCAATGTTTCTTGTCCACATGTTGAGCCATATCAGACC 960
Db 901 GAAGAGCCTAAATTAAGTCAATGTTTCTTGTCCACATGTTGAGCCATATCAGACC 960
Qy 961 GGTGATGCTGCTTACCAACATCTCTGCGGAAATGTTTAAACCTGCTGAGGTAATTCG 1020
Db 961 GGTGATGCTGCTTACCAACATCTCTGCGGAAATGTTTAAACCTGCTGAGGTAATTCG 1020
Qy 1021 ATACCCACTATGATGCTTACCACTTATGAGGCTATGTTTCTTCACTTCAATTTTAAG 1080
Db 1021 ATACCCACTATGATGCTTACCACTTATGAGGCTATGTTTCTTCACTTCAATTTTAAG 1080
Qy 1081 CAAATGCTATGCTTAAAGAAATGGAACCTGTGTCAATTTTGTGCCAAGTGAATG 1140
Db 1081 CAAATGCTATGCTTAAAGAAATGGAACCTGTGTCAATTTTGTGCCAAGTGAATG 1140
Qy 1141 GGTGATGCTGAACGACGCCGACAGACCTTGAATGGGTCTAAATTTAAAAAGGCT 1200
Db 1141 GGTGATGCTGAACGACGCCGACAGACCTTGAATGGGTCTAAATTTAAAAAGGCT 1200
Qy 1201 CATGTACAGGAAACACACAGCTGATATTTTATGATGCTTCTCATCATCTAT 1260
Db 1201 CATGTACAGGAAACACACAGCTGATATTTTATGATGCTTCTCATCATCTAT 1260
Qy 1261 TTCTGCTCCCATGCTGATGTTTGTGCAATTAATCAATCAGCTCCGTTACACC 1320
Db 1261 TTCTGCTCCCATGCTGATGTTTGTGCAATTAATCAATCAGCTCCGTTACACC 1320

Qy 1321 GTCCTACTGTATGCGCTTGCAGCTTTGATTCGGAAGATCTTATTAATCCCTATGATATG 1380
Db 1321 GTCCTACTGTATGCGCTTGCAGCTTTGATTCGGAAGATCTTATTAATCCCTATGATATG 1380
Qy 1381 GGTAGTACGAGTGTGTTAAGGCTGTTATGTCATGCTGATGATTAATTAACCTATTTCTTCTG 1440
Db 1381 GGTAGTACGAGTGTGTTAAGGCTGTTATGTCATGCTGATGATTAATTAACCTATTTCTTCTG 1440
Qy 1441 AATCAATTTGCCCAACGATATGCTTAAAGATTCGCTGAATACAAACAAATTAACCTATG 1500
Db 1441 AATCAATTTGCCCAACGATATGCTTAAAGATTCGCTGAATACAAACAAATTAACCTATG 1500
Qy 1501 ACTGCTATATGATACATATTTTCCGACCTGCTATCCCTTATAGCAATGAATTAAGAT 1560
Db 1501 ACTGCTATATGATACATATTTTCCGACCTGCTATCCCTTATAGCAATGAATTAAGAT 1560
Qy 1561 ATGGAATATGTTTCTGGAATCCAAATTAAGAAATCCGAGAAATTAAGATGTTGAAT 1620
Db 1561 ATGGAATATGTTTCTGGAATCCAAATTAAGAAATCCGAGAAATTAAGATGTTGAAT 1620
Qy 1621 ATTAGTACGAAATTAAGAAATGATGCTGCTGAATGATTAAGATTAAGATGGAAT 1680
Db 1621 ATTAGTACGAAATTAAGAAATGATGCTGCTGAATGATTAAGATTAAGATGGAAT 1680
Qy 1681 TCGATGTTGAAACATAGATTAATTTTATG 1713
Db 1681 TCGATGTTGAAACATAGATTAATTTTATG 1713

RESULT 7
US-08-669-524-2
; Sequence 2, Application US/08669524
; Patent No. 5843758
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, Robyn J.
; APPLICANT: NEMCOMB, Richard D.
; APPLICANT: ROBIN, Geoffrey C.
; APPLICANT: BOYCE, Thomas M.
; APPLICANT: CAMPBELL, Peter M.
; APPLICANT: PARKER, Anthony G.
; APPLICANT: OAKESHOTT, John G.
; APPLICANT: SMYTH, Kertie A.
; TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe Price Lebland & Becker
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,524
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Price, Robert L.
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 1451-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single

Db	961	GCTGATGTGCTTACCCAAACATCCCTGGGAAATGGTTAAANNCTCTGGGGATNTTCG	1020
Qy	1021	ATACCCACTATGATGGGTACACTTCATATAGGGTCATTTTTCACCTTCAATTCCTTAAG	1080
Db	1021	ATACCCACTATGATGGGTACACTTCATATAGGGTCATTTTTCACCTTCAATTCCTTAAG	1080
Qy	1081	CAAAATGCTATGCTGTGTTAAAGATTTGGAACCTTGTCATATTTTGTGCAAGTGAATTG	1140
Db	1081	CAAAATGCTATGCTGTGTTAAAGATTTGGAACCTTGTCATATTTTGTGCAAGTGAATTG	1140
Qy	1141	GCTGATGCTGACACGACGCCCCAGAGACCTTGGAATGGGTGCTAAATTTAAAAAGCT	1200
Db	1141	GCTGATGCTGACACGACGCCCCAGAGACCTTGGAATGGGTGCTAAATTTAAAAAGCT	1200
Qy	1201	CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTTTGCTGCACATCTAT	1260
Db	1201	CATGTTACAGAGAAACCAACAGCTGATATTTTATGATCTTTTGCTGCACATCTAT	1260
Qy	1261	TTCTGGTCCCAATGCAATCGTTTGTGGCAATTAAGTTCAATCACACCTCCGGTACACC	1320
Db	1261	TTCTGGTCCCAATGCAATCGTTTGTGGCAATTAAGTTCAATCACACCTCCGGTACACC	1320
Qy	1321	GTCATCTGTATGCGCTTCGACTTTGATTTGATGGAGATCTTATTAATCCCATGATATAG	1380
Db	1321	GTCATCTGTATGCGCTTCGACTTTGATTTGATGGAGATCTTATTAATCCCATGATATAG	1380
Qy	1381	CGTAGTGACGCTGTGTGTTAAGGGGTGTAGTCATGCTGATGAATTAACCATTTCTTCGG	1440
Db	1381	CGTAGTGACGCTGTGTGTTAAGGGGTGTAGTCATGCTGATGAATTAACCATTTCTTCGG	1440
Qy	1441	AATCAATTTGGCCAAACGTATAGCTTAAAGAATCGCGTGAATACAAACAAATTGACGTATG	1500
Db	1441	AATCAATTTGGCCAAACGTATAGCTTAAAGAATCGCGTGAATACAAACAAATTGACGTATG	1500
Qy	1501	ACTGGTATATGATGATACAAATTTGGCACACAGCTGTAATCTTATAGCAATGAATTTGAAGT	1560
Db	1501	ACTGGTATATGATGATACAAATTTGGCACACAGCTGTAATCTTATAGCAATGAATTTGAAGT	1560
Qy	1561	ATGCAAAATGTTTCTCTGGGATTCCAATTAAGAAATCCGACGAAGTATACAAAGTGTTCGAT	1620
Db	1561	ATGCAAAATGTTTCTCTGGGATTCCAATTAAGAAATCCGACGAAGTATACAAAGTGTTCGAT	1620
Qy	1621	ATTAGTGACGAATGAATAATGATGATGCGCTGGAATGGATGAAGTTTAAACAATGGGAA	1680
Db	1621	ATTAGTGACGAATGAATAATGATGATGCGCTGGAATGGATGAAGTTTAAACAATGGGAA	1680
Qy	1681	TCGATGTTTGAAAAACATATAGATTTATTTTAA	1713
Db	1681	TCGATGTTTGAAAAACATATAGATTTATTTTAA	1713
RESULT 8.			
US-09-068-960-14			
: Sequence 14, Application US/09068960A			
: Patent No. 6235515			
: GENERAL INFORMATION:			
: APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.			
: TITLE OF INVENTION: MALATHION CARBOXYLISSTERASE			
: FILE REFERENCE: Attorney Docket No. 6235515 501/9-051			
: CURRENT APPLICATION NUMBER: US/09/068.960A			
: EARLIER FILING DATE: 1998-05-20			
: EARLIER APPLICATION NUMBER: PCT/AU96/00746			
: EARLIER FILING DATE: 1996-11-22			
: EARLIER APPLICATION NUMBER: AU 6751			
: NUMBER OF SEQ ID NOS: 43			
: SOFTWARE: PatentIn Ver. 2.0			
: SEQ ID NO 14			
: LENGTH: 1710			
: TYPE: DNA			
: ORGANISM: Musca domestica			
: US-09-068-960-14			

Page 10

Query Match	10.68;	Score 181.2;	DB 3;	Length 1204;
Best Local Similarity	56.4%;	Pred. No. 3.8e-43;		
Matches 361;	Conservative	0;	Mismatches 273;	Indels 6;
				Gaps 1

```

RESULT 10
US-08-747-221B-52/C
; Sequence 52, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
;

```

Query Match	10.6%;	Score 181.2;	DB 3;	Length 1504;
Best Local Similarity	56.4%;	Pred. No. 3.8e-43;		
Matches 361, Conservative	0;	Mismatches 273;	Indels 6;	Gaps 1

QY	116	ATGCGAAGTGAAGGGGTTAAAGCTTTAACTGTCGTACGATGATTCACATACAGTTTC	1497
Db	1556	AAGGTACTCTTTAAAGGAAGAAAGCAATTATGTGAAAAGGAATGTCTTCATAGTTATT	235
QY	176	AGGGTATACCGTAGCCCAACCCGCACTGGGTAGCTGAGATTTTAAAGACCCAGCGAC	1437
Db	1496	CTGGATTCATATGCCAAACCTCTCTAGTATCTTAAGATTAAAGCCACTCAACCTG	295
QY	236	CAACACCTGGGATGTCGTGGTGATTTGGTCATCATCTAAGATAGTCAGTCAAGTTG	1377
Db	1436	CAGAACCTTGGTCAGAGTGTCTTGATGCTGATTAAGAAAGGATAGTGTAGATCAGTAC	355
QY	296	ATTTTTAAAGGGCAAGAGTGTGGCTCAGAGATTTCTTATACCTAGAGTCCTATAGCA	1317
Db	1376	ATTTTATTTAAAAAATTAAAGTAGGGGCTGGAAGATTGTTTAACCTCATGCTATAGTAC	415
QY	356	ATAATCTAATCCCGAACTAAAGCTCCGTTTGGTATGATACATACATAGTGTGGTTTAA	1257
Db	1316	CAAAACATCAGAGAAATACTCTTCCAGTAAATGATGTGATGCATAGGAGGAGGCTTCT	475
QY	416	TTATCGGTGAAMAATCATCTGTATGTATGTATGTCCTGATTAATTTCAATTAAGAAGATGG	1197
Db	1256	TCATGGGATCTGGAAATAGATATGTATAGTGGCTCGAATATTTGATGATTAATGAATTG	535
QY	476	TGTTGATTAACTATCATATATCGTTTGGGAGCTCTAGTGTTCATAGTTTAAATTCAGAAG	1137
Db	1196	TTTCGTTACTCTTAATTAATTCGATTAAGGTGTTTGGATTTTGAACCTGGGAATTAAG	595
QY	536	ACCTTAATGTGCCCCGATATGCGGCGCTTAAGATCAATCATATGCGCTTGGTGGATTA	1083
Db	1136	AA-----GGCCCTGGCAATGTTGGTTTGTATGAGCAGGCTTGAACCTCTAAATGGGTA	

TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-005-051-52

Query Match 10.6%; Score 181.2; DB 4; Length 1584;
Best Local Similarity 56.4%; Pred. No. 3.8e-43;
Matches 361; Conservative 0; Mismatches 273; Indels 6; Gaps 1;

QY 116 ATGGCAAGTGAAGCGCTTAAAGCTTAACTGTACATGATCTCTACAGTTTG 175
DB 1556 AAGTACTTAAAGAAAGAAAGCAATTAAGTAAAGAAAGAAAGTGTCCATAGTATT 1497
QY 176 AGGTTATACCGTACGCCCAACCGCCAGTGTAGCTGAGTAAAGACCCCGAC 235
DB 1496 CTGGAAATTCATATGCCAAACCTCCGTAGTATGAATTTAAGCACCCTCACTG 1437
QY 236 CAACACCTGGTGGTGTGGCGATTTGTGAATCATTAAGATTAAGTCAAGTTG 295
DB 1436 CAGAACCTTGTCAGGTGTTCTTCACTAGTAAAGAAAGGAATGTGTAGATCAGTAC 1377
QY 296 ATTTTATACGGGCAAAAGTGTGGCTCAGAGATTTGTATACCTAAGTGTATACGA 355
DB 1376 ATTTTATTAATAAAATTAAGTAGGGGCTGAAGATTTGTATACCTCATGTCTATGAC 1317
QY 356 ATATCTAATCCCAACTAAAGCTCCGTTTAACTATACATGATGCTGCTTAA 415
DB 1316 CAAAAACATCAGAAATCACTCTTCCAGTAAATGATGATGATGAGAGAGCTTCT 1257
QY 416 TTATGGTGAAATCATGTGATATGATGATGCTGCTGATTTATTTAAAGAGTGTG 475
DB 1256 TCATGGGATCTGGAATATGATATGATGATGCTGCTGATTTATGATGATGATG 1197
QY 476 TGTGATTACATCAATATGCTTTGGAGCTGATGCTTCTAAGTTTAAATTCAGAG 535
DB 1196 TTCTGGTACTTCAATATGATGATGATGCTTTTGGAGTTTGAACCTGGGATGAG 1137
QY 536 ACCTTAATGTCCCGGTAATGCGGCTTAAAGATCAATGATGCTGCTTGAATTA 595
DB 1136 AA-----GCCCTGGCAATGTTGGTTGATGACGAGTTGAAGCTCTAAATGGGTAA 1083
QY 596 AAATATGCGCAACTTTGGGCAATGCCATATATTAAGTCTTTGGTGAATG 655
DB 1082 AAACATATTTGATCTTGTGTTGATGACCCCAACATGATGATTTTGGAGATCAG 1023
QY 656 CCGTGTGCTGCTACCCAGTACATGATTTAAACGAACAACTGCGGCTTTTTCATC 715
DB 1022 CAGTGTGCTGCAATGTTGATTTGATGATGATGATTTTCCAAAGGACCTTTTCA 963
QY 716 GTGTTATCAATGATGCTGATTTGTCATGGC 755
DB 962 AAGCATCTCAAAAGTGAAGTCTTTTAACTCTGGC 923

RESULT 13
US-08-747-221B-36
Sequence 36, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation

STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610e1member 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 11..1594
US-08-747-221B-36

Query Match 10.6%; Score 181.2; DB 3; Length 2007;
Best Local Similarity 56.4%; Pred. No. 4.3e-43;
Matches 361; Conservative 0; Mismatches 273; Indels 6; Gaps 1;

QY 116 ATGGCAAGTGAAGCGCTTAAAGCTTAACTGTACATGATCTCTACAGTTTG 175
DB 39 AAGTACTTAAAGAAAGAAAGCAATTAAGTAAAGAAAGAAAGTGTCCATAGTATT 98
QY 176 AGGTTATACCGTACGCCCAACCGCCAGTGTAGCTGAGTAAAGACCCCGAC 235
DB 99 CTGGAAATTCATATGCCAAACCTCCGTAGTATGAATTTAAGCACCCTCAACTG 158
QY 236 CAACACCTGGTGGTGTGGCGATTTGTGAATCATTAAGATTAAGTCAAGTTG 295
DB 159 CAGAACCTTGTCAGGTGTTCTTCACTAGTAAAGAAAGGAATGTGTAGATCAGTAC 218
QY 296 ATTTTATACGGGCAAAAGTGTGGCTCAGAGATTTGTATACCTAAGTGTCTATACGA 355
DB 219 ATTTTATTAATAAAATTAAGTAGGGCTGAAGATTTTAACTCAATGCTATGATG 278
QY 356 ATATCTAATCCCGAATCAATGCTCCGTTTAACTATACATGATGCTGCTTGAATTA 415
DB 279 CAAACATCAGAAATCACTCTTCCAGTAAATGATGATGATGATGATGATGATGATG 338
QY 416 TTATCGGTGAATAATCATGATGATGATGATGATGATGATGATGATGATGATGATG 475
DB 339 TCATGGTACTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATG 398
QY 476 TGTGATTACATCAATATGCTTTGGAGCTGATGCTTCTAAGTTTAAATTCAGAG 535
DB 399 TTCTGGTACTTCAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 512
QY 536 ACCTTAATGCGGCAATGCGGCTTAAAGATCAATGCTGCTGCTGCTGCTGCTGCTG 595
DB 459 AA-----GCCCTGGCAATGTTGGTTGATGACCCCAACATGATGATTTTGGAGAT 512
QY 596 AAATATGCGCAACTTTGGGCAATGCCATATATTAAGTCTTTGGTGAATG 655
DB 513 AAACATATTTGATCTTGTGGTGAAGCTTAACTCTGGC 572

MOLECULE
FEATURE:

Db 500 TTAATTACAGATTGAACGCTTCGGTTTCCTGTCCATGAACACACA-----AAATCC 553

[illegible]

RESULT 2
US-09-738-626-1254
US-09-738-626-1254

```

Sequence 1254, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIHO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738, 626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1254
LENGTH: 1611
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1254

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Query Match	4.58;	Score 77.2;	DB 9;	Length 1611;
Best Local Similarity	50.28;	Pred. No. 5.5e-10;		
Matches 277;	Conservative 0;	Mismatches 263;	Indels 12;	Gaps 3;

QY 177 GGTATTACCGTAACGCCAACCGGAGGGGAGCTAGATTATTAACACCCACGAGAC 236
 Db 78 GGGATTTCCTTACGCGCCAAACACTGCGCGAATAATTCGCTTCGCGGACACCCGGGCGCG 137
 QY 237 AACACCCCTGGATGTGTGCGTATTTGTGCA--ATCATTAAGATTAAGTCAGTGCACAG 253
 Db 138 CAAAGAAATGGGACGCGCGCTGCAGATTTGCTCATATGTTCGGTGAAGTAGACTTCTAGCCAC 197
 QY 294 TGATTTTTAAACGGCAAGAAGTGTGTGCTCAAGAGATTGTCTAATACCTAAGTGTCTATAC 353
 Db 198 GTACCTCTGGAACAGATTAAGATTCCGGGGTTCAGAGACTGCCTTAACCTCATGTCTGCGCG 257
 QY 354 GAAATATCTAATATCCGGAACATAAAGCCCGCTTTTGATATACATACATGSGTGGATT 413
 Db 258 G-----CCTGATTTCCGAAGAAACCTTCCTGTTGTGTGATATCCACGGCGGTTCCCT 311
 QY 414 TATTATCGGTGA--AAATCATCTGATATGATATGTCCTGATATTATTCAATTAANAAGA 470

Db.	312	CATCATGGCGTCATCAACGCGAAAAAGGCGTGGCGGGATATTAACTCGTCACAAACATGAA	371
OY	471	TGTGGTGTGATTAAACAATTACATATCGTTTGGAGCTCAGTTTCTTAAGTTAAATTC	530
Db	372	TGTGCTACAGTGTGCGTTATTATTTCCGCCTCGGGGCTTTGGGCAATCATATCGCTTC	431
OY	531	AGAGACCTTAAATGTGCGCGGTAATGCGCGCTTAAAGATCAAGTCATGGCCTTGCCTT	590
Db	432	CGTGGGGAGGATTTGGCGTAGCCAAACCCGCGCTCAGATCAGTCACTCTCGCCCTGCAGTG	491
OY	591	GATTAAAAATTAATTGGCGCACTTTGGTGCAATCCGAGTAATTAATTACATCTTTGGTGA	650
Db	492	GGTAGCGCGTAATATCGAAGCAATTTGGGGATCTGACAAAGCTCACCTCATGGGCCA	551
OY	651	AAGTGCAGGTCCTGCTTACCCACTACATGATGTTAAACCGAAACACTCGCGTCTTTT	710
Db	552	ATCCGCGGGCGCTCGACAGAGTGTTGACATCATGTGTGTCGCCGCTCAGAGAGACTATT	611
OY	711	CCATCGTGGTAT 722	
Db	612	CCACGCGGCAT 623	

QY	711	CCATCGTGGTAT	722
Db	612	CCACCGCGCCAT	623

```

RESULT 3
US-09-748-739A-1
Sequence 1, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Malkins, Jeff D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1967
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
FEATURE:
NAME/KEY: CDS
LOCATION: (86)...(1891)
US-09-748-739A-1

```

Query Match	3.6%;	Score 62.2;	DB 10;	Length 1967;
Best Local Similarity	54.8%;	Pred. No. 5e-06;		
Matches 190; Conservative	0;	Mismatches 148;	Indels 9;	Gaps 3;

Qy	325	GAGAGATGTCATCTACTAAGTCGTATACGAATATATCAATATCCGGAACATAACGCCC	384
Db	437	GAGAGCTGTTATATCTCAATAAATGATATGATCTCCAGCACTAAAC--	493
Qy	385	GTTTATAGTATACATACATGTCGTCGTTTATATATCGTGAAATCATCGTATATAT	444
Db	494	GATATGATATGATTTATGTCGTGTCGTTTCAACGTGAAACATCATCTTTACATGTTAT	553
Qy	445	GGTCCTGATTTATTTCAATAAAAGCA--	501
Db	554	GATGGCAATTTCTGCTCGGTCGATTAAGAGATTATTTAGTGTCAATGAATATAGGCTG	613
Qy	502	GGAGCTCTAGGTTTCTAAGTTAAATTCACAGAAGCCTTATGTCGCCGGTAATAGCGGC	561
Db	614	GGGCCCCATGGGATCTTACTCTT---GCCAGGAAATCTGTAGGCTCCAGGAAACATGGGT	670
Qy	562	CTTAAAGATCAAGTATAGGCTTCCTGGTGGATTAATAAATAATTCGCCCAACTTGTGTGC	621
Db	671	TTATTTGATCAACAGTGGCTCTTCAGTGGGCTTCAAAAATAATATAGCAGCCTTTGGTGA	730
Qy	622	AATCCGATATATTTACATCTTTTGGTGAAAGTGCCTGCTGCCTC	668

Db 731 AATCTAAAGTAACTCTTTGGAGAAAGTCAGAGACGCTTC 777

RESULT 4

US-09-880-107-2271
Sequence 2271, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scheff, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 2271
LENGTH: 2381
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474
US-09-880-107-2271

Query Match

Best Local Similarity 3.6%; Score 62.2; DB 10; Length 2381;
Matches 190; Conservativity 54.8%; Pred. No. 5.5e-06;
Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGATTGCTATACCTAAGTGTCTATACGAATATCTAAATCCCGAAACTAAAGCTCC 384
DB 427 GAAGACTGTTATATCTAAAGTATGATTCACACCTAAAC--AAAAAATGCCACT 483
QY 385 GTTTAGATACATACATGCTGCTGTTTATTCGTCGAATCATCGATATGAT 444
DB 484 GTATTGATATGATTTATGCTGCTGTTTCAACCTGAAACATCATCTTACATGTTAT 543
QY 445 GGTCTGATTTATTCATTAAGAAAG--TGTGCTGTTGATTATACATATATCGTTG 501
DB 544 GATGCAAGTTTCGCTCGGCTGGAAGATTTATGATGTAATGAACTATAGGTG 603
QY 502 GGACCTAGTCTTCTAAGTTTAAATTCAGAGACCTTAATGCGCGTAAATGCCGC 561
DB 604 GGTCCCTAGGATTTCTAGCTT--GCCAGGAATCCTGAGCTCCAGGACATGGGT 660
QY 562 CTAAAGATCAAGTCATGCTTGCCTGCTGATTAATAATATTCGCCAATTTGGTGC 621
DB 661 TTAATTTGATCAACAGTTGCTTCAAGGCTTCAAAAAAATATAGAGCCTTTGGTGA 720
QY 622 AATCCGATATATTAACAGTCTTGTGTAAGTCCGCTGCTGCTC 668
DB 721 AATCTAAAGTAACTCTTTGGAGAAAGTCAGAGACGCTTC 767

RESULT 5

US-09-748-739A-3
Sequence 3, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3

LENGTH: 2416

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant

NAME/KEY: CDS
LOCATION: (214)...(1935)

US-09-748-739A-3

Query Match

Best Local Similarity 3.6%; Score 62.2; DB 10; Length 2416;
Matches 190; Conservativity 54.8%; Pred. No. 5.6e-06;
Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGATTGCTATACCTAAGTGTCTATACGAATATCTAAATCCCGAAACTAAAGCTCC 384
DB 481 GAAGACTGTTATATCTAAAGTATGATTCACACCTAAAC--AAAAAATGCCACT 537
QY 385 GTTTAGATACATACATGCTGCTGTTTATTCGTCGAATCATCGATATGAT 444
DB 538 GTATTGATATGATTTATGCTGCTGTTTCAACCTGAAACATCATCTTACATGTTAT 597
QY 445 GGTCTGATTTATTCATTAAGAAAG--TGTGCTGTTGATTATACATATATCGTTG 501
DB 598 GATGCAAGTTTCGCTCGGCTGGAAGATTTATGATGTAATGAACTATAGGTG 657
QY 502 GGACCTAGTCTTCTAAGTTTAAATTCAGAGACCTTAATGCGCGTAAATGCCGC 561
DB 658 GGTCCCTAGGATTTCTAGCTT--GCCAGGAATCCTGAGCTCCAGGACATGGGT 714
QY 562 CTAAAGATCAAGTCATGCTTGCCTGCTGATTAATAATATTCGCCAATTTGGTGC 621
DB 715 TTAATTTGATCAACAGTTGCTTCAAGGCTTCAAAAAAATATAGAGCCTTTGGTGA 774
QY 622 AATCCGATATATTAACAGTCTTGTGTAAGTCCGCTGCTGCTC 668
DB 775 AATCTAAAGTAACTCTTTGGAGAAAGTCAGAGACGCTTC 821

RESULT 6

US-09-748-739A-5
Sequence 5, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2416
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
NAME/KEY: CDS
LOCATION: (214)...(1935)
US-09-748-739A-5

Query Match

Best Local Similarity 3.6%; Score 62.2; DB 10; Length 2416;
Matches 190; Conservativity 54.8%; Pred. No. 5.6e-06;
Mismatches 148; Indels 9; Gaps 3;

QY 325 GAGATTGCTATACCTAAGTGTCTATACGAATATCTAAATCCCGAAACTAAAGCTCC 384
DB 481 GAAGACTGTTATATCTAAAGTATGATTCACACCTAAAC--AAAAAATGCCACT 537

Query Match	3.4%	Score	59	DB	10	length	2508
Best Local Similarity	53.2%	Pred. No.	3.9e-05				
Matches	125	Conservative	0	Mismatches	110	Indels	0
						Gaps	0

RESULT 12
US-09-974-300-1107
Sequence 1107, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085,500-US

CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1107
LENGTH: 657
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-1107

Query Match 3.4%; Score 57.8; DB 10; Length 657;
Best Local Similarity 49.9%; Pred. No. 3.8e-05;
Matches 174; Conservative 0; Mismatches 172; Indels 3; Gaps 1;

QY 377 AACGTCCTTTTATATACATACATGCTGCTTTTATATCG--TGAATATCATC 433
DB 30 ATCTGCTCTTATGCTGTGATTCATGGGCGCTTTTATCGCGCGGAGTGAAC 89
QY 434 GTGATATGATGCTGCTGATTTATTAATAAAGATGCTGTGATTAACATCAAT 493
DB 90 CGCTTATGACGGGACTCAGCTTCAAGTAAATTCAGACCTTAATGTCGCCGTA 149
QY 494 ATCTTTGGAGCTCTAAGTTTCTAAGTTTAAATTCAGACCTTAATGTCGCCGTA 553
DB 150 ATGCGCTCGGCGCTGCTTTTTCATCTATCTCAATGATGATCTCTACAGAGCA 209
QY 554 ATGCGCGCTTAAAGATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
DB 210 ATCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 269
QY 614 TTGCTGCAATCCGATATATTACAGCTTTGCTGTAAGTCCGCTGCTGCTGCTGCT 673
DB 270 TTGCGGAGACCGTACATACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 329
QY 674 ACTACATGATGTAAACGCAACAACTGCGGCTTTTCCATCGTGTAT 722
DB 330 CTGCTTTTGGCGATGCCGAACAAAGGCGCTTTTCCACAGGCCAT 378

RESULT 13
US-09-418-176-1
Sequence 1, Application US/09418176
Publication No. US20030040040A1

GENERAL INFORMATION:
APPLICANT: Das, Goutam
TITLE OF INVENTION: DNA molecules for Expression of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/418,176

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/624,398
FILING DATE: 04-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE96/00318

FILING DATE: 12-MAR-1996
PRIOR APPLICATION DATA: SE 9501939-4
APPLICATION NUMBER: 24-MAY-1995
FILING DATE: 24-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Thelma A. Chen Cleland
REGISTRATION NUMBER: 40,948
REFERENCE/DOCKET NUMBER: 1103326-0206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8200
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2428 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: mammary gland
FEATURE:
NAME/KEY: CDS
LOCATION: 82..2319
OTHER INFORMATION: /product= "bile-salt-stimulated
OTHER INFORMATION: lipase"
FEATURE:
NAME/KEY: exon
LOCATION: 985..1173
FEATURE:
NAME/KEY: exon
LOCATION: 1174..1377
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LOCATION: 1378..1575
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LOCATION: 1576..2415
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NAME/KEY: mat_peptide
LOCATION: 151..2316
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NAME/KEY: polyA_signal
LOCATION: 2397..2402
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NAME/KEY: repeat_region
LOCATION: 1756..2283
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LOCATION: 1888..1920
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NAME/KEY: repeat_unit
LOCATION: 1921..1953
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LOCATION: 1954..1986


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: LOCATION: 2185..2217
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: LOCATION: 2218..2250
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: NAME/KEY: repeat_unit
: LOCATION: 2251..2283
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: PUBLICATION INFORMATION:
: AUTHORS: Nilsson, Jeanette
: AUTHORS: Blackberg, Lars
: AUTHORS: Carlsson, Peter
: AUTHORS: Enerback, Sven
: AUTHORS: Herneli, Olle
: AUTHORS: Bjursell, Gunnar
: TITLE: cDNA cloning of human-milk
: TITLE: bile-salt-stimulated lipase and evidence for its
: TITLE: identity to pancreatic carboxylic ester hydrolase
: JOURNAL: Eur. J. Biochem.
: VOLUME: 192
: PAGES: 543-550
: DATE: Sept.-1990
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: Db 608 CTGGGAGCGCAATCTGCCAGTACATGAGCTTCGGGATCAGACATGGCATTCCTT 667
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: QY 590 GGATTAAATAATGCGGCAACTTTGGTGGCAATCCGATATATTAAGTCTTTGGTG 649
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: Db 668 GGGTGAAGAGAAATATCCGCGCTTCGGGGGGGACCCCAACAATCAGCTCTTCGGGG 727
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: QY 650 AAAGTGGCGGTGCTCTTACCCACTACATGATTTAAGCAACAAACTGGCGTCTT 709
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: Db 728 AGTCTGCTGGAGGTGCGCGCTCTCTGCAAGACCTCTCCCTACAAAGGCGCTCA 787
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: QY 710 TCCATCGTGTATCTAATGTCGGGTAATGCTATTTGTCATGGG 754
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: Db 788 TCCGGCGAGCATCAGCCAGAGCGGCGGTGGCCCTGATGTCCTGGG 832
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: RESULT 14
: US-09-969-347-220
: Sequence 220, Application us/09969347
: Patent No. US20020115085A1
:
: GENERAL INFORMATION:
: APPLICANT: Ebner, Reinhard
: TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
: TITLE OF INVENTION: Sets
: FILE REFERENCE: 689290-69
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: CURRENT APPLICATION NUMBER: US/09/969,347
: PRIOR FILING DATE: 2001-10-02
: PRIOR APPLICATION NUMBER: US/60/237,598
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: US/60/237,604
: PRIOR FILING DATE: 2000-10-03
: NUMBER OF SEQ ID NOS: 318
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 220
: LENGTH: 2428
: TYPE: DNA
: ORGANISM: Homo sapiens
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: US-09-969-347-220
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: Query Match
: Best Local Similarity 53.3%; Score 57; DB 10; Length 2428;
: Matches 120; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
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: QY 530 CAGAAGACCTTAATGTGCGGCGGTATGCGGCGCTTAAGATCAAGTCAATGCGCTT 589
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: Db 608 CTGGGAGCGCAATCTGCCAGTACATGAGCTTCGGGATCAGACATGGCATTCCTT 667
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: QY 590 GGATTAAATAATGCGGCAACTTTGGTGGCAATCCGATATATTAAGTCTTTGGTG 649
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: Db 668 GGGTGAAGAGAAATATCCGCGCTTCGGGGGGGACCCCAACAATCAGCTCTTCGGGG 727
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: QY 650 AAAGTGGCGGTGCTCTTACCCACTACATGATTTAAGCAACAAACTGGCGTCTT 709
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: Db 728 AGTCTGCTGGAGGTGCGCGCTCTCTGCAAGACCTCTCCCTACAAAGGCGCTCA 787
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: QY 710 TCCATCGTGTATCTAATGTCGGGTAATGCTATTTGTCATGGG 754
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: Db 788 TCCGGCGAGCATCAGCCAGAGCGGCGGTGGCCCTGATGTCCTGGG 832
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: RESULT 15
: US-09-954-531-1038
: Sequence 1038, Application US/09954531
: Patent No. US20020165180A1
:
: GENERAL INFORMATION:
: APPLICANT: Weaver, Zoe
: TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
: TITLE OF INVENTION: Gene Sets
: FILE REFERENCE: 689290-77
: CURRENT APPLICATION NUMBER: US/09/954,531
: PRIOR FILING DATE: 2002-05-02
: PRIOR APPLICATION NUMBER: US/60/233,133
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: US/60/234,009
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: US/60/234,034
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: US/60/234,509
: PRIOR FILING DATE: 2000-09-22
: PRIOR APPLICATION NUMBER: US/60/234,567
: PRIOR FILING DATE: 2000-09-22
: NUMBER OF SEQ ID NOS: 1392
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1038
: LENGTH: 2191
: TYPE: DNA
: ORGANISM: Homo sapiens
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: US-09-954-531-1038
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: Query Match
: Best Local Similarity 53.2%; Score 56.8; DB 9; Length 2191;
: Matches 215; Conservative 0; Mismatches 177; Indels 12; Gaps 4;
:
: QY 322 TCAGAGATGCTATACCTAGTGTATACGAATATTAATCCGAA---ACTAAA 378
:   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
: Db 436 TCTGAGAGCTGCTATCTCAGATCAACAGCGGCGCCATAGCATGAAGGCTTAAC 495
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: QY 379 CGTCCGTTTACATACATACATGCTGTTTATTATTCGGTGAATATCATGCTGAT 438
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Db 496 CTGCCGCTGATGCTGATGATCCACGCTGGCTTGTG--GCATGGCTTCCTGT 553
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Db 554 ATGATGTTCCATGCTGGCTGCT-TGGAGAACGTGTGTGTCATCCAGTACCGC 612
QY 499 TTGGGAGCTCTAGTCTTCTAAGTTAAATTCAGAGACCTTAATGTGCCGTAATGCC 558
Db 613 CTGGGTGCTCTGGCTT-----CTTCAGCACTGGAGACAGCAACCGCAACTG 666
QY 559 GGCTTAAGATCAAGTCATGGCTTGCCTTGGATTAAATAATGCGCAACTTGGT 618
Db 667 GGCTACCTGGACCAAGTGGCTGACCTACGCTGGGTCAGAGAAATATCGCCACTTGG 726
QY 619 GGCATCCCGATATATTTACAGTCTTGGTGAAGTCCGCTGCTTACCACTAC 678
Db 727 GGCACCCCTGACCGTTCACCATTTTGGGAGTCTGCGGGTGCAAGTGTGCTTCG 786
QY 679 ATGATGTTAACCGAACAACTCGCGCTTTTCCATCGTGTAT 722
Db 787 CTGTGTGTGCCCCCATATCCCAAGACTCTTCCAGGAGCCAT 830

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3060	99.6	570	18	AAW17768
5	2345	76.3	570	18	AAW17767
6	2006.5	65.3	572	22	ABBS7850
7	1412.5	46.0	567	22	ABBS7857
8	1408.5	45.8	554	22	ABBS7866
9	1389.5	45.2	572	22	ABBS7867
10	1324.5	43.1	554	22	ABBS9161

11	1302.5	42.4	566	22	ABBS1983	Drosophila melanog
12	1295.5	42.2	565	22	ABBS7746	Drosophila melanog
13	1238	40.3	542	22	ABBS7790	Drosophila melanog
14	1228.5	40.0	530	22	ABBS7868	Drosophila melanog
15	1184	38.5	602	23	AAW47598	Drosophila cell cy
16	1073	34.9	551	22	ABBS7788	Drosophila melanog
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27	785.5	25.6	550	22	AAE12910	Ctenocephalides fe
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39	711.5	23.2	575	23	ABBS79538	Carboxylesterase c
40	710	23.1	584	23	ABBS07676	Carboxylesterase d
41	673.5	21.9	527	22	ABBS62353	Drosophila melanog
42	623	20.3	570	19	AAW57860	C. felis esterase,
43	623	20.3	570	22	AAW57879	C. felis esterase,
44	623	20.3	570	22	AAE12915	Ctenocephalides fe
45	623	20.3	595	19	AAW57859	C. felis esterase,

ALIGNMENTS

RESULT 1	ID	AA78142	standard; Protein: 570 AA.
XX	AA78142		
AC	AA78142;		
XX	22-DEC-1995 (first entry)		
XX	OP-sensitive esterase E3.		
XX	Esterase; E3; bioremediation; organophosphate; carbamate;		
KW	Insecticide; pesticide; water decontamination; meat decontamination.		
XX	Lucilia cuprina.		
XX	MO9519440-A1.		
PN	20-JUL-1995.		
XX	13-JAN-1995; 95WO-AU00016.		
XX	13-JAN-1994; 94AU-0003347.		
PR	(CSIR) COMMONWEALTH SCI & IND RES ORG.		
PA	Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;		
PI	Parker AG, Robin GC, Russell RJ, Smyth K;		
PI	WPI: 1995-263870/34.		
DR	N-PSDB: AAQ91561.		
XX	Pure E3 esterase from Lucilia cuprina and related DNA - used to		
PT	eliminate residues of organo:phosphate and carbamate pesticides from		

PT water, meat etc.
 XX
 PS Example 3; Page 12-17; 38pp; English.
 XX
 CC CDNA from organophosphate (OP)-sensitive L. cuprina pupa CDNA
 CC library was amplified using cluster-specific esterase primers.
 CC Isolated clone Lc743, a probable full-length CDNA, was expressed
 CC using a baculovirus vector in insect cells and shown to encode
 CC an OP-susceptible E3 esterase useful in bioremediation.
 CC
 XX

SO Sequence 570 AA:

Query Match 100.0%; Score 3073; DB 16; Length 570;
 Best Local Similarity 100.0%; Pred. No. 7.8e-306; Indels 0; Gaps 0;
 Matches 570; Conservative 0; Mismatches 0;

QY 1 MNEVNSLMEKLLKWKIKCIENKFLNRYLTNETVVAETEKYKGVKRLTYDSDYSYFEG 60
 DB 1 MNEVNSLMEKLLKWKIKCIENKFLNRYLTNETVVAETEKYKGVKRLTYDSDYSYFEG 60
 QY 61 IPYAPPVGELRFKAPQRPPTMDGVRDCCNHKDSVQVDFITGKVCSEDCILYSYTN 120
 DB 61 IPYAPPVGELRFKAPQRPPTMDGVRDCCNHKDSVQVDFITGKVCSEDCILYSYTN 120
 QY 121 LNPETRKRVLYIHGGGFIIGENHRDMYGPDYFIKKDVLLINIQYRLGALGFLSNE 180
 DB 121 LNPETRKRVLYIHGGGFIIGENHRDMYGPDYFIKKDVLLINIQYRLGALGFLSNE 180
 QY 121 LNPETRKRVLYIHGGGFIIGENHRDMYGPDYFIKKDVLLINIQYRLGALGFLSNE 240
 DB 121 LNPETRKRVLYIHGGGFIIGENHRDMYGPDYFIKKDVLLINIQYRLGALGFLSNE 240
 QY 181 NVPGNAGLKDQVMAIRKNNCANFGNPDNTIVGESAGASTHYMMLTEQTRGLFHRG 240
 DB 181 NVPGNAGLKDQVMAIRKNNCANFGNPDNTIVGESAGASTHYMMLTEQTRGLFHRG 240
 QY 241 ILMGNAICPMANTOCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPODLIKLEKYL 300
 DB 241 ILMGNAICPMANTOCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPODLIKLEKYL 300
 QY 301 EERTNKVMPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMGMNTSYEGLEFTSILK 360
 DB 301 EERTNKVMPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMGMNTSYEGLEFTSILK 360
 QY 361 QMPMLVKLETCVNFVPSLADAEPTLLEMGAKIKKAHYTGPTPADNFMDCSHLY 420
 DB 361 QMPMLVKLETCVNFVPSLADAEPTLLEMGAKIKKAHYTGPTPADNFMDCSHLY 420
 QY 421 FWFPNHRLLQIRFNHTSGTPVLYLRFDPSDDLINPYRIMRSGRGVYSHADELTYFEW 480
 DB 421 FWFPNHRLLQIRFNHTSGTPVLYLRFDPSDDLINPYRIMRSGRGVYSHADELTYFEW 480
 QY 481 NQLAKRMPKESREYKTIERTMTGIMIOFATGNPNYSNEIEGMENVSMDPIKSDYVKCLN 540
 DB 481 NQLAKRMPKESREYKTIERTMTGIMIOFATGNPNYSNEIEGMENVSMDPIKSDYVKCLN 540
 QY 541 ISDELKMDVPEMDKIKOMESMFEKHRDL 570
 DB 541 ISDELKMDVPEMDKIKOMESMFEKHRDL 570
 RESULT 2
 ID AAW17765 standard; Protein: 570 AA.
 XX AAW17765;
 AC
 XX 08-AUG-1997 (first entry)
 DT
 XX Lc-alpha-E7 malathion susceptible clone Lc743 esterase E3.
 DE
 XX Malathion carboxylesterase; organophosphate; insecticide;
 KW pesticide; remediation; bioremediation; decontamination; esterase.
 XX Lucilia cuprina.
 OS
 XX
 FH Key Location/Qualifiers

FT Misc-difference 251
 FT /note= "amino acid 251 is Leu in resistant
 FT mutants"

XX W09719176-A1.

XX 29-MAY-1997.

XX 22-NOV-1996; 96NO-AU00746.

XX 23-NOV-1995; 95AU-0006751.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Boyce T, Brownlie JC, Campbell PM, Claudianos C;
 PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

XX WPI: 1997-298113/27.
 XX N-PSDB: AAT68596.

PT DNA encoding enzyme that degrades organophosphate pesticides
 useful for decontamination of soil, water, food etc

PS Disclosure: Fig 1: 52pp; English.

CC Esterase E3 (AAW17765) from a malathion susceptible strain of
 CC Lucilia cuprina differs from an esterase enzyme (see also
 CC AAW17768) from malathion resistant RM8 strains by a Trp for Leu
 CC substn. at amino acid position 251, owing to a mutation in the
 CC encoding DNA sequence (see also AAT68596). The resistant enzyme,
 CC termed malathion carboxylesterase, can be formulated for use in
 CC degrading environmental carboxylester or dimethyl general
 CC organophosphates.

XX Sequence 570 AA:

Query Match 100.0%; Score 3073; DB 18; Length 570;
 Best Local Similarity 100.0%; Pred. No. 7.8e-306; Indels 0; Gaps 0;
 Matches 570; Conservative 0; Mismatches 0;

QY 1 MNEVNSLMEKLLKWKIKCIENKFLNRYLTNETVVAETEKYKGVKRLTYDSDYSYFEG 60
 DB 1 MNEVNSLMEKLLKWKIKCIENKFLNRYLTNETVVAETEKYKGVKRLTYDSDYSYFEG 60
 QY 61 IPYAPPVGELRFKAPQRPPTMDGVRDCCNHKDSVQVDFITGKVCSEDCILYSYTN 120
 DB 61 IPYAPPVGELRFKAPQRPPTMDGVRDCCNHKDSVQVDFITGKVCSEDCILYSYTN 120
 QY 121 LNPETRKRVLYIHGGGFIIGENHRDMYGPDYFIKKDVLLINIQYRLGALGFLSNE 180
 DB 121 LNPETRKRVLYIHGGGFIIGENHRDMYGPDYFIKKDVLLINIQYRLGALGFLSNE 180
 QY 121 LNPETRKRVLYIHGGGFIIGENHRDMYGPDYFIKKDVLLINIQYRLGALGFLSNE 240
 DB 121 LNPETRKRVLYIHGGGFIIGENHRDMYGPDYFIKKDVLLINIQYRLGALGFLSNE 240
 QY 181 NVPGNAGLKDQVMAIRKNNCANFGNPDNTIVGESAGASTHYMMLTEQTRGLFHRG 240
 DB 181 NVPGNAGLKDQVMAIRKNNCANFGNPDNTIVGESAGASTHYMMLTEQTRGLFHRG 240
 QY 241 ILMGNAICPMANTOCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPODLIKLEKYL 300
 DB 241 ILMGNAICPMANTOCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPODLIKLEKYL 300
 QY 301 EERTNKVMPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMGMNTSYEGLEFTSILK 360
 DB 301 EERTNKVMPFGPTVEPYOTADCVLPKHPREMYKTAMGNSIPTMGMNTSYEGLEFTSILK 360
 QY 361 QMPMLVKLETCVNFVPSLADAEPTLLEMGAKIKKAHYTGPTPADNFMDCSHLY 420
 DB 361 QMPMLVKLETCVNFVPSLADAEPTLLEMGAKIKKAHYTGPTPADNFMDCSHLY 420
 QY 421 FWFPNHRLLQIRFNHTSGTPVLYLRFDPSDDLINPYRIMRSGRGVYSHADELTYFEW 480
 DB 421 FWFPNHRLLQIRFNHTSGTPVLYLRFDPSDDLINPYRIMRSGRGVYSHADELTYFEW 480
 QY 481 NQLAKRMPKESREYKTIERTMTGIMIOFATGNPNYSNEIEGMENVSMDPIKSDYVKCLN 540
 DB 481 NQLAKRMPKESREYKTIERTMTGIMIOFATGNPNYSNEIEGMENVSMDPIKSDYVKCLN 540

Db 481 NQLAKRMPKESREKXTERMTGIMIOFATGNPNYSNEIEGMENVSMDPIKKSDEYKCLN 540
 QY 541 ISDELKMDVPEMDKIKOMESMEFEKHDLF 570
 Db 541 ISDELKMDVPEMDKIKOMESMEFEKHDLF 570

RESULT 3

AAW17766
 ID AAW17766 standard; Protein: 570 AA.

AC AAW17766;

XX 08-AUG-1997 (first entry)

DE Malathion carboxylesterase.

XX Malathion carboxylesterase: organophosphate; insecticide;

KW pesticide; remediation; bioremediation; decontamination; esterase;

XX Lucilia cuprina.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 251

FT /label=Leu, Ser, Ala, Ile, Val, Thr, Cys, Met, Gly

FT /note="pref. Leu or Ser"

XX WO9719176-A1.

XX 29-MAY-1997.

XX 22-NOV-1996; 96WO-AU00746.

XX 23-NOV-1995; 95AU-0006751.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Boyce T, Brownlie JC, Campbell PM, Claudianos C;

XX PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

XX DR WPI; 1997-298113/27.

XX DNA encoding enzyme that degrades organophosphate pesticides -

PT useful for decontamination of soil, water, food etc

XX Claim 1; Fig 1: 52pp; English.

XX A malathion carboxylesterase (AAW17766) differs from the esterase

CC (AAW17765) of a malathion susceptible clone of Lucilia cuprina by

CC a substn. of the tryptophan residue at amino acid position 251.

CC The enzyme is capable of hydrolysing carboxylester and/or

CC dimethylloxon organophosphates and can be formulated for use in

CC bioremediation strategies for treating soil or water.

XX SQ Sequence 570 AA;

Query Match 99.6%; Score 3060; DB 18; Length 570;
 Best Local Similarity 99.8%; Pred. NO. 1,7e-304;
 Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 181 NVPGNAGLKDOVMALRMKNNKNCANEGNPNINITVFGESAGASTHYMLTROTGLFPHG 240
 Db 181 NVPGNAGLKDOVMALRMKNNKNCANEGNPNINITVFGESAGASTHYMLTROTGLFPHG 240
 QY 241 ILMGNAICPWANTOCQHRAFTLAKLAGYKGEDNDKDVLEFLMAKAPODLILKEKVLTL 300
 Db 241 ILMGNAICPWANTOCQHRAFTLAKLAGYKGEDNDKDVLEFLMAKAPODLILKEKVLTL 300
 QY 301 EERTNKVMEPPGPVPEYQADCVLPKHPRMVKVTAMGNSIPTMGNTSYGLEFTSTLK 360
 Db 301 EERTNKVMEPPGPVPEYQADCVLPKHPRMVKVTAMGNSIPTMGNTSYGLEFTSTLK 360
 QY 361 QMPVLVELETCVNFVPSLADARTAPETLEMGAKIKKAVTGTPPADNFMDCSHY 420
 Db 361 QMPVLVELETCVNFVPSLADARTAPETLEMGAKIKKAVTGTPPADNFMDCSHY 420
 QY 421 FMPFMHRLQLRFNHTSGTPVYLRFDFDSBDLINPYRIMSGRGVKVSHADELTFPFW 480
 Db 421 FMPFMHRLQLRFNHTSGTPVYLRFDFDSBDLINPYRIMSGRGVKVSHADELTFPFW 480
 QY 481 NQLAKRMPKESREKXTERMTGIMIOFATGNPNYSNEIEGMENVSMDPIKKSDEYKCLN 540
 Db 481 NQLAKRMPKESREKXTERMTGIMIOFATGNPNYSNEIEGMENVSMDPIKKSDEYKCLN 540
 QY 541 ISDELKMDVPEMDKIKOMESMEFEKHDLF 570
 Db 541 ISDELKMDVPEMDKIKOMESMEFEKHDLF 570

RESULT 4

AAW17766
 ID AAW17766 standard; Protein: 570 AA.

AC AAW17766;

XX 08-AUG-1997 (first entry)

DE Malathion carboxylesterase RM8Con.

XX Malathion carboxylesterase: organophosphate; insecticide;

KW pesticide; remediation; bioremediation; decontamination; esterase;

XX Lucilia cuprina.

OS Lucilia cuprina.

XX WO9719176-A1.

XX 29-MAY-1997.

XX 22-NOV-1996; 96WO-AU00746.

XX 23-NOV-1995; 95AU-0006751.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Boyce T, Brownlie JC, Campbell PM, Claudianos C;

XX PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;

XX DR WPI; 1997-298113/27.

XX DNA encoding enzyme that degrades organophosphate pesticides -

PT useful for decontamination of soil, water, food etc

XX Claim 6; Fig 1: 52pp; English.

XX A malathion carboxylesterase (AAW17768), designated RM-8Con, differs

CC from the esterase (AAW17765) of a malathion susceptible clone of

CC Lucilia cuprina by a substn. of the tryptophan residue at amino

CC comparison to reference susceptible clone LC743 (AAT68596) of
 CC Lc-alpha-E7. The enzyme is capable of hydrolysing carboxylester
 CC and/or dimethylloxon organophosphates and can be formulated for use
 CC in bioremediation strategies for treatment of soil or water.

XX Sequence 570 AA:

Query Match 99.6%; Score 3060; DB 18; Length 570;
 Best Local Similarity 99.8%; Pred. No. 1.7e-304;
 Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 MNFNYSLEMEKLMKWKIKCIENKFLNRLTNTNETVAETEGYKVKYKRLTYDDSYSEEG 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MNFNYSLEMEKLMKWKIKCIENKFLNRLTNTNETVAETEGYKVKYKRLTYDDSYSEEG 60
OY 61 IRYAOPVPGELRFPKAPQRPPTPMDGVDCCNHDKSVQVDFITGKVCSEDDCLYLSVTNN 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 IRYAOPVPGELRFPKAPQRPPTPMDGVDCCNHDKSVQVDFITGKVCSEDDCLYLSVTNN 120
OY 121 LMPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLINIOYRLGALGFLSINSEDL 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 LMPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLINIOYRLGALGFLSINSEDL 180
OY 181 NYPGNAGLKDQYVALRMKIKNNCANFGNPDNTTVEGSAASHTHYMMLTEOTRGLFHRG 240
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 NYPGNAGLKDQYVALRMKIKNNCANFGNPDNTTVEGSAASHTHYMMLTEOTRGLFHRG 240
OY 241 ILMGNAICPMWANTOCQOHRATFLAKAGYKGEDNDKVDLEFLMKAKPDLIKLEEKVLT 300
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 ILMGNAICPMWANTOCQOHRATFLAKAGYKGEDNDKVDLEFLMKAKPDLIKLEEKVLT 300
OY 301 EERTNKVMPFPGTTPRYOTADCVLPKHPRKEMVKTAMGNSIPTMGNTSYEGLEFSTILK 360
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 301 EERTNKVMPFPGTTPRYOTADCVLPKHPRKEMVKTAMGNSIPTMGNTSYEGLEFSTILK 360
OY 361 QMPLVKELETQVNFVPSSELADEARTAPETLENGAKIKAAHYGETPTADNEMDLCSHY 420
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 361 QMPLVKELETQVNFVPSSELADEARTAPETLENGAKIKAAHYGETPTADNEMDLCSHY 420
OY 421 FWPBMRRLQLRNHTSGTPVLYLRDPDSEDLINPYRIMSRGRGVKGVSHADELTYPFW 480
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 421 FWPBMRRLQLRNHTSGTPVLYLRDPDSEDLINPYRIMSRGRGVKGVSHADELTYPFW 480
OY 481 NOLAKRMPKESREYKTIERTMTGIMIOFATTGNDPYSNEIEGEMENVSDPIKSDVYKCLN 540
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 481 NOLAKRMPKESREYKTIERTMTGIMIOFATTGNDPYSNEIEGEMENVSDPIKSDVYKCLN 540
OY 541 ISDELKMIIDVPENDKIKQWESMEKRDLP 570
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 541 ISDELKMIIDVPENDKIKQWESMEKRDLP 570

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RESULT 5
 AAM17767
 ID AAM17767 standard: Protein: 570 AA.

XX AAM17767:

XX 08-AUG-1997 (first entry)

XX Md-alpha-E7 malathion resistant mutant.

XX Malathion carboxylesterase; organophosphate; insecticide;

XX pesticide; remediation; bioremediation; decontamination.

XX Musca domestica Rutgers strain.

XX Key Location/Qualifiers

XX Misc-difference 251 /note= "Ser-251 is tryptophan in the susceptible
 FT allele expression product"

XX W09719176-A1.

XX 29-MAY-1997.
 PD 22-NOV-1996; 96MO-AU00746.
 PF 23-NOV-1995; 95AU-0006751.
 PR (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA Boyce T, Brownlie JC, Campbell PM, Claudianos C;
 PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
 PS WPI: 1997-298113/27.
 DR N-PSDB: AAT68597.

XX DNA encoding enzyme that degrades organophosphate pesticides -
 PT useful for decontamination of soil, water, food etc
 PS Disclosure: Fig 3; 52pp; English.

CC A polypeptide (AAM17767) is the expression product of a malathion
 CC resistant allele of the Musca domestica Md-alpha-E7 gene, and
 CC contains a Ser for Trp substn. at amino acid position 251. The
 CC enzyme is capable of hydrolysing carboxylester and/or
 CC dimethylloxon organophosphates and can be formulated for use
 CC in bioremediation strategies for treatment of soil or water.

XX Sequence 570 AA:

Query Match 76.3%; Score 2345; DB 18; Length 570;
 Best Local Similarity 74.4%; Pred. No. 4.1e-231;
 Matches 424; Conservative 71; Mismatches 75; Indels 0; Gaps 0;

```

OY 1 MNFNYSLEMEKLMKWKIKCIENKFLNRLTNTNETVAETEGYKVKYKRLTYDDSYSEEG 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MNFNYSLEMEKLMKWKIKCIENKFLNRLTNTNETVAETEGYKVKYKRLTYDDSYSEEG 60
OY 61 IRYAOPVPGELRFPKAPQRPPTPMDGVDCCNHDKSVQVDFITGKVCSEDDCLYLSVTNN 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 IRYAOPVPGELRFPKAPQRPPTPMDGVDCCNHDKSVQVDFITGKVCSEDDCLYLSVTNN 120
OY 121 LMPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLINIOYRLGALGFLSINSEDL 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 LMPETKRPVLYIHGGGFTIGENHRDMYGPDYFIKKDVLINIOYRLGALGFLSINSEDL 180
OY 181 NYPGNAGLKDQYVALRMKIKNNCANFGNPDNTTVEGSAASHTHYMMLTEOTRGLFHRG 240
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 NYPGNAGLKDQYVALRMKIKNNCANFGNPDNTTVEGSAASHTHYMMLTEOTRGLFHRG 240
OY 241 ILMGNAICPMWANTOCQOHRATFLAKAGYKGEDNDKVDLEFLMKAKPDLIKLEEKVLT 300
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 ILMGNAICPMWANTOCQOHRATFLAKAGYKGEDNDKVDLEFLMKAKPDLIKLEEKVLT 300
OY 301 EERTNKVMPFPGTTPRYOTADCVLPKHPRKEMVKTAMGNSIPTMGNTSYEGLEFSTILK 360
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 301 ERTNKVMPFPGTTPRYOTADCVLPKHPRKEMVKTAMGNSIPTMGNTSYEGLEFSTILK 360
OY 361 QMPLVKELETQVNFVPSSELADEARTAPETLENGAKIKAAHYGETPTADNEMDLCSHY 420
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 361 QMPLVKELETQVNFVPSSELADEARTAPETLENGAKIKAAHYGETPTADNEMDLCSHY 420
OY 421 FWPBMRRLQLRNHTSGTPVLYLRDPDSEDLINPYRIMSRGRGVKGVSHADELTYPFW 480
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 421 FWPBMRRLQLRNHTSGTPVLYLRDPDSEDLINPYRIMSRGRGVKGVSHADELTYPFW 480
OY 481 NOLAKRMPKESREYKTIERTMTGIMIOFATTGNDPYSNEIEGEMENVSDPIKSDVYKCLN 540
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 481 NOLAKRMPKESREYKTIERTMTGIMIOFATTGNDPYSNEIEGEMENVSDPIKSDVYKCLN 540
OY 541 ISDELKMIIDVPENDKIKQWESMEKRDLP 570
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 541 ISDELKMIIDVPENDKIKQWESMEKRDLP 570

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RESULT 6

ABB57850 ID ABB57850 standard; Protein: 572 AA.

XX ABB57850;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 342.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmacological.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL01953.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions -

XX Disclosure; SEQ ID NO 342; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (AB16176-AB130511), expressed DNA

XX sequences (AB101840-AB16175) and the encoded proteins

XX (ABB57737-ABB72072).

XX The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 572 AA;

XX

XX

DB 241 ILQSGSALCPMAYNDITHNPIRIAKLVGYGENDKDYLEFLOVNAKKDLIREENVLT 300

QY 300 LEERTNKVMPFPGTVEPYQTADCVLPKHPREMYKTANGNSIPTMGNTSYGLFTSTIL 359

DB 301 LEERNMKNIMFAPGSLPEFSTPECVYSKPKEMKMTAMNSNIPMIGTSTYEGILMVEY 360

QY 360 KQMPMLVKELETQVNFVSELDADERTAPETLEMGAKIKKAAHYGETPTADNFDLCSHI 419

DB 361 KLMPQVLOQLDAGTPEFIRKELLATEPESKEKLSMSAQIRDVHRTSESTPNYDLCSTY 420

QY 420 YFMPFMRLLOLRNHTSGTPVLYLRFPDSEEDILNPRIMSGRGVSHADELYEYF 479

DB 421 YFVFPALRVSHRNAYAGAVYFRYDFDSEELFPRIIRLRGAGVSHADLSTQF 480

QY 480 WNOIAKRPKESREYKTIERTMTGMIOPATGPNPISNEIEGEMVSWDPKRSDEYKCL 539

DB 481 SSLARLRPKESREYKTIERTMTGMIOPATGPNPISNEIEGEMVSWDPKRSDEYKCL 540

QY 540 NISDELKMDYPEMDKIQWESMPEKHRDL 569

DB 541 NISDLKFTIDLPEWPKLWESLYDDNKDL 570

RESULT 7

ABB57857 ID ABB57857 standard; Protein: 567 AA.

XX ABB57857;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 363.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmacological.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL01960.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions -

XX Disclosure; SEQ ID NO 363; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

SQ Sequence 567 AA:

Query Match 46.0%; Score 1412.5; DB 22; Length 567;
Best Local Similarity 48.6%; Pred. No. 2.1e-135;
Matches 267; Conservative 105; Mismatches 164; Indels 13; Gaps 6;

QY 26 RLTTNEVVAETEGKVKYKRLTYDSDYSEEGIPYAOYPVGELEFKAPQRETPMDGV 85
D 19 RLRSNDVIADTYGKVKYKQSIYGNNSYSEGIPEFKAPVGELEFKAPVREHMSDV 78
QY 86 RDCNHRDKSVQYDFITGKCGSEDCLYLSTYNNLNLPETKRPVLYIHGGELIGENHR 145
D 79 KRCHVAKACQVNYITLQVQSEDCLYLVNRYELPHRPLVLYIGGEGOMGASR 138
QY 146 DMGPDYFIKRDVYLNIQYRLGALGFLSINSEDLNVPNAGLKDOVMALRMKNCANF 205
D 139 DLVSPOYIMHEVLYVYISRLALGFLSLADELDVPGNAGLKDOVMALRMKNCQFT 198
QY 206 GGNPDITVGEESAGAASHTYMLTEQTRGLFHRGILMSGNAICPMANTQCO-HRAFTLA 264
D 199 GGDNDITVGEESAGASTHYMLTDQAKGLFHKTIIMSSALAPMAQPTTHINMPYRLA 258
QY 265 KLAGYGEDNDKDVLEFLMKAKPODLIKLEKYLLEERTNKY-MRPEGTVPYQTAOC 323
D 259 QATGYTGADANDRIEFAHLKKCKASSMLKVAEDITTEERHQRULTMFSFGTIEPYLPHC 318
QY 324 VLPKHPREYKWTAMGNSIPTMGNTSYEGLEFSTILKOMPLVKELETGVNPESELA 383
D 319 VIRKSLFEMRDMCGNSIPVIGNSFEGILMPPEVKNKPELLCOGDCDENLAPQ--DA 375
QY 384 ERTAPTELEMGAKIKKAHTGTET--TADNFDLCSHIYFEPHRLQLRPNHTSGRP 440
D 376 HDEQORAKFAKVKRLTYGDRTPGKRKTLLEYSDLSFYKFWGHIRHTLSRAHNAFLAP 435
QY 441 VYLPRDPESEDLINPYRIMRSGRGVYSHADELTFPFMNOLAKRMPRESREYKTEEM 500
D 436 TFLYRDPDSKH-FNIMRIITGRKVRGCHADDSLYLFYMAAKLKRRTAEFKITIKRL 494
QY 501 TGTWIOFATTGNP---YSNEIEGMENVSMDPIKSKDEYVKKCLNISDELKMDIVPEMDKI 556
D 495 VSVNVAEFAISGDPNIPWQDEKEQPRGAMLPISKDKVFOCLINSHDVHIDLPEAKEL 554
QY 557 KOMESMEK 565
D 555 RLMDCLTYDR 563

RESULT 8
ABB57866
ID ABB57866 standard; Protein; 554 AA.
XX
AC ABB57866;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide seq ID NO 390.
XX
KW Drosophila: developmental biology; cell signalling; insecticide; pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN MO200171042-A2.
XX
PD 27-SEP-2001.
XX
PE 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX

PI Venter JC, Adams M, Li PWD, Myers EM;
XX
DR WPI: 2001-656860/75.
DR N-PSDB: ABL01969.
XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX

PS Disclosure: SEQ ID NO 390; 21pp + Sequence Listing; English.
XX

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL57737-ABR72072).
CC (ABR57737-ABR72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPD
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 554 AA:

Query Match 45.8%; Score 1408.5; DB 22; Length 554;
Best Local Similarity 48.5%; Pred. No. 5.1e-135;
Matches 269; Conservative 95; Mismatches 178; Indels 13; Gaps 6;

QY 18 IENKFLNRYRLTNETVVAETEGKVKYKRLTYDSDYSEEGIPYAOYPVGELEFKAPQ 77
D 2 VDFKYOQRRYRTSEKTVSTYTGPIKGVKRSIYQSVSFERRIFAPRPVGELEFKAPQ 61
QY 78 RPTPMDGVADCCNHDKSVQVDFITGKCGSEDCLYLSTYNNLNLPETKRPVLYIHGG 137
D 62 PBEVTEVASTCSQGPRLQKHVEEMTDGSEDCLYLVNRYELNLYPTPMYPMWYIGG 121
QY 138 FLIGENHRDMYGPDYFIKRDVYLNIQYRLGALGFLSINSEDLNVPNAGLKDOVMALRM 197
D 122 PFGGASRRCYSPODLLRNDVYISINRYRLGFLCLDDPDLVPGNAGLKDOVMALRM 181
QY 198 IKNNCANFGNPDNITVGEESAGAASHTYMLTEQTRGLFHRGILMSGNAICPMANTQCO 257
D 182 YKANSRFGDSANITIFGDSASAVHYMMITEQTHGLFHKALCMSGNTLSPMAVTPQR 241
QY 258 HRAFTLAKAGYKGEDNDKDVLEFLMKAKPODLIKLEKYLLEERTNKYMRPEGTVPY 317
D 242 NMPYRLAVQAGTAGENNTRDYWEFLKNAKGSBITKANGELCIDEEKKRIEFSFGPIEP 301
QY 318 YOTADCVLPKHPREYKWTAMGNSIPTMGNTSYEGLEFSTILKOMPLVKELETGVNPE 377
D 302 YVTSCHVPPKRIEMRTAMSNINIPLLIGVSNBGLLYSEKINPKCLNLDRCRFVPR 361
QY 378 SELDAERTAPTELEMGAKIKKAHTGTETPAD--NMDLCSHIYFEPHRLQLRPN 434
D 362 TEL-NMDRESALCREYGOQLRCQYGDYTPSLDLEHVLQWVSHYEFPIYRTVLSLQ 420
QY 435 HTSGPYVLYRFEDESEDLINPYRIMRSGRGVYSHADELTFPFMNOLAKRMPRESREY 494
D 421 YARSAPTYLRFDPDSKH-FNHLRLTSGKVRGCHADDSLYLFYSLAKLKNHTREY 479
QY 495 KTIEMTGIWIOFATTGNP-YSNEIEGMENVSMDPIKSKDEYVKKCLNISDELKMDIV 550
D 480 KCIERLVGLMTHTFAACGPNPDPEQEDL---WQPVPAAEVKEQLCLNISDELKMDIV 535
QY 551 PEMDKIKOMESMEK 565
D 536 PDLKKLMWVESFRR 550

RESULT 9
ABB57867
ID ABB57867 standard; Protein; 572 AA.


```

XX XX Drosophila melanogaster polypeptide SEQ ID NO 30.
DE DE
XX XX Drosophila: developmental biology; cell signalling; insecticide;
KM KM pharmaceutical.
XX XX Drosophila melanogaster.
OS OS
PN PN WO200171042-A2.
XX XX
PD PD 27-SEP-2001.
XX XX
XX XX 23-MAR-2001; 2001WO-US09231.
PF PF
PR PR 23-MAR-2000; 2000US-191637P.
PR PR 11-JUL-2000; 2000US-0614150.
XX XX
PA PA (PEKE ) PE CORP NY.
PI PI
PI PI Venter JC, Adams M, Li PWD, Myers EW;
XX XX
XX XX WPI: 2001-656860/75.
DR DR N-PSDB; ABL01849.
XX XX
XX XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT PT interactions -
XX XX
XX XX Disclosure: SEQ ID NO 30; 21pp + Sequence Listing; English.
XX XX
XX XX The invention relates to an isolated nucleic acid detection reagent
CC CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC CC useful in developmental biology and in elucidating cell signalling and
CC CC cell-cell interactions in higher eukaryotes for the development of
CC CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC CC sequences (AB101840-AB16175) and the encoded proteins
CC CC (AB57737-AB572072).
CC CC The sequence data for this patent did not form part of the printed
CC CC specification, but was obtained in electronic format directly from WIPO
CC CC at ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX XX Sequence 565 AA;
SQ SQ
Query Match 42.2%; Score 1295.5; DB 22; Length 565;
Best Local Similarity 45.2%; Pred. No. 2,1e-123;
Matches 265; Conservative 98; Mismatches 186; Indels 37; Gaps 12;
QY 1 MNFNLSMEKLKWKIKCIENKFLNRLTNTNETVVAETEXGKGVKRLVYDSS-YSPF 59
DB 1 MEIRGVGDLLKMGTKRLIGHKIVORYRLGTQTKVCTRDGVGRHRRRLVDEEMTFPE 60
QY 60 GIPVQPPVGELEFRAPORPTPMDGVRDCCNHHKDSVOVDFTTGVCSSEDCVLVSYTN 119
DB 61 GIPFQAPVGELEFRAPORPTPMDGVRDCCNHHKDSVOVDFTTGVCSSEDCVLVSYTN 120
QY 120 NLNPTKRPVLVYTHGGFIIENHRDMYGPDTFKKQVNLINIOYRIGALGFLSLNSD 179
DB 121 RRSRSPKPLVYTWITGGFQGEAGRDYSPDYFMQODVVVTFYRVGALGFLSLARD 180
QY 180 LNVPGNAGLKDOVALRMVTKNCCANFGNPNDIITFEGESAGASAHYMWLFEOTGGLFHR 239
DB 181 LDVPGNAGLKDOVALRMVTKNCCANFGNPNDIITFEGESAGASAHYMWLFEOTGGLFHR 240
QY 240 GILMSGNAICPWANTQCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKQDOLIKLEKYL 299
DB 241 AIMQSGSMCEWANEPSRMAAYRLACQGYSGSENEKEVFRYIQAPASEMAAQGITLV 300
QY 300 LEEKRNKVMFPFGPYVEYQTFADCVLPKHPREMYKTANGNSIPTMMGNTSYGLF-FISI 358
DB 301 QEERQOYVLFPTTPEVPEYITRDVCLPCHREMLPEAWGNDPLLLGGSFSGFLSYOST 360
QY 359 LKQMDLVKLEETGVNFVPSLEADAERTAPETLEMGAKIKKAHYTGPTADNFMDL--- 415

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DB 361 LHDEEHMLSAFV---LIPREIRE-KSTQSHLKDLLRQK-----VDFPDATRG 406
QY 416 -----CSHI---YFPEPMRLQLRENHNSGTPVLYRDPFDEDLINPRIMSGRG 465
DB 407 RMEFNECHLISLVKHFHWGIIHRTVLAISHADATPTLYLRFPVDSFH-FNHRQVWCGKH 465
QY 466 VKGVSHADELTYPFNQOLAKRMPKRESREKTERMTGMIQOFATGPNPSNEIEGHN 525
DB 466 VRGVSHADDLSTLYFHILLANKVKDKSSMEYOTQRLGVGMVAFAKNDNCPQI---GPTT 522
QY 526 WDP1-KKSDVYKCLINSDLMKIDVPEMDKIKOMESMEKRDLP 570
DB 523 WEALDEKGPOM--CLNIGKQLEFIYLPESKQRINDRLYDKN-DLF 565
RESULT 13
ABB57790
ID ABB57790 standard; Protein; 542 AA.
XX XX
XX XX ABB57790;.
AC AC
XX XX 26-MAR-2002 (first entry)
DT DT
XX XX
DE DE Drosophila melanogaster polypeptide SEQ ID NO 162.
XX XX
XX XX Drosophila: developmental biology; cell signalling; insecticide;
KM KM pharmaceutical.
XX XX
OS OS Drosophila melanogaster.
XX XX
XX XX WO200171042-A2.
XX XX
XX XX 27-SEP-2001.
PD PD
PF PF 23-MAR-2001; 2001WO-US09231.
PR PR
PR PR 23-MAR-2000; 2000US-191637P.
PR PR 11-JUL-2000; 2000US-0614150.
XX XX
XX XX (PEKE ) PE CORP NY.
PA PA
PI PI Venter JC, Adams M, Li PWD, Myers EW;
XX XX
XX XX WPI: 2001-656860/75.
DR DR N-PSDB; ABL01893.
XX XX
XX XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT PT interactions -
XX XX
XX XX Disclosure: SEQ ID NO 162; 21pp + Sequence Listing; English.
XX XX
XX XX The invention relates to an isolated nucleic acid detection reagent
CC CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC CC useful in developmental biology and in elucidating cell signalling and
CC CC cell-cell interactions in higher eukaryotes for the development of
CC CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC CC sequences (AB101840-AB16175) and the encoded proteins
CC CC (AB57737-AB572072).
CC CC The sequence data for this patent did not form part of the printed
CC CC specification, but was obtained in electronic format directly from WIPO
CC CC at ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX XX Sequence 542 AA;
SQ SQ
Query Match 40.3%; Score 1238; DB 22; Length 542;
Best Local Similarity 45.7%; Pred. No. 1.6e-117;
Matches 251; Conservative 93; Mismatches 177; Indels 28; Gaps 11;
QY 31 ETVVAETEXGKGVKRLVYDSSYSGIYAAPVGELEFRAPORPTPMDGVRDCCN 90
DB 31 ETVVAETEXGKGVKRLVYDSSYSGIYAAPVGELEFRAPORPTPMDGVRDCCN 90

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Db 8 ETCETLTPVGQIKGVKRLSYDDPFSEFKIPFAKPELGELEFRAPVADPMSGVLCTH 67
 Qy 91 HNDKSVQDFITGKVCSEDLCLYLSVTNNLNLPETKRPVLVYIHGGFLLIGENHRDMYGP 150
 Db 68 YAEKPTQKRLREIEGGEDCLYLVNSQKLSEKRLPVYMYIYGAVTGEATRELXGP 127
 Qy 151 DYFIKRDVLLINIOYRLGALGFLSLNSEDLVNPGNAGLKDOVMALRWIKNCANCGNPD 210
 Db 128 DYFMTKDVLTLYNLRVDCLEGLSLKDPFLKYPGNAGLKDQVLAALKWKQYLSNNGDS 187
 Qy 211 NITVGESEGAASHTYHMLTEQTRGLFHNGILMSGNALICPMANTQCOHRAFTLAKLAGYK 270
 Db 188 NITVEESAGGCTHFMCTEOTRGLFAITPMISGTVHMYMANNAEDAFRLAQONGET 247
 Qy 271 GEDNDKDVLEFLMKAKRPODLIKLEEKVLTLEERTNKVMPREPRVPEYQADCVLPKHNR 330
 Db 248 GEMDAKAVLEYLQGVAPADLV--NHNLTPREHNRNGLLEAFSPVTEAVYGECCVYKPRPV 305
 Qy 331 EMVKITAMGNSIPTMGNTSEYEGLEF---TSLIKQMPMLVKELETCVNPVPSLADAE-R 385
 Db 306 EMARDAMSNFPVMLGTSFEGLEMTPAVSANKALDLSQD-----PRLVAVDVR 357
 Qy 386 TA---PETLEMGAKIKKAVTGETPTAD--NEMDLSHIYEWEPHMLLQLEFNTSGT 439
 Db 358 TVSEKENLEYSORLMAKATGYSRPSSELLNMLDFYSYKIFWHGFRTEFNALTYAK-A 416
 Qy 440 PVLVYRPDESDCLINPYRIMKSGRGYK-GVSHADELTFFENQOLAKRMPKESREKITE 498
 Db 417 PLYVYRPDESPN-FNEYRAKFCGDKIKTGVAHADLSYLFNAGSMKLDKTSAEYRTIE 475
 Qy 499 RMGVIWQFPTGNGPNYSNIEGEMENSWDPIKKSDEYVKCLNTSDELMKIDVEMDKIKO 558
 Db 476 RMGIVTAFAATSNPCPELGHLE--WKPSYKNDP-KRYINISDQVTLIDPEYEKLOI 531
 Qy 559 WESMEFKHR 567
 Db 532 WDNLYKPNQ 540

RESULT 14
 ABB57868 standard; Protein: 530 AA.
 ID ABB57868
 AC ABB57868;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 396.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX
 OS Drosophila melanogaster.
 PN
 PD WO200171042-A2.
 XX
 DT 27-SEP-2001.
 XX
 PE 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 PI
 PI Venter JC, Adams M, Li PWD, Myers EW;
 DR WPI: 2001-656860/75.
 DR N-PSDB: ABL01971.
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX
 PS Disclosure; SEQ ID NO 396; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB10840-AB116175) and the encoded proteins
 CC (AB57737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SO Sequence 530 AA;
 Qy 40 GKVKGVKRLTYDSDYSYFEGIPYAPVGELEFRAPQRPYMDGVDRDCCNKKDSVQVD 99
 Db 5 GYVKGKNTIMGSGYFSEFKIPFAKRPVGLDRKAPAVRPMQELDCTSPADKPIQTH 64
 Qy 100 FITGKVCSEDLCLYLSVTNNLNLPETKRPVLVYIHGGFLLIGENHRDMYGPDYFIKRDV 159
 Db 65 MFPRKYGASEDCLYLVNYYVKKLPDRLRPVWYIYGAVTGEATRELXGP 124
 Qy 160 LNIQYRLGALGFLSLNSEDLVNPGNAGLKDOVMALRWIKNCANFGGPNITVFGESA 219
 Db 125 IYVAVRIGALGFLSLDLPQNLVPGNAGLKDOVMALRWVQONIEAFGDSNNITLFGESA 184
 Qy 220 GAASHTYHMLTEQTRGLFHNGILMSGNALICPMANTQCOHRAFTLAKLAGYGEENDKYL 279
 Db 185 GASTHFLALSPQTEGLIKALVMSGSYVLCPTQPRNNMAYRLQKLYGDNDKDAIF 244
 Qy 280 EFLMKAKPODLIKLEKVLTLEERTNKVMPREPRVPEYQADCVLPKHPREMYTAGN 339
 Db 245 EFLRMSGGEIYKATATVLSNDEKHHRLFAFGVYVEYRTTHYVAAQPHLMQNSH 304
 Qy 340 SIPTMGNTSYEGLEFSTSLIKQMPMLVKELETCVNPVPSLADAEARTPETLE-MGAKIK 398
 Db 305 RIPMFGGTSFEBLIFYPEVSRPATLDEVGNCKNLPSDL--GLNDPKLEENYGLQK 362
 Qy 399 KAHVTEPTADN--FMDLSHIYFWPMMHLLQLEFNTSGTVYLYRPDESDCLIN 455
 Db 363 KAYFGDEPCNOANMKFLELCYSREFMHIYRAALNRVROSS-APYILRFPHDSK-LCN 420
 Qy 456 PYRIMSGRGVKGSHADELTFFENQOLAKRMPKESREKITERMTGIWQFATGPNYS 515
 Db 421 ATRIVLCGHOMRGVCHGDDCLYFHSMLSHQSPDSEHKVITGMVDVTSFAHGDPP-- 478
 Qy 516 NETEGMENSWDPIKKSDEYVKCLNTSDELMKIDVEMDKIKO-WESMEFKHR 567
 Db 479 -NCESIKSLKFAPIENVTN-FKCLINIGDQFEVWALPELOKIEPVMSYFAPMK 529

RESULT 15
 AAM47598 standard; Protein: 602 AA.
 ID AAM47598
 AC AAM47598;
 XX
 DT 12-FEB-2002 (first entry)
 XX
 DE Drosophila cell cycle progression protein #27.
 XX
 KW Antiproliferative; cytoskeletal; cardiac; immunosuppressive; meiosis;
 KW antiinflammatory; antiproliferative; dermatological; antifungal; mitosis;
 KW antiparasitic; antimalarial; antineoplastic; antitubercular; cell division;
 KW cell cycle progression protein; tumour; proliferative disorder;
 KW cardiovascular; autoimmune; dermatological disorder.

[illegible][illegible]

Search completed: April 4, 2003, 09:13:00
Job time : 47.0154 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:10:33 ; Search time 19.0734 Seconds

(without alignments)
2872.940 Million cell updates/sec

Title: US-09-776-910-8

Perfect score: 3073
Sequence: 1 MNFNVSIMKELKWKIKICIN.....PEMDKIKQWSEKRDLE 570Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

PIR-73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1038	33.8	540	2	A35986
2	1035	33.7	540	2	S53370
3	1025	33.4	540	2	S53371
4	929	30.2	503	2	S53372
5	691	22.5	564	2	A34325
6	593	19.3	578	2	F89068
7	593	19.3	658	2	T32053
8	585.5	19.1	547	2	S53233
9	578.5	18.8	489	2	B69680
10	571.5	18.6	583	2	T25690
11	568.5	18.5	564	1	S36787
12	568.5	18.5	602	1	ACHU
13	567	18.5	552	2	S36786
14	565.5	18.4	596	1	ACRYE
15	564.5	18.4	614	2	JH0314
16	558.5	18.2	599	1	A38868
17	557	18.1	746	2	A25363
18	556.5	18.1	614	2	JH0811
19	549.5	17.9	583	1	S10712
20	548.5	17.8	561	2	S47655
21	547.5	17.8	561	2	S47655
22	545	17.7	614	2	C39768
23	538	17.5	562	2	S27782
24	537	17.5	584	2	S48724
25	536	17.5	511	2	D70944
26	536	17.4	548	2	T32907
27	536	17.4	557	2	A47162
28	535	17.4	544	2	A34089
29	535	17.4	544	2	A41426

30	535	17.4	544	2	B40122	carboxylesterase (
31	535	17.4	548	2	A28022	carboxylesterase (
32	534	17.4	544	2	C41426	carboxylesterase (
33	534	17.4	544	2	A40122	carboxylesterase (
34	533.5	17.4	544	2	H41426	carboxylesterase (
35	533.5	17.4	691	2	JE0150	acetylcholinestera
36	533	17.3	544	2	F41426	carboxylesterase (
37	530	17.2	544	2	B41426	carboxylesterase (
38	530	17.2	544	2	D41426	carboxylesterase (
39	528.5	17.2	545	2	S58982	carboxylesterase (
40	528.5	17.2	545	2	S58968	carboxylesterase (
41	528.5	17.2	545	2	S58977	carboxylesterase (
42	528	17.2	544	2	E41426	carboxylesterase (
43	527.5	17.2	544	2	E41426	carboxylesterase (
44	527.5	17.2	545	2	S58972	carboxylesterase (
45	526.5	17.1	545	2	S58980	carboxylesterase (

ALIGNMENTS

RESULT 1

esterase B1 - southern house mosquito

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)

C:Date: 16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change 21-Jul-2000

C:Accession: A35986

R:Mouches, C.; Pauplin, Y.; Agarwal, M.; Lemieux, L.; Herzog, M.; Abadon, M.; Beyssat

Proc. Natl. Acad. Sci. U.S.A. 87, 2574-2578, 1990

A:Title: Characterization of amplification core and esterase B1 gene responsible for

A:Reference number: A35986; MUID:90207238; PMID:2320576

A:Accession: A35986

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-540 <MOD>

A>Note: The authors translated the codon CGT for residue 213 as Ala, and CGT for resi

C:Superfamily: cholinesterase; cholinesterase homology

Query Match	33.8%	Score 1038;	DB 2;	Length 540;
Best local similarity	37.9%	Pred. No. 1,4e-72;		
Matches 206;	Conservative 114;	Mismatches 201;	Indels 22;	Gaps 8;
QY	31	ETVAETETGKVKVKRLTYDDSYFEGIPYQPPVGEIRFRAPOPTWMDVRC--	88	
DB	4	ESLIVQTRKGVKRVNLSLQGEYVFOGIPYARABEGELFRFAPVPPOKMTLDCQ 63		
QY	89	-----CNHKDKSVQYDFITGKVGSEDCLYSVYNNLNPETKRPVLVYIHGGFTIGENH 144		
DB	64	QCEPCYHFDRLQ-----KIVGCEDSLKINVFKEINPSTPLVYMLTYIGGFTIGTS 117		
QY	145	RDWGPVYFIKKDVLINIOYRIGALGFLSUNSDLVNPNAGLKDQYALRWIKNNCAN 204		
DB	118	TELGPFLVQKDLIVLSFNVRIGALGFLCQSDQDVPNAGLKDQYALRWILENTIAA 177		
QY	205	FGGPNMTITVGEASASTHYMLTEQTRGLFIRGILMSGNALCPRANQOCORAFITLA 264		
DB	178	FGGPKRVTLTLAGSAGASVQVHLISDASKDLFRRIRLWMSGSTVSSWLTQRWVEXLA 237		
QY	265	KLAVYKEDNDKDVLEFLMKAKPODLIKLEEKVLTLEERTKVMFPPTVEPYQTADCV 324		
DB	238	KALGWDOGGSSGLRLFRRAKRPEDIYAHQKLLTDQMODDITTPGPTVEPYLTGCI 297		
QY	325	LPKHREVMVKTAWGNSIPTMKNSTSYGLFTSTLKQMPMLVKELETCVNPSELDAAE 384		
DB	298	IPKAPFEMARATWMDKIDIMIGTSEGLDLQIKILHPELLSHPHLFLGWPNPL--K 354		
QY	385	RTAETLEMGAKIKKAHTGETPRADN---PMDCSHYTFPFRHRLDLRFNNTSGPV 441		
DB	355	ISMKEEIFAKLKQRYPPDISPMENNLGVVHMSDQVFNHGHRTLLAAR--SRAT 413		
QY	442	YLTFEDSDLDLIPRYIMSGRGVGVSHADELTTFYFMNOLAKRMKESREYTIERT 501		

Db 414 FVYRICLDE-FYNNHYRIMIDPKLGTGTAHADELSTYLFNFMTQOVPGKETFEYRGLQTL 472
 QY 502 GIIWOFATGPNYSNEIEGEMENVMPIKSDVEYKCLNT-SDELKIDVPEMDKIQWE 560
 Db 473 DVFSAFVINGDPNCG-MTAKSGVVEFPNAGTKPTFKCLNTANDGVAVDYDPADRLDMMD 531
 QY 561 SMF 563
 Db 532 AMY 534

RESULT 2

S53370
 carboxylesterase (EC 3.1.1.1) B2 - southern house mosquito
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
 C:Date: 15-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000
 C:Accession: S53370.544211
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
 Biochem. J. 305, 651-658, 1995
 A:Title: The independent gene amplification of electrophoretically indistinguishable B
 A:Reference number: S53370; MUID:95134253; PMID:7530448
 A:Accession: S53370
 A:Molecule type: mRNA
 A:Residues: 1-540 <VNU>
 A:Cross-references: EMBL:232694; NID:9475067; PIDN:CAA83643.1; PID:9475068
 A:Experimental source: strain PeIR
 A:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase

Query Match 33.7%; Score 1035; DB 2; Length 540;
 Best local similarity 37.8%; Pred. No. 2.3e-72; Indels 22; Gaps 8;
 Matches 205; Conservative 114; Mismatches 202;

QY 31 ETVVAETEVKGVKRVLTVDYSSFEQIPYAPVGLRFAKAPRPPMDSVRC-- 88
 Db 4 ESLTVQTKGVPVGRKSVSLDGEVYFQGIYARAPGELRFAKAPVPPQWMTETLDCSQ 63
 QY 89 ----CNHKDKSVQVDFITGKVCSEDCLYSTNNLNPETKRPVLYIHGGFIIENH 144
 Db 64 QCEPCYHFDRLQ-----KIVGCEDSLKINFAKINPSKPLVMLYIGGGFTGTS 117
 QY 145 RDWNGPRYFIKRDVLTINIOYRGLGFLSLNSEDLVNPGNGLKQDYMALRWIKNCGAN 204
 Db 118 TELGPDLVQKDLVLSFNYRIGALGFLCCSEODGVGNAGLKDQNLATRWLVENIGA 177
 QY 205 FCGNPDNITVFGESAGASTHYMLTEQTRGLFHRGILMSGNAICPMANTOCORAFILA 264
 Db 178 FCGDPKRVTLVGHSAAGASVOYHILSDASKDLFQRAIVSGSYNSWSLRTORNVYKLA 237
 QY 265 KLAGYKGEDNDKVDLEFLMAKAPODLILKEKYLTLEERTNKVMPPFGTVPEYOTADCV 324
 Db 238 KAIGMDGGGSGEALRFLRAKRPEDIVANODEKLLTDODMODLFTFPFGTVPEYLTQCM 297
 QY 325 LPKHRENVKKTWANGSITPMGNTSYEGLEFSTILKQMPVLEKTVCFVSESLADAE 384
 Db 298 IKKEPEMARKTWMDKIDIMIGTSEBGLLQKIKLOPRLSHPHILGNVPPNL--K 354
 QY 385 RTAPETLEMGAKIKRAHYTGETPADN---FMDLCSHYTFEPMHRLQLRFNHTSGTV 441
 Db 355 ISMEKRIEFAKIKORYYDSSPSMENNIGYHMSDREVFHGHILRTILARAAR-SRART 413
 QY 442 YLYRFDSEDLINPYRIRMSRGVGVSHADELYTFPMNOLAKRMPKESREYKTIERTM 501
 Db 414 FVYRICLDE-FYNNHYRIMIDPKLGTGTAHADELSTYLFNFMTQOVPGKETFEYRGLQTL 472
 QY 502 GIIWOFATGPNYSNEIEGEMENVMPIKSDVEYKCLNT-SDELKIDVPEMDKIQWE 560
 Db 473 DVFSAFVINGDPNCG-MTAKSGVVEFPNAGTKPTFKCLNTANDGVAVDYDPADRLDMMD 531
 QY 561 SMF 563
 Db 532 AMY 534

RESULT 3

S53371
 carboxylesterase (EC 3.1.1.1) B1 - southern house mosquito
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
 C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
 C:Accession: S53371
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
 Biochem. J. 305, 651-658, 1995
 A:Title: The independent gene amplification of electrophoretically indistinguishable
 A:Reference number: S53370; MUID:95134253; PMID:7530448
 A:Accession: S53371
 A:Molecule type: mRNA
 A:Residues: 1-540 <VNU>
 A:Cross-references: EMBL:232695; NID:9475069; PIDN:CAA83644.1; PID:9780238
 A:Experimental source: strain MRES
 A:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase

Query Match 33.4%; Score 1025; DB 2; Length 540;
 Best local similarity 37.3%; Pred. No. 1.4e-71; Indels 24; Gaps 10;
 Matches 203; Conservative 120; Mismatches 197;

QY 31 ETVVAETEVKGVKRVLTVDYSSFEQIPYAPVGLRFAKAPRPPMDSVRC-- 88
 Db 4 ESLTVQTKGVPVGRKSVSLDGEVYFQGIYARAPGELRFAKAPVPPQWMTETLDCSQ 63
 QY 89 ----CNHKDKSVQVDFITGKVCSEDCLYSTNNLNPETKRPVLYIHGGFIIENH 144
 Db 64 QCEPCYHFDRLQ-----KIVGCEDSLKINFAKINPSKPLVMLYIGGGFTGTS 117
 QY 145 RDWNGPRYFIKRDVLTINIOYRGLGFLSLNSEDLVNPGNGLKQDYMALRWIKNCGAN 204
 Db 118 TELGPDLVQKDLVLSFNYRIGALGFLCCSEODGVGNAGLKDQNLATRWLVENIGA 177
 QY 205 FCGNPDNITVFGESAGASTHYMLTEQTRGLFHRGILMSGNAICPMANTOCORAFILA 264
 Db 178 FCGDPKRVTLVGHSAAGASVOYHILSDASKDLFQRAIVSGSYNSWSLRTORNVYKLA 237
 QY 265 KLAGYKGEDNDKVDLEFLMAKAPODLILKEKYLTLEERTNKVMPPFGTVPEYOTADCV 324
 Db 238 KAIGMDGGGSGEALRFLRAKRPEDIVANODEKLLTDODMODLFTFPFGTVPEYLTQCM 297
 QY 325 LPKHRENVKKTWANGSITPMGNTSYEGLEFSTILKQMPVLEKTVCFVSESLADAE 384
 Db 298 IKKEPEMARKTWMDKIDIMIGTSEBGLLQKIKLOPRLSHPHILGNVPPNL--K 354
 QY 385 RTAPETLEMGAKIKRAHYTGETPADN---FMDLCSHYTFEPMHRLQLRFNHTSGTV 441
 Db 355 ISMEKRIEFAKIKORYYDSSPSMENNIGYHMSDREVFHGHILRTILARAAR-SRART 413
 QY 442 YLYRFDSEDLINPYRIRMSRGVGVSHADELYTFPMNOLAKRMPKESREYKTIERTM 500
 Db 414 FVYRICLDE-FYNNHYRIMIDPKLGTGTAHADELSTYLFNFMTQOVPGKETFEYRGLQTL 471
 QY 501 TGIIWOFATGPNYSNEIEGEMENVMPIKSDVEYKCLNT-SDELKIDVPEMDKIQWE 559
 Db 472 DVFTFAVINGDP-NCSMTAKSGVVEFPNSQTKPTFKCLNTANDGVALVDYDPADRLDMMD 530
 QY 560 ESMF 563
 Db 531 DAMY 534

RESULT 4

S53372
 carboxylesterase (EC 3.1.1.1) B - southern house mosquito (fragment)
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
 C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
 C:Accession: S53372; S44212
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
 Biochem. J. 305, 651-658, 1995
 A:Title: The independent gene amplification of electrophoretically indistinguishable

A:Reference number: S53370; MUID:95134253; PMID:7530448
A:Accession: S53372
A:Molecule type: mRNA
A:Residues: 1-503 <NAV>
A:Cross-references: EMBL:232696
A:Experimental source: Pelss
R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
submitted to the EMBL Data Library, April 1994
A:Description: The independent gene amplification of indistinguishable esterase B electrophoretic
A:Reference number: 544211
A:Accession: 544212
A:Molecule type: mRNA
A:Residues: 'SA', 1-503 <NAV>
A:Cross-references: EMBL:232696; NID:9475070; PID:9475071
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match 30.2%; Score 929; DB 2; Length 503;
Best Local Similarity 36.9%; Pred. No. 3.6e-64;
Matches 187; Conservative 104; Mismatches 194; Indels 22; Gaps 8;

QY 67 PVGLRRAPRPTPMDCVRC-----CNHKDSVOVDFTGKVCSEDCLYSVYTN 120
DB 3 PEGELRFAVPQNMWETLDTQCEPCYHSDRLQ-----KIVGCEDSLKIWEAKE 56
QY 121 LNPETKRPVLYYHGGGFTIGENHRDMYGPDYFIKKDVLINIOYRGLAGLSNSED 180
DB 57 INPSKPLDVMYLYGGGTETGTELTGPDLVOKDVLVSFNRIGALFLCOOSYOD 116
QY 181 NVPGNAGLKDQVMAIRWIKNCANFGNPDNITVGSAGASTHYMLTEOTRGLFHRG 240
DB 117 GVPAGAGLQDQNLAIKRWLENIAMFGDPKRVTLVGHAGAGASVOYHILSDASDLFRA 176
QY 241 ILASGNAICPMANTQCOHRAFTLAKAGYKCEDNDKDLLEFLMAKPODLIKLEKVT 300
DB 177 IVMSGSTYNSLSLTKRQMWKELAKAIGMDGSGSGLAFRLAKAPEDIIVANOEKLT 236
QY 301 EERTNKVFPFGPTPEPYOTADCVLPKPRMVKTWAMGNSPTJMGNTSYGLFTSTLK 360
DB 237 QDMODDITPFGPTPEPYOTADCVLPKPRMVKTWAMGNSPTJMGNTSYGLFTSTLK 296
QY 361 QMPMLVKELETCVNFPSLEDAERTABELMGAKIKAHVGTETPADN---FMDCS 417
DB 297 LQPLLSHPHFLGNIIPNL---KISMEKRIEFAKIKORYVPPSSPMANNLGYVHMS 353
QY 418 HIYFEPHRLDLRFNHTSGTPVLYLRFDSDELIPYIKMSGRGVKGVSHADELT 477
DB 354 DRVFMHGHRTILAAAR-SRARTFVYRICDSE-FYNNHYRIMIDPKLRGTAHDEL 411
QY 478 FFMNOLAKRMPKRESEKTYTIRMGTGWIQFAFTGPNYSNEIGMENVMDPIKSD 537
DB 412 LFSNFTQVLPKRTFETVIGLQTLVDVFTAFVINGDP-NCSMTAKSGVFEPSQTKPTFK 470
QY 538 CLNT-SDELKMIIDVPEMDIKOMESMF 563
DB 471 CLNIANDGLAFVDYDADRLDMWDAMY 497

RESULT 5
A34325
juvenile-hormone esterase (EC 3.1.1.59) precursor - tobacco budworm
C:Species: Heliothis virescens (tobacco budworm)
C:Date: 22-Jun-1990 #sequence_revision 25-Sep-1992 #text_change 13-Sep-1998
R:Accession: A34325
R:Hanzi, T.N.; Abdel-Aal, Y.A.I.; Harshman, L.G.; Hammock, B.D.
J. Biol. Chem. 264, 12419-12425, 1989
A:Title: Isolation and sequencing of cDNA clones coding for juvenile hormone esterase from the silkworm, Bombyx mori.
A:Reference number: A34325; MUID:89308671; PMID:2745451
A:Accession: A34325
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-564 <HAN>

A:Cross-references: GB:J04955; NID:9159222; PID:9159223
C:Superfamily: juvenile-hormone esterase
C:Keywords: carboxylic ester hydrolase

Query Match 22.5%; Score 691; DB 2; Length 564;
Best Local Similarity 33.3%; Pred. No. 1.4e-45;
Matches 173; Conservative 102; Mismatches 208; Indels 36; Gaps 19;

QY 23 LNYRLTNETVVAETEGKVGKRLVYDSDYSFEGIPYAPQVGLRERAPRPT 82
DB 18 LAMQETNSRYVAHLDSSGILGVPR-SADGIKFAFSLGVPAKQVGLRERLEPLPW 76
QY 83 DGVDRCCNHRKKSVOVDFTGKVC---SEDCLYSVYTN---NNNPEKTK-----RPLV 131
DB 77 DNLIMATNEGPICFOTDVLGRMAASMSSEACIYANIHVPMQSL-PRVKGTPPLRPLV 135
QY 132 YHGGFTIGENHRDMYGPDYFIKKDVLINIOYRGLAGLSNSEDLPVGNAGLQD 191
DB 136 FHHGGGFAFGSHEDLHGPFLVTRKNVIVTFNRLANVFGLSMNT--TKIPGNAGLQD 193
QY 192 VMAIRWIKNCANFGNPDNITVGSAGASTHYMLTEOTRGLFHRGILMSGNAICPW 251
DB 194 VTLKRWQNRKAKNFGGDSPTITIGQASASAHLLTSLKATGELFKRAILMSGTGMSYF 253
QY 252 ANTOCOHRAFTLAKAGYK---EONDKDLLEFLMAKPODLIKLEKVTLEERTNKVME 309
DB 254 FTTSPFLFAVYISKOLLQGLGMDGSEIHRQLDLPAB--KLEANVAVLEQIG--LT 308
QY 310 PEGPTE--PYOTADCVLPKPRMVKTWAMGNSPTJMGNTSYGLFTSTLKQMPMLVKE 368
DB 309 TELPIVESPLDGVTTIIDDDPEILAEGRKNVPLLIPTSECTFFNRLNPLVYKI 368
QY 369 LETCVNFPSELADAERAPETL-EMGAKIKAHVGTETPADNMDLCSHYTFPMHR 427
DB 369 QDNPTIILIPKRL--LEMPPELMELAKTIERKYNG--TISIDNVKSCSDGFYEPALK 425
QY 428 LLOLFNHTSGTPVLYLRFDSDELIPYIKMSGRGVKGVSHADELTPE--NMOLKR 486
DB 426 LAQKR-AETGAPFLVLYFAIEGQNSITK-KVM--GLNHEGVGHIEDLTLYFKVMSSEA 481
QY 487 M---PKSEKRYKTIERTMTGWIQFAFTGPNYSNEIGME 522
DB 482 LHASPSN-DVKMKMLMTGFLNFIKSCQPTCEDNNSLE 519

RESULT 6
F89068
protein T28C12.4b [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
R:Accession: F89068
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: F89068
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-578 <SPD>
A:Cross-references: GB:chr_V; PIDN:AAH66160.1; PID:g2315734; GSPDB:GN00023; CESP:T28C
C:Genetics:
A:Gene: T28C12.4b
A:Map position: 5
C:Superfamily: cholinesterase; cholinesterase homology

Query Match 19.3%; Score 593; DB 2; Length 578;
Best Local Similarity 29.1%; Pred. No. 5.8e-38;
Matches 172; Conservative 98; Mismatches 220; Indels 102; Gaps 26;

QY 22 FLNRLTNETVVAETEGKVGKRLVYDSDYSFEGIPYAPQVGLRERAPRPT 81
DB 22 FLNRLTNETVVAETEGKVGKRLVYDSDYSFEGIPYAPQVGLRERAPRPT 81

F:88-115,275-286,423-542/Disulfide bonds: #status experimental
F:105/Binding site: substrate (TTP) #status experimental
F:722/Active site: Ser #status experimental
F:346,461/Active site: Glu, His #status predicted
F:437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:593/Disulfide bonds: Interchain #status experimental

```
Query Match          18.4% Score 565.5 DB 1: Length 596;
Best Local Similarity 27.8%, Fred. No. 8.4e-36;
Matches 165; Conservative 107; Mismatches 213; Indels 109; Gaps 22;

QY 33 VVAEEFGYGVKVKRTLYTDDSYSEFEGIPYAQPVGELREKFAQRPPIPMQGVRCCHNK 92
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dp 27 LNVNKSGLKVMGT-RVPLVSSHLSIAFLGPAEPVGNFRFRPEKKKWSGVNASTYRP 85
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 93 DKSVDYDFITGKAYCG-----SEDCLYSYVTNNINLPETKRPVLYIHGGGFI 139
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dp 86 NNCQQ--YYDEQRPFGSGSEMMNPKESEDCLYLNIWVPSRPKS-TIVWVIYGGGFY 142
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 140 IGENHNDMYGRDF-IKKDVLLINIQRLGALGFLSLNSEDNLVPGNAGLKQDVMLRMT 198
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dp 143 SGSTLDLYNGKTLATVEVVLVLSRYVAGFGLHGSQ-EAPGVGLDDRMALQWY 201
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 199 KNNCANGNDNITVYGESAGASTHYMMLTQTRGLFRGLMSGNAICPMAN--TQ 255
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dp 202 HDNIOFEGGPRKTYTIGESAGSVGHILSPGSRDLFRALIGSPNCPMASVVAE 261
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 256 CQHRAPFLAKLAGKGEQNDKVLFEFLMKARPDILKLEEVLTLEERTKKVMPREPGTV 315
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dp 262 GRRRAVELGRNLNC-NLNSDELLHCLREKKRQELILVENVLPFD--STFRSEYPI 317
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 316 ERYOTADCVLPKRPREMYKTMAGNSIPTMGNTSYEGEFLFSILKOMPLVELETGVNF 375
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dp 318 DGE-----FFPETSLESMNSGNFKTKQILLGVNKGDSGF--LLYGAGFSKDSSES--- 366
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 376 VPESLADERTAPETLEMGAKIKKAH-----VTGETPADNPM----- 414
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dp 367 -----KISRDEPFMSGVKLSVPHANDLGDAATLOYTWMDDNNGCIKNRGDIDTVG 417
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 415 ---LCSHYTFEPMRRLQLRFNHTSGPYVLRFEDESDILNPRYMRSGRGVGS 470
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dp 418 DHNVICPLMHF--VNKYTF-----GNGYTLFFNHRASNLVWPEWM-----GVI 460
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 471 HADELTFEPMNOIAKRMKESREYKTIERMGTGIWFOFATGPNYSNIEIGME----- 522
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dp 461 HGIEIEFVGLRPVKELNTAEEALSRIMHWATFAATGNP--NEPISOESKMPLEFTT 518
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 523 -----NVSMDPLPKSD--EYVKCLNISDEL-KMIDVPEM--DKIKOWESMEPK 565
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dp 519 KEQFTIDLNTEPMKVHQRLRVOMCVPMNOFLPKLLNATEFIDBAERQMKTEFFHR 572
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

RESULT 15

JH0314
acetylcholinesterase (EC 3.1.1.7) precursor - mouse

C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1999
C:Accession: JH0314

R:Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstrom, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990

A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alte

A:Reference number: JH0314, MUID:90380423; PMID:2400605

A:Accession: JH0314

A:Molecule type: mRNA

A:Residues: 1-614 <RAC>

A:CROSS-references: EMBL:X56518; NID:949844; PIDN:CA39867.1; PID:949845

A:Experimental source: brain

C:Superfamily: Cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve

F:1-31/Domain: signal sequence #status predicted <SIG>

F:32-614/Product: acetylcholinesterase #status predicted <MAT>

F:63-569/Domain: cholinesterase homology <CHK>

F:100-127,288-303,440-560/Disulfide bonds: #status predicted

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 4, 2003 09:09:07 ; Search time 10.6371 Seconds

(without alignments)
2222.359 Million cell updates/sec

Title: US-09-776-910-8
Perfect score: 3073
Sequence: 1 MNFVSLMKLKKIKCIEN.....PENDKIKWESMEKRDLE 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892.

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	1038	33.8	540	1 EST1_CULPI	P16834 culex pipie
2	690	22.5	564	1 EST1_HELVI	P12992 heliothis v
3	606	19.7	633	1 ACES_ELEBL	O42275 electrophor
4	583.5	19.0	489	1 PNBA_BACSU	P37967 bacillus su
5	575.5	18.7	634	1 ACES_BRARE	O6d63 brachydanio
6	568.5	18.5	564	1 ESTP_MYZPE	P35502 myzus persi
7	568.5	18.5	602	1 CHLE_HUMAN	P06276 homo sapien
8	567	18.5	552	1 ESTE_MYZPE	P35501 myzus persi
9	564.5	18.4	614	1 ACES_MOUSE	P21836 mus musculu
10	562	18.3	586	1 ACES_MOUSE	P04058 torpedo cal
11	558.5	18.2	611	1 ACES_TORCA	O62763 felis silve
12	558	18.2	574	1 CHLE_HORSE	P81908 equus cabal
13	557	18.1	649	1 ACES_DROME	P07140 drosophila
14	556.5	18.1	614	1 ACES_RAT	P37136 rattus norv
15	555.5	18.0	613	1 ACES_BOVIN	P23795 bos taurus
16	552.5	18.0	629	1 ACES_LEPDE	O27677 leplitorais
17	552	18.0	590	1 ACES_TORMA	P07697 torpedo mar
18	551	17.9	581	1 ACES_BUNFA	O92035 bungarus fa
19	548.5	17.8	561	1 EST1_MESAU	O64419 mesocricetu
20	547.5	17.8	584	1 ACES_RABIT	O29499 oryctolagus
21	547.5	17.8	614	1 ACES_HUMAN	P22303 homo sapien
22	545	17.7	581	1 CHLE_RABIT	P19192 oryctolagus
23	538	17.5	562	1 EST1_CARBR	O04456 caenorhabdi
24	536	17.4	557	1 SASB_ANAPL	O04791 anas platyr
25	535	17.4	544	1 EST6_DROME	P08171 drosophila
26	524	17.1	603	1 CHLE_MOUSE	O03311 mus musculu
27	523.5	17.0	545	1 ESTB_DROPS	P25726 drosophila
28	523	17.0	542	1 EST6_DROMA	P47982 drosophila
29	522	16.9	544	1 EST6_DROSI	O08662 drosophila
30	518.5	16.9	544	1 ESTP_DROME	P18167 drosophila
31	517	16.8	532	1 EST2_RABIT	P14943 oryctolagus
32	516.5	16.8	566	1 EST1_PIG	O29550 sus scrofa
33	516	16.8	545	1 ESTC_DROPS	P25725 drosophila

34	514.5	16.7	547	1 ESTA_DROPS	P25727 drosophila
35	511.5	16.6	561	1 EST4_RAT	O64573 rattus norv
36	507.5	16.5	565	1 EST10_RAT	P16303 rattus norv
37	506	16.5	597	1 BAL_BOVIN	P30122 bos taurus
38	505	16.4	549	1 EST1_RAT	P10959 rattus norv
39	501	16.3	554	1 ESTN_MOUSE	P23953 mus musculu
40	500.5	16.3	561	1 EST5_RAT	O63010 rattus norv
41	499	16.2	599	1 BAL_MOUSE	O64285 mus musculu
42	496	16.1	664	1 ACES_ANOST	P56161 anopheles s
43	495.5	16.1	554	1 ESTW_MOUSE	O63880 mus musculu
44	495	16.1	612	1 BAL_RAT	P07882 rattus norv
45	492	16.0	562	1 EST1_CAREEL	O04457 caenorhabdi

ALIGNMENTS

RESULT 1	EST1_CULPI	STANDARD:	PRT:	540 AA.
AC	P16834;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	01-FEB-1994 (Rel. 28, Last annotation update)			
DE	Esterase B1 precursor (EC 3.1.1.1).			
GN	Bl.			
OS	Culex pipiens (House mosquito).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;			
OC	Culicoidae; Culex.			
OX	NCBI_Taxid=7175;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-TM-R;			
RX	MEDLINE=90207238; PubMed=2320576;			
RA	Mouches C., Pauplin Y., Agarwal M., Lemieux L., Herzog M.,			
RA	Abadon M., Beyssat-Arnaudy V., Hyrien O., de Saint Vincent B.R.,			
RA	Geophilou G.P., Pasteur N.;			
RT	"Characterization of amplification core and esterase B1 gene			
RT	responsible for insecticide resistance in Culex."			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:2574-2578(1990).			
CC	-1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON			
CC	MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.			
CC	-1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a			
CC	carboxylic anion.			
CC	-1- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF			
CC	BOTH A AND B ARE KNOWN.			
CC	-1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL: M32328; AAA28289.1; -			
DR	PIR: A35986; A35986.			
DR	HSSP: P21836; IMA.			
DR	InterPro: IPR002018; CarbesteraseB.			
DR	InterPro: IPR000379; Ser_estrs_site.			
DR	Pfam: PF00135; Coesterase; 1			
DR	PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.			
DR	PROSITE: PS00941; CARBOXYLESTERASE_B.2; FALSE_NEG.			
KW	Hydrolase; Serine esterase; Glycoprotein; Multigene family; Signal.			
FT	SIGNAL	1	?	
FT	CHAIN	?	540	ESTERASE B1.
FT	ACT_SITE	191	191	BY SIMILARITY.
FT	ACT_SITE	442	442	BY SIMILARITY.
FT	DISULFID	68	81	BY SIMILARITY.
FT	CARBOHYD	452	452	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	540 AA;	60806 MW;	F73B25B3A7157C95 CRC64;

ID	ACCS_ELEBL	STANDARD:	PRT:	633 AA.
AC	042275			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Acetylcholinesterase precursor (EC 3.1.1.7) (Ache).			
OS	Electrophorus electricus (Electric eel).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;			
OX	NCBI_TaxID=8005;			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RX	MEDLINE=98070504; PubMed=9407087;			
RA	Simon S., Massoulie J.;			
RT	"Cloning and expression of acetylcholinesterase from Electrophorus.			
RT	Splicing pattern of the 3' exons in vivo and in transfected mammalian			
RT	cells.";			
RL	J. Biol. Chem. 272:33045-33055(1997).			
CC	-1- FUNCTION: RAPIDLY HYDROLYSES CHOLINE RELEASED INTO THE SYNAPSE.			
CC	-1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.			
CC	-1- SUBUNIT: DIMERS AND COLLAGEIN-TAILED FORMS, IN WHICH CATALYTIC			
CC	TERMINI ARE ASSOCIATED WITH ANCHORING PROTEINS THAT ATTACH THEM			
CC	TO THE BASAL LAMINA OR TO CELL MEMBRANES. IN THE COLLAGEIN-TAILED			
CC	FORMS, SUBUNITS ARE ASSOCIATED WITH A SPECIFIC COLLAGEN; COLO,			
CC	WHICH TRIGGERS THE FORMATION OF ISOFORM T TETRAMERS FROM DIMERS.			
CC	-1- MISCELLANEOUS: NO OTHER ISOFORMS EXIST. THIS PROTEIN CORRESPONDS			
CC	TO THE T ISOFORM IN OTHER SPECIES.			
CC	-1- SIMILARITY: BELONGS TO THE CARBOXYL ESTERASE TYPE-B FAMILY.			
CC	-----			
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CC	OR SEND AN EMAIL TO license@sib-sib.ch .			
CC	-----			
DR	EMBL: AF030422; AAB86606.1; -			
DR	HSSB: P04058; ISOM.			
DR	InterPro: IPR002018; Carboxylase.			
DR	InterPro: IPR000397; Cholinesterase.			
DR	InterPro: IPR000397; Ser-estr- site.			
DR	Pfam: PF00135; Coesterase; 1.			
DR	PRINTS: PR00878; CHOLINESTERASE.			
DR	PROSITE: PS00122; CARBOXYL ESTERASE_B.1; 1.			
DR	PROSITE: PS00941; CARBOXYL ESTERASE_B.2; 1.			
KW	Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;			
KW	Neurotransmitter degradation; Glycoprotein.			
KM	Neurotransmitter degradation; Glycoprotein.			
FT	SIGNAL	1	23	POTENTIAL.
FT	CHAIN	24	633	ACETYLCHOLINESTERASE.
FT	ACT_SITE	225	225	BY SIMILARITY.
FT	ACT_SITE	352	352	BY SIMILARITY.
FT	ACT_SITE	494	494	BY SIMILARITY.
FT	DISULFID	91	118	BY SIMILARITY.
FT	DISULFID	279	290	BY SIMILARITY.
FT	DISULFID	427	579	BY SIMILARITY.
FT	DISULFID	630	630	INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD	133	133	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	184	184	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	283	283	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	368	368	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	511	511	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	591	591	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	591	591	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE	633 AA:	71814 MW:	FC92FE7E4ADB84C3	CRC64:

Query Match	19.7%	Score 606	DB 1	Length 633
Best Local Similarity	29.9%	Pred. No. 3.5e-39		
Matches 184	Conservative 94	Mismatches 228	Indels 110	Gaps 24
QY	TNEVVAETEGKVGKVGKRLVYDDSY--VSFEGIVYAOPPELRFKAPQRPMPDGVAD	87		
Db	25 TDPELITMTRLQYOGCT-RLVPYRDSHYATLGLTIFAEERPLQKMKFPPPEPKKPNVDYD	83		
QY	88 CCHNKKQSVQ-VDFITGKVCV-----SEDLVLSVYTNININPETKRP---VLVY	132		
Db	84 ARDYSACVQYVDTSYPSFGSGTEEMNPNRMSEDLVLTNVWY----PATPRHNLTVMWY	139		
QY	133 IHGGFIIIGENRMDWYGDYFIKQD-VVLTINQVYLGALGFLTSSSEDLNVGNGNLKQY	191		
Db	140 IYGGGFYGGSSSLVDYDGRYLAHSHKRVVSVSNMYVSAGFATLNG-SAEAGANGLLDQ	198		
QY	192 VVALFWIKNNCANFEGCNPDNITVGEESAGASTHYMLTEQTRGLFHRGILMSGNAICPW	251		
Db	199 RIALQWODNIHFEGGNPKQVITFEGSAGAAVGHMLLSPDSRPKFTRAILQSGVYNGPW	258		
QY	252 ANT---QCONRAFTLAKLAGYKIGENDKQDYLEFLMKAKPQDILKEEKVLTLEERTNKVM	308		
Db	259 RTVSFDEARRRAIKLGRILVQCP-DQNDPDLIDLCKRSKQPDIDDEWLPLF---SGLFR	314		
QY	309 PFPGFTVEYQADCVLRPHREMYKWTAMGNSIPRMNGTSTYEGLFETSLIKQMPLYKE	368		
Db	315 FSFVVID-----GVYFPDTPREALMNSGNFKQTQIILGVNQNQGSYF-LIIGAGQFSKD	367		
QY	369 LETCV--NFVPSELADERTAPETLEMGAK-----IKKRAHYGETPTAD	410		
Db	368 NESLITREDF-----LOGVMASVPHANEIGLEAVILQYTDMDMEDNP IKREAMDIVGDH	423		
QY	411 NFMDCSHYFEPHRLQ-----LRFNHT-----SGTPYLLRFPEDSD	452		
Db	424 NVVCPLOHFAKMYAOLSLQGTGTASQCNGLMGNSGASNSGNSQVSYLLYMFPHRASN	483		
QY	453 IINPRIMSGRGVGVSHADELYTFEWMQLAKRMPKESREKTEIRMGVIOFATTGN	512		
Db	484 LVMPERM-----GVHGYEIEFVFGPLERKLRLNTYLEERKLSRMMKYANFARTGN	535		
QY	513 PYSNIEGN--ENVSWDPPIKSDYEVKCLINISDEK-----MIDVP	551		
Db	536 PIN-INVDGIDSRMRWPFTSTYOKHVGILN-TDSLKVHKLGSQCALMNRFLPRLNT	593		
QY	552 EM--DKIKOWESMEFK	565		
Db	594 ENIDDAEROMKAEFHR	609		
RESULT 4				
PDBA_BACSU				
ID	PDBA_BACSU	STANDARD:	PRT:	489 AA.
AC	P37967;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Para-nitrobenzyl esterase (EC 3.1.1.-) (PNB carboxy-esterase) (PNBCE).			
GN	PNBA.			
OS	Bacillus subtilis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1423;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 1-22 AND 211-223.			
RX	STRAIN=NRRL B8079;			
RX	MEDLINE=9512891; PubMed=7828905;			
RA	Zock J., Cantwell C., Swartling J., Hodges R., Pohl T., Sutton K.,			
RA	Rostek P. Jr., McGilivray D., Queener S.;			
RT	"The Bacillus subtilis pnbA gene encoding p-nitrobenzyl esterase:			
RL	cloning, sequence and high-level expression in Escherichia coli.";			
RL	Gene 151:37-43(1994).			
RP	[2]			
SEQUENCE OF 1-22 AND 211-223, AND CHARACTERIZATION.				

QY 421 FWFPMRLQLFRNHTSG---TPVLYRDEPDSDDLNPRIIMSGHGVGVSHADELT 477
 DB 414 FCGYCSKAAQ-----HIAAKNTAPVYEFEGYSGNYSYVAFPKSYRSGSPHGDFTNN 469
 QY 478 -----FFWQOLAKRMKRESREKTERMTGWIWOFATTGNPYSNEIGEMVNSMDPI 529
 DB 470 VLKVDFTVYDNE-----EDKKMKITWNIWATFIKSGVDPDENSE-----IWLPV 515
 QY 530 KKSD-EVYKCLNISDE 544
 DB 516 SKNPADLFRFTKITQ 531

RESULT 7
 CHLE_HUMAN STANDARD: PRT: 602 AA.
 ID CHLE_HUMAN
 AC P06276;
 DT 01-JAN-1988 (Rel. 06, last sequence update)
 DT 01-AUG-1988 (Rel. 08, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
 DE (Choline esterase II) (Butyrylcholine esterase)
 DE (Pseudocholinesterase).
 GN BCHE OR CHEL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90212557; PubMed=2322535;
 RA Arpaegus O.; Kott M.; Vatsis K.P.; Bartels C.F.; La Du B.N.;
 RA Lockridge O.;
 RT "Structure of the gene for human butyrylcholinesterase. Evidence for
 RT a single copy.";
 RT Biochemistry 29:124-131(1990).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE-Fetal;
 RX MEDLINE=8721856; PubMed=3035536;
 RA Prody C.A.; Zeyin-Sonkin D.; Ghatt A.; Goldberg O.; Soreg H.;
 RA "Isolation and characterization of full-length cDNA clones coding for
 RT cholinesterase from fetal human tissues.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE-Brain;
 RX MEDLINE=88016155; PubMed=3477799;
 RA McLennan C.; Adkins S.; Chaconnet A.; Vaughan T.A.; Bartels C.F.;
 RA Kott M.; Rosenberry T.L.; La Du B.N.; Lockridge O.;
 RA "Brain cDNA clone for human cholinesterase.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
 RL [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE-Skin;
 RX Strausberg R.;
 RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RN SEQUENCE OF 29-602.
 RP TISSUE-Plasma;
 RX MEDLINE=87109144; PubMed=3542989;
 RA Lockridge O.; Bartels C.F.; Vaughan T.A.; Wong C.K.; Norton S.E.;
 RA Johnson L.L.;
 RA "Complete amino acid sequence of human serum cholinesterase.";
 RT J. Biol. Chem. 262:549-557(1987).
 RL [6]
 RN DISULFIDE BONDS.
 RX MEDLINE=88007487; PubMed=3115973;
 RA Lockridge O.; Adkins S.; La Du B.N.;
 RA "Location of disulfide bonds within the sequence of human serum
 RT cholinesterase.";
 RT J. Biol. Chem. 262:12945-12952(1987).

RN [7]
 RP REVIEW.
 RX MEDLINE=89149758; PubMed=3067729;
 RA Lockridge O.;
 RT "Structure of human serum cholinesterase.";
 RL Bioessays 9:125-128(1988).
 RN [8]
 RP VARIANT ATYPICAL GLY-98.
 RX MEDLINE=8912896; PubMed=2915989;
 RA McGuire M.C.; Nogueira C.P.; Bartels C.F.; Lightstone H.; Hajra A.;
 RA van der Spek A.F.L.; Lockridge O.; La Du B.N.;
 RA "Identification of the structural mutation responsible for the
 RT dibucaine-resistant (atypical) variant form of human serum
 RT cholinesterase.";
 RT Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
 RN [9]
 RP VARIANT IDE-358.
 RX MEDLINE=96287386; PubMed=8680411;
 RA Iida S.; Kinoshita M.; Fujii H.; Moriyama Y.; Nakamura Y.; Yura N.;
 RA Moriwa K.;
 RT "Mutations of human butyrylcholinesterase gene in a family with
 RT hypocholinesterasemia.";
 RL Hum. Mutat. 6:349-351(1995).
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED
 CC OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A
 CC DISULFIDE BOND.
 CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
 CC -1- DISEASE: MUTANT ALLELES OF CHEL ARE RESPONSIBLE FOR
 CC HYPOCHOLINESTERASEMIA RESULTING IN SUXAMETHONIUM SENSITIVITY.
 CC HOMOZYGOUS PERSONS SUSTAIN PROLONGED APNEA AFTER ADMINISTRATION
 CC OF THE MUSCLE RELAXANT SUXAMETHONIUM IN CONNECTION WITH SURGICAL
 CC ANESTHESIA.
 CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
 CC ORGANOPHOSPHATE ESTERS.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
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 CC -----
 DR EMBL: M32391; AAA99296.1; -;
 DR EMBL: M32389; AAA99296.1; JOINED.
 DR EMBL: M32390; AAA99296.1; JOINED.
 DR EMBL: M16541; AAA98113.1; -;
 DR EMBL: M16474; AAA52015.1; -;
 DR EMBL: BC018141; AAH18141.1; -;
 DR PIR: A00772; ACBU.
 DR PIR: A26613; A26613.
 DR PIR: A33769; A33769.
 DR PIR: A33887; A33887.
 DR HSSP: P21836; IMAA.
 DR Genew: HGNC:983; BCHE.
 DR MIM: 177400; -;
 DR InterPro: IPR002018; Carpesteraseb.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_estrs-site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_2; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE; signal; Disease mutation;
 DR HydroLase: Serine esterase; Glycoprotein; signal; Disease mutation;
 KW Polymorphism.
 FT SIGNAL 1 28
 FT CHAIN 29 602 CHOLINESTERASE.
 FT ACT_SITE 226 226 BY SIMILARITY.
 FT ACT_SITE 353 353 BY SIMILARITY.
 FT ACT_SITE 466 466 BY SIMILARITY.

FT	DISULFID	93	120
FT	DISULFID	280	291
FT	DISULFID	428	547
FT	DISULFID	599	599
FT	CARBOHYD	45	45
FT	CARBOHYD	85	85
FT	CARBOHYD	134	134
FT	CARBOHYD	269	269
FT	CARBOHYD	284	284
FT	CARBOHYD	369	369
FT	CARBOHYD	483	483
FT	CARBOHYD	509	509
FT	CARBOHYD	514	514
FT	VARIANT	98	98
FT			
FT			
FT	VARIANT	271	271
FT			
FT	VARIANT	358	358
FT			
FT	VARIANT	418	418
FT			
FT	VARIANT	567	567
FT			
QO	SEQUENCE	602 AA:	68418 MR:

C9836409D9057E27 CRC64:

```

INTERCHAIN.
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
D -> G (IN ATYPICAL FORM, DIBUCAINE-
RESISTANT)
/FTId-VAR_002360.
T -> M (IN FLUORIDE-1).
/FTId-VAR_002361.
L -> I (IN HYPOCHLOINESTERASEMIA).
/FTId-VAR_002362.
G -> V (IN FLUORIDE-2).
A->-T (IN K VARIANT, WITH REDUCED ENZYME
ACTIVITY).
/FTId-VAR_002364.
```

[illegible]

DB	550	WISFPPK	556
RESULT 8			
ESTE_MYZPE			
ID	ESTE_MYZPE	STANDARD:	PRT: 552 AA.
AC	P35501:		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	01-OCT-1994 (Rel. 30, Last annotation update)		
DE	Esterase E4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).		
OS	Myzus persicae (Peach-potato aphid)		
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;		
OC	Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;		
OC	Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.		
OX	NCHI_TaxID=13164;		
RM	[1]		
RE	SEQUENCE FROM N.A., AND SEQUENCE OF 24-63.		
RC	STRAIN=R3 / isolate 794J;		
RX	MEDLINE=93384534; PubMed=8373371;		
RA	Field L.M., Williamson M.S., Moores G.D., Devonshire A.L.;		
RT	"Cloning and analysis of the esterase genes conferring insecticide resistance in the peach-potato aphid, Myzus persicae (Sulzer).";		
RL	Biochem. J. 294:569-574(1993).		
CC	-1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.		
CC	-1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a carboxylic anion.		
CC	-1- MISCELLANEOUS: THIS ESTERASE CONFERS INSECTICIDE RESISTANCE.		
CC	-1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.		
CC	-----		
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CC	-----		
DR	EMBL: X74554; CNA52648.1; .		
DR	PIR: S36786; S36786.		
DR	HSSP: P21836; IMAA.		
DR	InterPro: IPR002018; CarbesteraseB.		
DR	InterPro: IPR000379; Ser_estr_site.		
DR	Pfam: PF00135; Coesterase_1.		
DR	PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.		
DR	PROSITE: PS00941; CARBOXYLESTERASE_B.2; FALSE_NEG.		
KW	Hydrolase; Serine esterase; Glycoprotein; Signal.		
FT	SIGNAL	1	23
FT	CHAIN	24	552
FT	ACT_SITE	214	214
FT	ACT_SITE	339	339
FT	ACT_SITE	463	463
FT	DISULFID	89	106
FT	DISULFID	266	277
FT	CARBOHYD	81	
FT	CARBOHYD	269	
FT	CARBOHYD	371	
FT	CARBOHYD	404	
FT	CARBOHYD	443	
SO	SEQUENCE	552 AA;	61348 MM; B97B6272DF7209 CRC64;
Query Match	18.5%;	Score 567;	DB 1; Length 552;
Best Local Similarity	29.3%;	Pred. No. 3e-36;	
Matches 167;	Conservative 88;	Mismatches 226;	Indels 88; Gaps 22;
QY	28	TNTEETVAETEXKGVKRLTVYDSDYSYFEGICVYADPPVQELRFKAPQRETPMDGYRD	87
DB	22	SASNTPKVQVHSGIAGGEFTYVNRKITYSLGIRYASPPVQNNFKEPQVQPLGAWN	81
QY	88	CCNHDKSVQVDFITG-KVCGSEDLILSYVTNNINPEFK-----RPVLYIHGGFFITGE	142
DB	82	ATVPASACIGIEFGGSKTIGEDCLFNVYPPKLPQENSAGDLMNVVHGGGYGGE	141


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DB 46 GOLRGI-RLAAGPGVSAFLGIPFAEPVGSRRPMPERAPMSGVLDATFQNVQYV 104
      ::::: || ::||::||| ||| ::||| ::|||
QY 99 DFTGKACG-----SECDLYLSVTNNLNPEKRVLYIYHGGGITGENHMDY 148
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 105 DTLYPEGEGEMNNPNRESECDLYLWVMPYRPASPTVLLIMYGGGSGAASLDYV 164
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 149 GPDYFK-KQVVLINIDYRLGALGFLSNSEDLNVPGNAGLKQVMAIRIKNNCANEGG 207
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 165 DGRFLAOVEAVALYSMYRGTFGLALPG-SREAPGNVLLDQRLALQWQENIAFGG 223
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 208 NPDNITVFGSAGASTHYVMTQETRGFLRHGILMSGNAICPWANT---OCOHRAFTLA 264
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 224 DPMSTLFGSAGASGMHILSLPSRSLFHRAVLQSGTPNGRWATYSAGEARRATLLA 283
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 265 KLAGYK---GEDNDKDYLEFLMAKAPODLIKLEKVLTLTEETNNKVPFGPYEYQTA 321
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 284 RLVGCPGPGAGAGDTEIACLRTRPADLDVHEWHVLPQ---SIFRFSVVPVVDGDFLS 340
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 322 DCVLPKPRRMVKTAMGNSIPTMGNSTYEGLEFETSLKMPMLYKLELCVNFVSELA 381
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 341 DT-----PEALINTGPDQIDVLGVVKKDGSIF--LVYGVPGFSKNESLISRA-OFLA 392
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 382 DAEETAPETLEMGAKIKKAHVTG---ETPTADNFMDCSHIYFWPMHRL---OLRF 433
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 393 GVRIGVPGASDLAAEAVALVHTDMLHPEDPT--HLRDAMSAV---VEDHNVGCVQAOLAG 447
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 434 N-HITSGTPLYLRPFDESEDLINPRIRMSRGYKGYSHADELTFYFWNOLAKRMPRESR 492
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 448 RLAAOGARVAYIJEHRASLTWPLWM-----GVPHGYEIEFIFGLDPLDSLANTTE 499
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 493 EYKTEHMTGIMIOFATGTPGPNYSIEGMENVSMDPIKSDVEYKCNINDELKIDIV-- 550
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 500 ERIFAQNLKMYTNFAATGDP--NDPRDSKSPQMPPTTTAAQYVSIN---LKPLEYRR 553
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 551 -----PEN-----DKIKOMESMFEK 565
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 554 GLRAQTCAFWNRFLPKLLSATDTLDEAEARQWKAEFHR 590
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RESULT 10
ACCS_TORCA
ID ACES_TORCA STANDARD; PRT; 586 AA.
AC P04058;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACNE).
OS Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hypnosqualea; Pristiogaster; Batoidae;
OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX NCBI_TaxId=7787;
RN [1]
RP SEQUENCE OF 10-586 FROM N.A.
RX MEDLINE=86118676; PubMed=3753747;
RA Schumacher M., Camp S., Maulet Y., Newton M., McPhee-Quigley K.,
RT Taylor S.S., Friedmann T., Taylor P.,
RL "Primary structure of Torpedo californica acetylcholinesterase
deduced from its cDNA sequence."
RL Nature 319:407-409(1986).
RN [2]
RP SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=89066695; PubMed=3198606;
RA Schumacher M.;
RT "Multiple messenger RNA species give rise to the structural diversity
in acetylcholinesterase."
RL J. Biol. Chem. 263:18979-18987(1988).
RN [3]
RP SEQUENCE OF 552-558.
RX MEDLINE=88087239; PubMed=3335534;
RA Gibney G., MacPhee-Quigley K., Thompson B., Vedvick T., Low M.G.,
RL Taylor S.S., Taylor P.;
RN [13]
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

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RT "Divergence in primary structure between the molecular forms of
acetylcholinesterase."
RL J. Biol. Chem. 263:1140-1145(1988).
RN [4]
RX ALTERNATIVE SPLICING.
RP MEDLINE=90166618; PubMed=2306366;
RA Maulet Y., Camp S., Gibney G., Rachlinsky T.L., Ekstrom T.J.,
RT Taylor P.;
RL "Single gene encodes glycopospholipid-anchored and asymmetric
acetylcholinesterase forms: alternative coding exons contain inverted
repeat sequences."
RL Neuron 4:289-301(1990).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=87008586; PubMed=3759980;
RA McPhee-Quigley K., Vedvick T.S., Taylor P., Taylor S.S.;
RT "Profile of the disulfide bonds in acetylcholinesterase."
RL J. Biol. Chem. 261:13565-13570(1986).
RN [6]
RP STRUCTURE OF THE GPI-ANCHOR.
RX MEDLINE=94079692; PubMed=8257440;
RA Wehlert A., Varon L., Silman I., Homans S.W., Ferguson M.A.;
RT "Structure of the glycosyl-phosphatidylinositol membrane anchor of
acetylcholinesterase from the electric organ of the electric-fish,
Torpedo californica."
RL Biochem. J. 296:473-479(1993).
RN [7]
RP GPI-ANCHOR.
RX MEDLINE=96176849; PubMed=8597567;
RA Bucht G., Hjalmarsson K.;
RT "Residues in Torpedo californica acetylcholinesterase necessary for
processing to a glycosyl phosphatidylinositol-anchored form."
RL Biochim. Biophys. Acta 1292:223-232(1996).
RN [8]
RP MUTAGENESIS.
RX MEDLINE=91017542; PubMed=2217185;
RA Gibney G., Camp S., Dionne M., McPhee-Quigley K., Taylor P.;
RT "Mutagenesis of essential functional residues in
acetylcholinesterase."
RL Proc. Natl. Acad. Sci. U.S.A. 87:7546-7550(1990).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=91343928; PubMed=1678899;
RA Sussman J.L., Harel M., Frolow F., Oefner C., Goldman A., Toket L.,
RL Silman I.;
RT "Atomic structure of acetylcholinesterase from Torpedo californica: a
prototypic acetylcholine-binding protein."
RL Science 253:872-879(1991).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
RX MEDLINE=96363673; PubMed=8747462;
RA Harel M., Klewegt G.J., Ravelli R.B., Silman I., Sussman J.L.;
RT "Crystal structure of an acetylcholinesterase-fasciculin complex:
interaction of a three-fingered toxin from snake venom with its
target."
RL Structure 3:1355-1366(1995).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=97143314; PubMed=8989325;
RA Raves M.L., Harel M., Pang Y.P., Silman I., Kozlikowski A.P.,
RL Sussman J.L.;
RT "Structure of acetylcholinesterase complexed with the nootropic
alkaloid, (-)-piperazine A."
RL Nat. Struct. Biol. 4:57-63(1997).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=99249780; PubMed=10231521;
RA Bartolucci C., Perola E., Cellai L., Brufani M., Lamba D.;
RT "Back door' opening implied by the crystal structure of a
carbamoylated acetylcholinesterase."
RL Biochemistry 38:5714-5719(1999).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

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[illegible]

Query Match	18.3%	Score 562	DB 1	Length 586
Best Local Similarity	28.4%	Pred. No. 86-36		
Matches 106	Conservative 96	Mismatches 211	Indels 112	Gaps 22
Qy	33	VVAETGYKVKCVKRLTYDDSYSPFGIYAAPRGELRFKAPRPPWMDGVRCCNKH	92	
Db	27	LVNFKSGVMGT-RVPLVSHISAFILGIPAEPRPGNMFRPRDEKKRQSGVMASTYR	85	
Qy	93	DKSVYDFETIGKAVCG-----SEDCILASYTNLNLPERRKRVLYIYINGGFI	139	
Db	86	NMCCQ--YYDEQPPGSGSEMMNPRENSEDCILNINWVSPRRKS-TTVVVIYIGGFY	142	
Qy	140	IGENHRMWPDPVF-IKKDVLINIQYKRALGELISNEDLVNPGNAGLKQVWALMI	198	
Db	143	SGSSLTIDVYMGKTLATEEVLVLSYRGAFFGLAHGSO-EAPGVAGLDQRAALQW	201	
Qy	199	KNCGANFGNPDNIYVPGESAGASTHYMMLTEORGLFHKGILMSGALICPMAN---	255	
Db	202	HDNIQFEGGDPKVTITGESAGASVGHMILSPGRDLFRALIIOSGSPNCMAVSVAE	261	
Qy	256	CGHRAFTLAKLAGYKGEDNDKDVLEFLMAKAPODILKLEEVULLBERTYKVMFPPGPIV	315	
Db	262	GRRRAVELGRNLNC-NINSDDELHCLREKKPQEDLIDVEMVLPED---SIFRFSEVPYI	317	
Qy	316	EPYQADCVLRKHPREYKATAMGSIPTVMGNTSYEGLEFTSILKOMPLKYLETCVNF	375	
Db	318	DGE-----FFPISLESMLNSGNEKKQIILLGVAKDGSFF-LIYGAFGFSKDS-	366	
Qy	376	VPSELADERTAPETLENGAKIKKAAH-----YNGEPTPDNFD-----	414	
Db	367	-----KISREDPMSGVALSVPHANDGLAVTLQYTTMDNDNNGKRRDGLDIDVG	417	
Qy	415	-----LCSHYTFMPMRLLOLRFNHTSGTPVLYRDEDESDLLNPKIMSGRGVYS	470	
Db	418	DHNVICLPMF--YAKTKF-----GNGYLYTFEHRNASNLVMEWM-----GYI	460	
Qy	471	HADLTFFFNOLAKRMPRESREYTIIRMGIGIIOFATGNGYSLEIGEMENVSMDIK	530	
Db	461	HGYIEIEVGLPLVKELINTAAEEALSRIIMHYATFAKGN--NEPHSOES-FWP---	514	
Qy	531	KSDEYKCLINISDELKDIV-PEMDKIRO-----WESMEEK	565	
Db	515	-----LFTTKQKFIIDLNEPKVHQRLRVQSCVFMNOFLPK	551	

ORGANOPHOSPHATE ESTERS.

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

CC HSSP: P21836; JANA. CarbesteraseB.
 DR InterPro: IPR002018; Cholinesterase.
 DR InterPro: IPR000379; Ser-ester-ase.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTERASE.
 DR PROSITE: PS00142; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolyase; Serine esterase; Glycoprotein.
 FT ACT_SITE 198 198 BY SIMILARITY.
 FT ACT_SITE 325 325 BY SIMILARITY.
 FT ACT_SITE 438 438 BY SIMILARITY.
 FT DISULFID 252 252 BY SIMILARITY.
 FT DISULFID 400 400 BY SIMILARITY.
 FT DISULFID 519 519 BY SIMILARITY.
 FT DISULFID 571 571 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 486 486 N-LINKED (GLCNAC. . .).
 FT SEQUENCE 574 AA; 65641 MW; 07755EE9FB9CB33E CRC64;

Query Match 18.28; Score 558; DB 1; Length 574;
 Best Local Similarity 29.24; Pred. No. 1,6e-35;
 Matches 167; Conservative 100; Mismatches 232; Indels 72; Gaps 21;

OY 31 ETVAAETPYGVKVKRRLTVYDSDYSFEGIPYAPVGLRFRKAPQRTPTWDGV----- 85
 DB 2 EDLITTTNGKVRGM-NLPYLGTVTAFLGIPYAPVGLRFRKAPQRTPTWDGV----- 85
 OY 86 --RDCCNKKDKSVQVDFITGKVC-----SEDCLYLSVYTNLNLPEKRVLYIHGGF 138
 DB 61 YANSCYQVNTDQSF-P-GFGSEMMNPNTLSDCLLWVMPAPRK-NATVMIVYGGF 118
 OY 139 IIGENHRDMYGPDPYFIKDD-VLLINIOYRLGALGFLSNDLNVPGNAGLKQVMAIRN 197
 DB 119 QGTSSLPYDQKFLARVERIVVSMNYRGALGFLA-SENPRAPGMGLFDQDLAOW 177
 OY 198 IKNNCANEGNPNTVRESNGASTHYMMTEOTRGLFIRGLIMSGNAICPANT--- 254
 DB 178 VQKINIAFGNPRSVTLFEGESAGASVSLHLSPSQGLFTRALIQSSSNAPAVTSLY 237
 OY 255 QOCHRAFTLAKLAGYKGEENDKDVLEFLMKAPQDLIKLEKVTLEERTKVMFPGPT 314
 DB 238 EARNRLTLAKRMGC-SRDNETEMIKCLRDKPOEILNEVYVYD---TLISVNEGPT 293
 OY 315 VEPYQADCVLPKHPREMYKTANGSIPTPMGNTSEGLEFTSILKOMPLVKELETGVN 374
 DB 294 VDGGLFLDM-----PDLQLQGFRTQTLVGNKDEGAF--LVYGAPEKDNNSIT- 345
 OY 375 FVPSGLADART-APETLEMGAKIKRAHYTG--ETPTADNEMD-----LCSHY 420
 DB 346 -TRKEFEGKLFPPRVSERGESILFHYMDMDQDAEYRGLADVDVYDNIICPALE 404
 OY 421 FWFPMHRLDLRENHSGTVLYLYRDEDEDLINRYIRMSRGVGVSHADELYFFW 480
 DB 405 FTRKFSFL-----GNDAFYFFEFHRSTKLPBEMW-----GVHNGEIEFVG 447
 OY 481 NQLAKRMKESREYKTIERMGIWIOFATGPNPSNEIEGMENV--WDPIKSDSEYK 538
 DB 448 LPLERVYVYTABELLSISIKRANFAKGNP-----NOTQNNSTFWPFKSTDEKYL 502
 OY 539 LNISDELKIDVPEMDKIKOMESMFEKHRDL 569
 DB 503 LNTSPKVTYTKLRADQCRFWTLFFPKVLEL 532

RESULT 13
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 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AcHe).
 GN ACE OR CG17907.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 (1)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87080281; PubMed=3024971;
 RX Hall L.M.C., Spierer P.,
 RT "The Ace locus of Drosophila melanogaster: structural gene for
 acetylcholinesterase with an unusual 5' leader."
 RL EMBO J. 5:2949-2954(1986).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=MH19; Canton-S, and Oregon-R; TISSUE=Embryo, and pupae;
 RC MEDLINE=90064544; PubMed=2511327;
 RX Fournier D., Karch F., Bride J.-W., Hall L.M.C., Berge J.-B.,
 RA Spierer P.;
 RT "Drosophila melanogaster acetylcholinesterase gene. Structure,
 evolution and mutations."
 RL J. Mol. Biol. 210:15-22(1989).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkley;
 RC MEDLINE=20196006; PubMed=10731132;
 RX Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abril J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch L., Beasley E.M.,
 RA Bailew R.M., Basu A., Baxendale J., Bickelstein P., Brotler P.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borovaya D., Botchan M.R., Bouck J., Cadieu E., Center A., Chandra I.,
 RA Burks K.C., Busam D.A., Butler H., Cadenhead L.B., Davies P.,
 RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson B., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Fierman C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Foster K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Glisler A., Gong F., Gorrell J.H., Gu Z., Hernandez J.R., Houck J.,
 RA Harris N.L., Harvey D., Heilmann T.J., Heilmann J., Heilmann J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegam C.,
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liou X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkllov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Pollard J., Puri V., Reese M.G.,
 RA Palazolo M., Peltan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Skupski M.P., Smith T.,
 RA Shue B.C., Spradling A.C., Turner R., Ventler E., Wang A.H., Wang X.,
 RA Spier E., Spradling A.C., Turner R., Ventler E., Wang A.H., Wang X.,
 RA Svirskas R., Tector C., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Wang Z.-Y., Wassarman D.A., Weisslock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zavei J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 [4]

RP SUBUNITS.
 RX MEDLINE=89005711; PubMed=3139459;
 RA Fournier D., Bide J.-M., Karsch F., Borge J.-B.;
 RT "Acetylcholinesterase from *Drosophila melanogaster*. Identification of
 RT two subunits encoded by the same gene.";
 RL FEBS Lett. 238:333-337(1988).
 RN [5]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=92112889; PubMed=1730712;
 RA Mulero A., Fournier D.;
 RT "Post-translational modifications of *Drosophila* acetylcholinesterase.
 RT in vitro mutagenesis and expression in *Xenopus* oocytes.";
 RL J. Biol. Chem. 267:1695-1700(1992).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC IT CAN HYDROLYZE BUTYRYLTHIOCHOLINE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H₂O = choline + acetate.
 CC SUBUNIT: THE ACTIVE ENZYME SEEMS TO BE COMPOSED OF THE NON-
 CC COVALENT ASSOCIATION OF A 55 KDA AND A 16 KDA POLYPEPTIDE. TWO
 CC ACTIVE UNITS ARE LINKED TOGETHER BY A DISULFIDE BOND AT THE C-
 CC TERMINUS OF THE 55 KDA PEPTIDE.
 CC -1- SUBCELLULAR LOCATION: LINKED TO THE MEMBRANE OF THE NEURONAL
 CC CHOLINERGIC SYNAPSE BY A GPI-ANCHOR.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X05893; CAA29326.1; -
 DR EMBL: AE003699; AAP54915.1; -
 DR PIR: A25363; A25363.
 DR PIR: A33469; A33469.
 DR HSSP: P21836; IMAA.
 DR FLYBASE: FBgn0000024; Ace.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTRASE.
 DR PROSITE: PS00122; CARBOXYL ESTERASE_B.1; 1.
 DR PROSITE: PS00941; CARBOXYL ESTERASE_B.2; 1.
 KM Hydrolyase; Serine esterase; Synapse; Membrane; Nerve; Signal;
 KM Neurotransmitter degradation; GPI-anchor; Glycoprotein.
 FT SIGNAL 1 38
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 FT CHAIN 39 649
 FT CHAIN 39 649
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 FT CARBOHYD 331 331
 FT CARBOHYD 531 531
 FT CONFLICT 99 99
 SQ SEQUENCE 649 AA: 71785 MW: 5863737FF99028C0 CRC64;
 Query Match 18.1%; Score 557; DB 1; Length 649;
 Best Local Similarity 27.8%; Pred. No. 2, 2e-35;
 Matches 172; Conservative 93; Mismatches 223; Indels 130; Gaps 25;

QY 91 HKDSVO--VDFTTG-----KVGSEDCLYSYVT----- 118
 DB 100 LSATQVEREYEPGSGEETWNPNTVSEDCLYINWPAKALRLRGANGGEHPNGK 159
 QY 119 -----NNLNPEYTKR--PVLYYINGGFTIGENHRDYGPDYFK-KDVLINTQYR 166
 DB 160 QADTDHLIHNGNPQNTNGPLILIMYIGGFMGSGATLDIYMDIMAVGNVYASFOYR 219
 QY 167 LGALGFSLNSE-----DLVNPAGNAGKDOVMALRMKNCANGCPNDITVGESAGA 221
 DB 220 VGFAGFHLIAPEMPSEPAEBAFGVGLMDALATRLMKDNAHAGCNPEWWTLEGESAGS 279
 QY 222 ASTHYMMLTQTRGLPFRGLIMSGNALICPWANTQCCORAFPLAKYKGDNDKDLFEF 281
 DB 280 SYVAQGLMSVYTRGLVYKRGMAQSTMAFMSH-WTSEKAVEIGAL-----INDCNCNAS 333
 QY 282 LMKAKPDLI---KLEEKVLTLEE---RTNKVMPFGPVEPYQTADCVLPKPRBMVK 334
 DB 334 MKTNPFAHVMSCMRSYDAKTISVQWMNSYGLISFPSPAPID-----GAFLPADPMTLMK 388
 QY 335 TAMGNSIPTMMGNSYSGLEF-----TSILQMPMLVKELETGVFVPSSEL 380
 DB 389 TADLKDYDILMGVNRDGTFFLYDFIDYDKDATALPRD-----KYLE-IMNNIFGKA 442
 QY 381 ADAERTAPETLEMGAKIKKAHVIGE-TPRADNFMDLCSHI---YFMPMHRILQLRFNHT 436
 DB 443 TQAEEREA-----IIFQYTSWEGNPGYQNOQIGRAVDHFFCTPTNEYAQLALER- 492
 QY 437 SCGPVYLYRFDPSDDLINPVRIMSGRGV-KGVSHADELYTFFWNOLAKRMPRESREYK 495
 DB 493 -GASVHYHYF-----THRTSTSLMGEMGVLHGDLEYFEGQPL-----NNSIQYR 537
 QY 496 TIE-----RMTGIMIOFATGNPNPSNLEIGENSNMPRIKSDVYKCLNISDL-KMID 549
 DB 538 PVRELKRLMSAVIEFAKGNP-----ADGGEWPNFSKEDPVYIIFSTDKIEKRL 591
 QY 550 VPENDKIKOWESMPFKHR 567
 DB 592 GPLAARCSFMDYLPKYR 609
 RESULT 14
 ACES_RAT STANDARD: PRT: 614 AA.
 ID ACES_RAT
 AC P37136;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM T).
 RX MEDLINE=93107932; PubMed=8417155;
 RA Legay C., Bon S., Vernier P., Coussen F., Massoulie J.;
 RT Cloning and expression of a rat acetylcholinesterase subunit:
 RT generation of multiple molecular forms and complementarity with a
 RT Torpedo collagenic subunit.";
 RL J. Neurochem. 60:337-346(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS H AND R).
 RX MEDLINE=93114454; PubMed=8417973;
 RA Legay C., Bon S., Massoulie J.;
 RT "Expression of a cDNA encoding the glycolipid-anchored form of rat
 RT acetylcholinesterase.";
 RL FEBS Lett. 315:163-166(1993).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H₂O = choline + acetate.
 CC SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
 CC -1- CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGEN-

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: AF061815; AAC64270.1; .
DR EMBL: AF061813; AAC64270.1; JOINED.
DR EMBL: AF061814; AAC64270.1; JOINED.
DR PIR: S10712; S10712.
DR HSP: P22303; 2CLT.
DR GlycosylatedB: P23795; .
DR Interpro: IPR002018; Carboxylesterase.
DR Interpro: IPR000997; Cholinesterase.
DR Interpro: IPR000379; Ser_estr_site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PRO0878; CHOLINESTERASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydroxylase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW Neurotransmitter degradation; Glycoprotein; Alternative splicing.
FT SIGNAL 1 30
FT CHAIN 1 31 613
FT ACT_SITE 233 233 ACETYLCHOLINESTERASE.
FT ACT_SITE 233 233 BY SIMILARITY.
FT ACT_SITE 364 364 BY SIMILARITY.
FT ACT_SITE 477 477 BY SIMILARITY.
FT DISULFID 99 126 BY SIMILARITY.
FT DISULFID 287 302 BY SIMILARITY.
FT DISULFID 439 559 BY SIMILARITY.
FT DISULFID 610 610 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 494 494 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 574 613 DTIDEAKONKAEPHMSSTYVHMKNOFDHYSKODRCSDL
-> ASEPCTCGSPAHGEAPRRPGLPLPLLLFLLSRL
-> ASEPCTCGSPAHGEAPRRPGLPLPLLLFLLSRL
FT CONFLICT 46 46 R-> E (IN REF. 2).
FT CONFLICT 169 169 T-> V (IN REF. 2).
FT CONFLICT 212 212 W-> S (IN REF. 2).
FT CONFLICT 323 323 S-> H (IN REF. 2).
FT CONFLICT 352 352 H-> V (IN REF. 2).
FT CONFLICT 424 424 L-> W (IN REF. 2).
FT CONFLICT 524 524 D-> A (IN REF. 2).
FT CONFLICT 549 554 EVRRGL-> GVPOAS (IN REF. 2).
FT CONFLICT 571 571 S-> N (IN REF. 2).
SQ SEQUENCE 613 AA: 67663 MM: 698D4F0DF8624B12 CRC64;

Query Match 18.1%; Score 555.5; DB 1; Length 613;
Best Local Similarity 30.9%; Pred. No. 2,7e-35;
Matches 163; Conservative 84; Mismatches 229; Indels 51; Gaps 17;

QY 40 GKVGAVRLTYVDDSYYSFEGIPYAPVGLRKAFQRPYPMGVDCCNKKDKSVQ-V 98
D 45 GRLKGL-RLMAPRGVSAFLDIPPAEPVGRPLPEPRKRPVGLNATAFQGVQYV 103
QY 99 DFIFGKVGCG-----SEDCLYLSVYTNLNPETKRPLVLYIHGGFPIGENHNRDMY 148
D 104 DTLPGREGTAMNPNKRLSDCLYNWTPYPPSSFTPLVWITYGGFTSGASSLDVY 163
QY 149 GPDIYIKRD-VLLINIOYRLGALFLNSEDLNVPNGNLKQVMAIRWIKNCANFGG 207
D 164 DGRFLTQAEGLVLSMNRVGAFFGLALPG-SREAPGVGLDRLALQWQEVNAAFGG 222
QY 208 NPDNITYFGESAGASTHYKMLTEOTRGLFHRLGILMSGNAICPWANT---OCQHRATFLA 264
D 223 DPTSVTLTFGESAGASVGMHLSPSPRGLFHRVLOSAPNGAPWATVGVGEARRATLLA 282
QY 265 KLAGYK---GSDNKKDVLKLEKAKKPODLKLEKVLTLERTNKKVMPREGTVEPYOTA 321
D 283 RLVCPPGAGAGNDTELVACLRAPADLVDEKRVLPQF---SVFRFSFVYVDGDFLS 339
QY 322 DCVLPKHPREKAVKTAWGNSIPTMGNTSYEGIFTSILKQMPMLVKELETGVNFPSELA 381

D 340 DT-----PEALINAGDEHGLQVLGVVKKDEGSYE-LVYGAPGFSKDNESLISRA-OFIA 391
QY 382 DAERTAPETLEMGAKIKKAHVTG----ETPT--ADNFMDCSHIYFPPMIRLL-QLRFN 434
D 392 GVRVGVPOASDLAEAVVLYHTDMLHPEDPARLREALSDVVDHNVCCPVQOLGRILA-- 449
QY 435 HTSGTPVLYRFDPDSEDLINPYRIMSGRGKGVSHADELTYPFWQLAKRMPKESREY 494
D 450 -AGCARVYAYIFEHRASTLSWPLMM-----GVPHGYELIEFIFGLPLEBSLWYTIER 500
QY 495 KTIEMTGIWIOFATYTGNPISNETEGMENVSMDPIKSDDEVYKCLNTI 541
D 501 TFAOQLRMRYMANEFARTGDP--NDPRDPKAPQWPPPYTAGAQQYVSINL 545

Search completed: April 4, 2003, 09:13:36
Job time: 13.6371 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:09:58 ; Search time 56.8533 Seconds
(without alignments)
2065.788 Million cell updates/sec

Title: US-09-776-910-8
Perfect score: 3073
Sequence: 1 MNPNVSLMKIKKIKICIN.....PEMDKIKQWSEMEKRDLE 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21: *
1: sp.archaea: *
2: sp.bacteria: *
3: sp.fungi: *
4: sp.human: *
5: sp.invertebrate: *
6: sp.mammal: *
7: sp.mhc: *
8: sp.organelle: *
9: sp.phage: *
10: sp.plant: *
11: sp.podent: *
12: sp.virus: *
13: sp.vertibrate: *
14: sp.unclassified: *
15: sp.virus: *
16: sp.bacteriap: *
17: sp.archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3073	100.0	570	5	Q25252 lucilia cup
2	2431	79.1	570	5	Q9XZ70 musca domes
3	2348	76.4	570	5	Q9U409 haemaphys
4	2006.5	65.3	572	5	Q9VIB5 drosophila
5	1966.5	64.0	556	5	Q24201 drosophila
6	1412.5	46.0	567	5	Q9VIB3 drosophila
7	1411.5	45.9	558	5	Q24202 drosophila
8	1408.5	45.8	554	5	Q9VIB0 drosophila
9	1389.5	45.2	572	5	Q9VIB1 drosophila
10	1378.5	44.9	572	5	Q24203 drosophila
11	1353.5	44.0	565	5	Q9N159 drosophila
12	1330.5	43.3	566	5	Q961M0 drosophila
13	1324.5	43.1	554	5	Q9VIC2 drosophila
14	1322.5	43.0	554	5	Q24195 drosophila
15	1306.5	42.5	564	5	Q9N161 drosophila
16	1302.5	42.4	566	5	Q9W243 drosophila

17	1295.5	42.2	565	5	Q9VIC3 drosophila
18	1276.5	41.5	553	5	Q24194 drosophila
19	1248.5	40.6	345	5	Q9N153 drosophila
20	1238	40.3	542	5	Q95030 drosophila
21	1238	40.3	542	5	Q9VIB9 drosophila
22	1233.5	40.1	549	5	Q24204 drosophila
23	1230	40.0	542	5	Q24198 drosophila
24	1228.5	40.0	530	5	Q91715 drosophila
25	1123	36.5	540	5	Q8W089 drosophila
26	1114	36.3	540	5	Q92025 drosophila
27	1112	36.2	540	5	Q8W088 drosophila
28	1109	36.1	540	5	Q23733 drosophila
29	1073	34.9	551	5	Q9VIC1 drosophila
30	1069.5	34.8	543	5	Q8SZ45 drosophila
31	1069.5	34.8	548	5	Q24196 drosophila
32	1053	34.3	446	5	Q9N155 drosophila
33	1045	34.0	540	5	Q9G095 drosophila
34	1036	33.7	540	5	Q91920 drosophila
35	1035	33.7	540	5	Q23734 drosophila
36	1025	33.4	540	5	Q23735 drosophila
37	1022.5	33.3	541	5	Q9VIC0 drosophila
38	1019.5	33.2	541	5	Q24197 drosophila
39	995	32.4	541	5	Q9N158 drosophila
40	955.5	31.1	568	5	Q9VIB6 drosophila
41	940.5	30.6	467	5	P91597 culix pipie
42	938.5	30.5	42	5	P91596 culix pipie
43	937	30.5	401	5	Q9N160 drosophila
44	934.5	30.4	467	5	P91598 culix pipie
45	933	30.4	505	5	Q23736 culix quing

ALIGNMENTS

RESULT 1
ID Q25252 PRELIMINARY; PRT; 570 AA.
AC Q25252: Q25247;
DC 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Alpha esterase (LCAE7) (Carboxylesterase).
GN LCAE7.
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestriidae; Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LS7;
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
RL Insect Mol. Biol. 5:0-0(0).
RN [2]
RP SEQUENCE OF 70-181 FROM N.A.
RC STRAIN=LS7;
RA Newcomb R.D., East P.D., Russell R.J., Oakeshott J.G.;
RL Insect Mol. Biol. 0:0-0(0).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; U56636; AAB67728.1; -;
DR EMBL; U49421; AAA92012.1; -;
DR HSSP; P37967; IOE3.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000379; Ser-estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
SQ SEQUENCE 570 AA; 65416 MW; 399D72B3A0F338FD CRC64;
Query Match 100.0%; Score 3073; DB 5; Length 570;
Best Local Similarity 100.0%; Pred. No. 2,2e+246;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 KM HydroLase: 570 AA; 65613 MW; 18DA0A9A4AB970D CRC64;
 SQ SEQUENCE

Query Match 76.4%; Score 2348; DB 5; Length 570;
 Best Local Similarity 73.9%; Pred. No. 3.3e-186;
 Matches 421; Conservative 66; Mismatches 83; Indels 0; Gaps 0;

QY 1 MNFVSLMEKRLKIKICLENKFLNRLTNTNETVAETEGYGVKKRLTYVDDSYSEEG 60
 DB 1 MNFVSLMEKRLKIKICLENKFLNRLTNTNETVAETEGYGVKKRLTYVDDSYSEEG 60
 QY 61 IPYAPRGVGLRFRKAPQRPPTMDGVRDCCNKKDKSVQVDFITGKCGSEDCLYLVYNN 120
 DB 61 IPYAPRGVGLRFRKAPQRPPTMDGVRDCCNKKDKSVQVDFITGKCGSEDCLYLVYNN 120
 QY 121 LNPETKRPVLVYIHGGGFTIGENHRDMYGPDYFIKKDVVLINIOYRLGALGFLNSDEL 180
 DB 121 LNPETKRPVLVYIHGGGFTIGENHRDMYGPDYFIKKDVVLINIOYRLGALGFLNSDEL 180
 QY 181 NVPGNAGLKDQVMAALRWIKNNCANGNPDNITYVGEAGASATHYMLTQTRGLFHRG 240
 DB 181 NVPGNAGLKDQVMAALRWIKNNCASFGSDPTLFGESAGASTHYMMITQARGLFHR 240
 QY 241 ILMSGNAICPMANTQCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPDLILKEKVLTL 300
 DB 241 VLMGTAACIAVHQQCOHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPDLILKEKVLTL 300
 QY 301 EERTNKVAFPRGPRVYQYADCVLPKHPREKVTAMGNSIPTMMGNTSYGGLFETSLK 360
 DB 301 EELDKVAFAGPTPEYEDCVLPKPNREMLKTAMGNSIPTLIGNTSYGGLFETSVGK 360
 QY 361 QMPMLVKELETCVNPVPELADAEPTALEMGAIKKIKKAVTGPTRADNMDCSITY 420
 DB 361 QMPMLVKELETCVNPVPELADAEPTALEMGAIKKIKKAVTGPTRADNMDCSITY 420
 QY 421 FMFPMHRLQLRFNHTSGTPYLYKRFDPSEDLINPYRIMSGRGVSHADELTFYFM 480
 DB 421 FMFPMHRLQLRFNHTSGTPYLYKRFDPSEDLINPYRIMSGRGVSHADELTFYFM 480
 QY 481 NOLAKRPKESREKRTIRMGIMIQFTTGNPNYSNEIEGEMVSWDPDIKSDEYVKCLN 540
 DB 481 NOLAKRPKESREKRTIRMGIMIQFTTGNPNYSNEIEGEMVSWDPDIKSDEYVKCLN 540
 QY 541 ISDELKMLDVPMDKIKOWESFEKHRDLF 570
 DB 541 ISDELKMLDVPMDKIKOWESFEKHRDLF 570

RESULT 4
 QYVIBS
 ID QYVIBS PRELIMINARY: PRT: 572 AA.
 AC QYVIBS;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Alpha-EST7 protein (GI13950P).
 GN ALPHA-EST7 OR CG1112.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Morten J.R., Yandell M.D., Zhang O., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abriil J.F., Agbayan A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotilier P.,
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA De Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibsagwan C.,
 RA Jajall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Slden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zheng G., Zhou Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Fise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Paclob J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celiker S.,
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/FILIPASE FAMILY.
 DR EMBL: AE003671; AAF54010.1; -
 DR EMBL: AY051473; AAK92897.1; -
 DR HSSP: P21836; IMAA
 DR FlyBase: FBgn0015575; alpha-Est7.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 KW HydroLase.
 SO SEQUENCE 572 AA; 65435 MW; 693D9360DA1BAE27 CRC64;

Query Match 65.3%; Score 2006.5; DB 5; Length 572;
 Best Local Similarity 64.0%; Pred. No. 7.3e-158;
 Matches 365; Conservative 91; Mismatches 113; Indels 1; Gaps 1;

QY 1 MNFVSLMEKRLKIKICLENKFLNRLTNTNETVAETEGYGVKKRLTYVDDSYSEEG 60
 DB 1 MNFVSLMEKRLKIKICLENKFLNRLTNTNETVAETEGYGVKKRLTYVDDSYSEEG 60
 QY 61 IPYAPRGVGLRFRKAPQRPPTMDGVRDCCNKKDKSVQVDFITGKCGSEDCLYLVYNN 120
 DB 61 IPYAPRGVGLRFRKAPQRPPTMDGVRDCCNKKDKSVQVDFITGKCGSEDCLYLVYNN 120
 QY 121 LNPETKRPVLVYIHGGGFTIGENHRDMYGPDYFIKKDVVLINIOYRLGALGFLNSDEL 180
 DB 121 LNPETKRPVLVYIHGGGFTIGENHRDMYGPDYFIKKDVVLINIOYRLGALGFLNSDEL 180
 QY 181 NVPGNAGLKDQVMAALRWIKNNCANGNPDNITYVGEAGASATHYMLTQTRGLFHRG 240
 DB 181 NVPGNAGLKDQVMAALRWIKNNCASFGSDPTLFGESAGASTHYMMITQARGLFHR 240


```

OY 241 ILMSGNAICPWA-NTOCORAFITLAKLAGYKEDNDKVLLEFLKAKKAPODILKLEKVL 299
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 ILOSSAICPMAYNDIDHNPYRIAKLAVGKEDNDKVLLEFLONVAKKDLINVEENVLT 300
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 300 LEERNKWKMPGPTVEYOTADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFTSIL 359
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 LEERNKWKMPGPTVEYOTADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFTSIL 360
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 360 KOMPLVKELETGVNVPSELDAERTAPETLEMGAKIKKAVHGVETPADNEMDLCSH 419
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 KLMPOVLOOLDAGTPEIPKELLATEPESKEKLDWSAQIRDVHRTGSESTPDNYDLCSY 420
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 420 YEFEPALRVVSHHAYAAAPYEFYRYDSEBELLEFPYRMLRGVAGVSHADLSYOF 480
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 421 YEFEPALRVVSHHAYAAAPYEFYRYDSEBELLEFPYRMLRGVAGVSHADLSYOF 480
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 480 WNOIARMPKESREKYTERMTGIMTGFATGPNYSNEIEGEMNSMPRIKSDSVYK 539
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 481 SSLARLPKESREKYTERMTGIMTGFATGPNYSNEIEGEMNSMPRIKSDSVYK 540
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 540 NISDELKMTDVPKMDIKOMESMEKRD 569
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 541 NISDELKMTDVPKMDIKOMESMEKRD 570
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 5

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O24201 PRELIMINARY: PRT: 556 AA.
ID O24201:
AC O24201: 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Alpha esterase (Fragment).
GN ALPHA-EST7 OR AET OR CG1112.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Ephydroidea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Robin C., Medveczky K.M., Russell R.J., Oakeshot J.G.;
RL J. Mol. Evol. 0:0-0(0).
CC 1. SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL: U51050; AB01149.1; -.
DR HSP: P21856; IMAA; alpha-est7.
DR Flybase: FBgn001575; alpha-est7.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser-esterase.
DR Pfam: PF00135; Coesterase; 1.
DR Prosite: PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolase.
FT NON_TER 1 1
FT NON_TER 556 556
SQ SEQUENCE 556 AA: 63397 MW: AF0F80A1D3C34425 CRC64:

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Query Match 64.0%; Score 1966.5; DB 5; Length 556;

Best Local Similarity 64.9%; Pred. No. 1.5e-154; Indels 1; Gaps 1;

Matches 359; Conservative 85; Mismatches 108; Indels 1; Gaps 1;

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OY 18 IENKFLYRLTJNETVAETEGYKGVKRLTYDDSYSEFECIPYAPQPVGELRKAQ 77
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 IEHVQOYRSTNETVADTEYGVQKIRKLSLXDPYSFESGIPYAPQPVGELRKAQ 61
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 78 RPTMDGVRDCNHNKDSVOVDITGKVGSEDCLYSYTNLNPETKRPVLYVTHGG 137
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 RPTMDGVRDCNHNKDSVOVDITGKVGSEDCLYSYTNLNPETKRPVLYVTHGG 121
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 138 FTIGENHMDYGPDIKAVYLVINIOYRGAGFELINSEDLNVEGNALQOVVALRW 197
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 122 FTIGENHMDYGPDIKAVYLVINIOYRGAGFELINSEDLNVEGNALQOVVALRW 181
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 198 IKNNCANFGNPDNTYVGSAGASTHYMMLTEOTRGLEPHRGITLMSGNAICPWA-NTOC 256
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 182 IKNNCANFGNPDNTYVGSAGASTHYMMLTEOTRGLEPHRGITLMSGNAICPWA-NTOC 241
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 257 OHRATFLAKYKEDNDKVLLEFLKAKKAPODILKLEKVLLEERNKWKMPGPTVE 316
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 242 TNPYRIAKLAVGKEDNDKVLLEFLONVAKKDLINVEENVLTLEERNKWKMPGPTVE 301
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 317 PYOTADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFTSILKOMPLVKELETGV 376
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 302 PESTPECVISKEPKEMKRAMNSIPMFIIGNTSYEGLEFTSILKOMPLVKELETGV 361
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 377 PSELDAERTAPETLEMGAKIKKAVHGVETPADNEMDLCSHIFWPMHRLDLRFNHT 436
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 362 PSELDAERTAPETLEMGAKIKKAVHGVETPADNEMDLCSHIFWPMHRLDLRFNHT 421
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 437 SGTPYLYRDPDSEDLINPYRIMRSGRGVAGVSHADLSYOFSSILARRPKESREYN 481
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 422 AGAVYFRRYDSEBELLEFPYRMLRGVAGVSHADLSYOFSSILARRPKESREYN 481
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 497 IERTGIMTGFATGPNYSNEIEGEMNSMPRIKSDSVYK 556
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 482 IERTGIMTGFATGPNYSNEIEGEMNSMPRIKSDSVYK 541
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 557 KQWESMEKRD 569
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 542 KQWESMEKRD 554
    |||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 6

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O9YIB3 PRELIMINARY: PRT: 567 AA.
ID O9YIB3:
AC O9YIB3: 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Alpha-EST8 protein.
GN ALPHA-EST8 OR CG1112.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BERKELEY;
RC MEDLINE-20196006; PubMed-10731132;
RX Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwey L.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein F., Brotlier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadwell E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Evans J.E., Gabor C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fodor C., Gabor C., Gabor C., Gabor C., Gabor C., Gabor C., Gabor C.,
RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Hartvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin L., Houston K.A., Howland T.J., Wei M.-H., Ibegyan C.,
RA Jaitani M., Kalish J., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Moberg C., Morris J., Mostrel A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

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ID 09YIB0 PRELIMINARY: PRT; 554 AA.
 AC 09YIB0:
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Alpha-EST9 protein.
 GN ALPHA-EST9 OR CG1128.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxId=7227;
 ON (1)
 RX SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RP MEDLINE=20196006; PubMed=10731132;
 RX Adams M.D., Cealniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abdl J.F., Agdayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 Butts K.C., Cawley S., Dahike C., Davenport L.B., Davies P.,
 Cherry J.M., Delcher A., Deng Z., Cadieu E., Center A., Chandra I.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 Jaitli M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 Jaitli M., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Klimel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merulov G., Mishina N.V., Mobarry C., Morris J., Moshell A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon R., Nuskern D.R., Paclet J.M.,
 Palczolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Palczolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Ralner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Sidenkamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Sylvestre R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Massaman D.A., Weinstein G.M., Wu D., Yang S., Yao Q.A.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster."
 RT Science 287:2185-2195(2000)
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
 CC EMBL: AE003671; AAF54014.1; -
 DR HSSP: P37967; IOE3.
 DR FlyBase: FBgn0015577; alpha-Est9.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser-estrs_site.
 DR Pfam: PF00135; Coesterase_1.
 DR PRINTS: PR00878; CHOLNESTRASE.
 DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
 KM Hydrolyase.
 SQ SEQUENCE 554 AA: 63670 MW: 0A72368389DFC2B CRC64:

Db 2 VDEKVOARRRTSKRYVSTTYGPIKGVKRSIIYGOSYFSEFRIIPAKPPVGLNRYKAPQ 61
 QY 78 RPTPDGVRDCNNKDKSVQVDFITGKVGSEDCILSYVNNLNPETKRPVLYIHGGG 137
 Db 62 PPEVTEVRSTSGGPPRLOKHVFEMTDSGDCILYINVTYTKLTKPMPVWVIYGGG 121
 QY 138 FIFGHNHDMYGPDPYFIKIDVLLINIQRLGALGELSLSNEDLVNNGNGLKQVWALRM 197
 Db 122 FQFGASRECSYDVLNREDVVISINRLGPIGLFCLDPELDVPONAGLKQVWALRM 181
 QY 198 IKNNCANFGNDNITVVGESAGASPHYMLTEOTGLFPHRGLMSGNALCMWANTQOQ 257
 Db 182 VKANCSRFEGDSANITIFGDSASASVHYMTTQTHGLFPAKALCMGNTLSPMAVTPQR 241
 QY 258 HFAETLAKLAGYKGDNDKVDLEFLMKAKPODLIKLEKVLTLDEERNKMPFPGPVPR 317
 Db 242 NMPYRLAVAGTAGENRNDPWEFLKNAKGSIIKANGLCIDDEKKEIGFSGVPIER 301
 QY 318 YQPADCVLRKHPREKVTWAGNSITPMGNTSYEGLFSTILKQMPILYKELTCVNFVP 377
 Db 302 YVTSHCVPKPKPIEMKRTAMSNIPILLIGVSNEGILLSETKTNPKCLNELDCRRVVP 361
 QY 378 SELADERTAPETLENGAKIKRAHYGENTPAD---NEMDLSHYTFEPHRLLOLRFN 434
 Db 362 IEL-NMDRESALCREYGDQROCYGDKTPPSIDTLEHYLOWVSHYFEPYRVLRLQ 420
 QY 435 HTSGTPVLYLRPDPSEDLINPRIRSRGVKGVASHADELYFPWNLAKRMPKESREY 494
 Db 421 YARSAPTLYLRFPDSDKH-PNHLRLISCGKKNRGCTHGGDLSLEYNSLARLKNHTREY 479
 QY 495 KTIKRMGIMIOFATTGNP-YSNEIEGEMVSW---DPIKSDVEYKCNINISDELKMDIV 550
 Db 480 KCIERLYOLMWHFAACGNPNRDEQEDL---WQVPDPAVERKHOLCLNIDELKVIDV 535
 QY 551 PEMDKIKOWMESMEFK 565
 Db 536 PDLKLWMESEFFRR 550
 RESULT 9
 ID 09YIB1 PRELIMINARY: PRT; 572 AA.
 AC 09YIB1:
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Alpha-EST9 protein.
 GN ALPHA-EST9 OR CG1128.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxId=7227;
 ON (1)
 RX SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RP MEDLINE=20196006; PubMed=10731132;
 RX Adams M.D., Cealniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
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 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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 Butts K.C., Cawley S., Dahike C., Davenport L.B., Davies P.,
 Cherry J.M., Delcher A., Deng Z., Cadieu E., Center A., Chandra I.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

DB 480 YLSYNSLARKLNHTRKCIERLWLTWHPACGNPFDEOEDL-----WQVPDPATVE 535
 QY 533 DEVYKCLNIDSLKMDVPEMDKIKOMESMFEK 565
 DB 536 KNOCLKNIDSLKMDVPEMDKIKOMESMFEK 568

RESULT 11

Q9N159 PRELIMINARY: PRT: 565 AA.

AC Q9N159: 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Alpha-esterase 2.
 GN AE2A OR AE2.
 OS Drosophila buzzatii (Fruit fly).
 OC Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
 OC Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
 OC Ephydroidea: Drosophilidae: Drosophila.
 OC NCBI_taxid=7264;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Robin C., Claudianos C., Russell R.J., Oakeshott J.G.:
 RT "The alpha-esterase cluster of Drosophila buzzatii."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AF216210; AAF26723.1; .
 DR HSSP: P37967; 10E3.
 DR Flybase: FBgn0029452; DbuzAe2A.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLNSTRASE.
 DR HydroLase.
 SQ SEQUENCE 565 AA: 64618 MW: 0BC92E956B21006E CRC64;

Query Match 44.0%; Score 1353.5; DB 5; Length 565;
 Best Local Similarity 46.2%; Pred. No. 1.1e-103; Indels 25; Gaps 9;
 Matches 262; Conservative 110; Mismatches 170;

QY 11 LMKIKICLNKFLNRTNENYVAETEGKGVKRLTVDDSYR-SFEGIPYAQPPVG 69
 DB 10 LMGAKFVGHKVOQRLSHTIVATNGRGRLKRTVYQELVYCAFEGLPYAKPPLG 69
 QY 70 ELRFKAPQRPRTWGVYRDCCNHKSQVDFITGKVCSEDCLYSYTNNINPETKRPV 129
 DB 70 ELRFKAPQRPRTWGVYRDCCNHKSQVDFITGKVCSEDCLYSYTNNINPETKRPV 129
 QY 130 LVIYHGGFTIGENHNDMGPRDYFIKKDVLINIOYRICALGFLSLNSEDLVNPGNAGIK 189
 DB 130 MVIYGGGFGKGEASRDYISPDYFMKNVLYTINRLALGFLSLKDKDLDPGNAGIK 189
 QY 190 DQWALRWIKNNCANFGNPDNITVFGESAGASTHYMLTQTRGLRHGLMSGNAIC 249
 DB 190 DQWALRWIKNNCANFGNPDNITVFGESAGASTHYMLTQTRGLRHGLMSGNAIC 249
 QY 250 PMANTQCOHRAFTLAKLAGYKGEDNDKVLEFLMKAKPOLLKLEKVLTLERTKVMF 309
 DB 250 AMATPDRNNALRLAROMGYKGTDSIEDILRYLTKASARQIASHDEIYILDEFREFLYL 309
 QY 310 PEGTVEPYQTADVLPKHPREWKATMGNSIPTMGNTSYEGILFTSILKOMPVLKEL 369
 DB 310 AFGIVEPYESENKVPKREKMLATMGNSILPIYVGNSEFGLFYSQVLRANDPVMVTF 369
 QY 370 ETCVNFVPSLADERTAPLE--MGAKIKRAHYGTETPADNF---MDLCSHITYWEPW 425
 DB 370 H---NITREV--SESSPEQLQVLRKOLYFGDEORBCMKLEFALDIFSHQIWHDL 424
 QY 426 HRLQLRNNHSGPVIYLRDPDSIEDLINPYRIMRSGRGVSHADELTYEFWNOJAK 485

DB 425 HRNVAARLTYPADPTLYLRFEDSPH--FNQFRLVCGDVRGVSHGDIYSLEYVNLAT 483
 QY 486 RMDKESREKXTERMTGVIQIOPATIGNP-----YSENEGEMNVSMDPIKRS-DEVYKCL 539
 DB 484 KLSKSPPEYLLTKRMVGMWTTFAANSDEPNCMTATSNK-----WTVYQHTPRAHNCF 535
 QY 540 NISDELKMDVPEMDKIKOMESMFEK 566
 DB 536 NISSEMIMLPATALAIWDTFYDKN 562

RESULT 12

Q961N0 PRELIMINARY: PRT: 566 AA.

AC Q961N0: 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE GH15053p.
 GN ALPHA-EST2 OR CG2505.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
 OC Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
 OC Ephydroidea: Drosophilidae: Drosophila.
 OC NCBI_taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BERKELEY;
 RC Stipledon M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champé M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacleb J., Parada V., Park S., Phouananaong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AY051497; AAK92921.1; .
 DR Flybase: FBgn015570; alpha-Est2.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000379; Ser-estrs_s1te.
 DR Pfam: PF00135; Coesterase; 1.
 DR HydroLase.
 SQ SEQUENCE 566 AA: 64664 MW: 84C4FF4E3C0CF312 CRC64;

Query Match 43.3%; Score 1330.5; DB 5; Length 566;
 Best Local Similarity 44.7%; Pred. No. 9.2e-102; Indels 13; Gaps 7;
 Matches 255; Conservative 115; Mismatches 187;

QY 1 MNFVSLMEKLLKIKICLNKFLNRTNENYVAETEGKGVKRLTVYD-DSYSEF 59
 DB 1 MEVOVGWPKLTKKGAOLVGHKVOYRLSTGHVYILDTKGGVYRGRLKRTVYDKEPYFAFE 60
 QY 60 GTPAOPPVGELRFKAPQRPRTWGVYRDCCNHKSQVDFITGKVCSEDCLYSYTNNIN 119
 DB 61 GTPAOPPVGDLRFKAPQRPPEPQVLTCTNSKPMQRMILGIVEGSEDCLYHNVYK 120
 QY 120 NLNPEKRPVLYIHGGFTIGENHNDMGPRDYFIKKDVLINIOYRICALGFLSLNSED 179
 DB 121 ALKSEKPLPVYIYGGGFGKGEASRDYISPDYFMKNVLYTINRLALGFLSLKDKK 180
 QY 180 LNVGNGNLKQWVALRMKNNCANFGNPDNITVFGESAGASTHYMLTQTRGLRHLR 239
 DB 181 LDVPNAGLKVQWVALRMKNNCANFGNPDNITVFGESAGASTHYMLTQTRGLRHLR 240
 QY 240 GILMSGNAICPMWANTOCORAFRTLAKLAGYKGEDNDKVLEFLMKAKPOLLKLEKVL 299
 DB 241 ALMSGCALSMKSVESPDNNNAFLAQNIGYKGEDKADVLSFLSKVCARQIAAIDOVIN 300
 QY 300 ILEERTNKVFPPEGPVVEYQTADVLPKHPREWKATMGNSIPTMGNTSYEGILFTSIL 359
 DB 301 IDEVSEFLFAGVPIEYEDHCVPRKHKDLSEAMGNDIPIYVGNSEFGLFYSQV 360
 QY 360 KOMPVLKELTYEFCVNFVPSLADERTAPLE--MGAKIKRAHYGTETPADNF---MDLC 416

Db 361 RKDPAWLNKFNH---NILPREVRETSLEGGDL-LVRLKQLYFNNEQMSMEMFEALNIF 416

Qy 417 SHITFPMRHLQLRNHNHSGTVPYLYLRFPDSEDILNIPYRIRSGRGVSHADELT 476

Db 417 SHRIWMDTHFRILAROSYAKRTPTLYLRFDSPH-FNCFRRLVCGDRIRGVAHADEL5 475

Qy 477 YEFNOLAKRMRKREKTERMTGIWIOFATGNPNSIEGMENSWMDPIK-KSDEY 535

Db 476 YLFNIIASLKDKSSMEKTERVNGWMTSPASSGNPCPE---LGSAKWEAVOLKENAV 532

Qy 536 YKCLINISDELKMDVPEMDKIKOWESMEK 565

Db 533 EKCFCNISHDLEMRDLPESSDCLAVMDTFEPR 562

RESULT 13

ID QYVIC2 PRELIMINARY; PRT; 554 AA.

AC QYVIC2

DT 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)

DE Alpha-EST2 protein.

GN ALPHA-EST2 OR CG2505.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,

RA Wen K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abell J.F., Agbayan A., An H.-J., Andrews-Piannoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,

RA Burtka K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher S., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,

RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzzy D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacib J.W.,

RA Palazono K., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Styrtas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

DR EMBL: AE003671; AAF54003.1; -

DR HSSP: P37967. 10E3.

DR FlyBase: FBgn0015570; alpha-Est2.

DR InterPro: IPR002018; CarbinesteraseB.

DR InterPro: IPR000997; Cholinesterase.

DR InterPro: IPR000379; Ser_estr_site.

DR Pfam: PF00135; Coesterase; 1.

DR PRINTS: PR00878; CHOLINESTRASE.

KW Hydrolase.

SO SEQUENCE. 554 AA; 63254 MW; 6E4AC221A45B02D CRC64;

Query Match 43.1%; Score 1324.5; DB 5; Length 554;

Best local similarity 45.6%; Pred. No. 2.8e-101;

Matches 252; Conservative 112; Mismatches 176; Indels 13; Gaps 7;

Qy 18 IENKFLNRYLTNETVAETEGYKVKVRLTYVD-DSYSEFEGIPYAOPIYGLRFRAP 76

Db 6 VGHKVOQYRLSTGHTVIIDTKYGVGRLOKRTYVDKEFYAFEGIPYAKPPVGLRFRAP 65

Qy 77 QRPFTMGVRCOCNKKDSYQVDFITKGVCSGECCLTYSTNNLNPNPETKRVLYYING 136

Db 66 QPPEWGVLCNTRNSKPMQNMMLGIVESEDC.LHNVYKALKSEKPLVYIWIYGG 125

Qy 137 GFIIGENHRDYGDPDYFTKKDVLINIOYRLGALGFLSLNSEDNLVPGNAGLQDVMLR 196

Db 126 GFGKEASRDYSPDYFMKKPVFAINYRLAALGFLSLKDKRLVPGNAGLQDVMLR 185

Qy 197 WIKNNCANFGNPDNIYVGESAGASTHYWMLTEOTRGLFHRGLMSGNAICPMANTOC 256

Db 186 WISONIAHFNGBPNNTITMGESAGASVHVMTTQTRGLFKAIAWOSCALSEWVESPD 245

Qy 257 QHRAFTLKLAGEKEDNDKDVLEFLMKAKPPDCLKLEKRYLTERTNKVMEPPRPY 316

Db 246 NNMAFLQNIQYKGEDEADADVLSTKVCARQAIADODVNLNDEVSFLFAFGPVLE 305

Qy 317 PYOTADCVLPKPRRMVYTAGNSIPTMGNTSYEGLEFSTSLKOMPMLVKELETCVNFV 376

Db 306 PYETHCVLPKRRHKLSEBANGNDIPYIVGNSFGLSTSYOLVRDPAWLNKFNH---NIL 362

Qy 377 PSELADERTAPETLEMKAKIKAHVGTETPAADF---MDLCSITTEFPMRHLQLE 433

Db 363 PREVETSSLEGGDL-LVRLKQLYFNNEQMSMEMFEALNIFSHROIWMDTHFRILARQ 421

Qy 434 NHTSGTPYLYLRFPDSEDILNIPYRIRSGRGVSHADELTTFYFNOLAKRMPKRES 493

Db 422 STAPKTPYLYLRFPDSDH-FNCFRRLVCGDRIRGVAHADELSTLYFNIIASLKDKSSNE 480

Qy 494 YKTERMTGIWIOFATGNPNSIEGMENSWMDPIK-KSDEYVCLNIDELKMDVPE 552

Db 481 YKTERMTGIWIOFATGNPNSIEGMENSWMDPIK-KSDEYVCLNIDELKMDVPE 537

Qy 553 MDKIKOWESMEK 565

Db 538 SDCLAVMDTFEPR 550

RESULT 14

ID Q24195 PRELIMINARY; PRT; 554 AA.

AC Q24195

DT 01-NOV-1996 (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Alpha esterase.

GN ALPHA-EST2 OR AE2 OR CG2505.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RJ Robin C., Medveczky K.M., Russell R.J., Oakesholt J.G.,

RL J. Mol. Evol. 0:0-0(0).

CC	-1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR	EMBL: U51044; AAB01143.1; -.
DR	HSSB: P37967; 10E3.
DR	flybase: FBgn0015570; alpha-Est2.
DR	InterPro: IPR002018; Carboxylesterase.
DR	InterPro: IPR000379; Ser_ester_ssite.
DR	Pfam: PF00135; Coesterase_1.
KW	Hydrolase.
SEQUENCE	554 AA; 63242 MW; 17B4CCD344E2PDBE CRC64.
Query Match	43.0%; Score 1322.5; DB 5; Length 554;
Best Local Similarity	45.6%; Pred. NO. 4.1e-101;
Matches 252;	Conservative 109; Mismatches 179; Indels 13; Gaps
OY	18 IENKELNRLTNETNYVAETETGKKGKGVKRLTYD-DSTYSFEGIPADPAGELERKAP 76
DB	6 VGHKVOOYRLTGHVILDTKYGVNGLDKRYKYDYDEPFAFEGELIYAPRPQDLERAP 65
OY	77 ORPTPDGVRDCCNHKDKSVQVDFITGKCSGSDCYLTSVYNNLNLPETKRPVLYIHGG 136
DB	66 QREPRQGVLCCTTNKSKRMQRMMLGITYEGSDCHLWVYALKSEKPLPIVWYIGG 125
OY	137 GFLIENHDMYGRDYFIKKDVLINIOYRLGALGFLSLNSBDLNPAGAGLKDOYMAIR 196
DB	126 GFQKGASRDIYSPDYFMKRVYFVAINYRLALGFLSLDKPKLDVPGNGLDOYMAIR 185
OY	197 WIKNNCANGNPNDITVGESAGASTHYMMLTEQTRGLEFHRIILMSGNAICPMANTOC 256
DB	186 WISQNTIAQFQGDNDNTLTMGESAGSVHYMMTTEQTRGLEFHRIALMQSGALSEWESPD 245
OY	257 QHSAPFLAKLAGYKGEDNDKDVLEFLMKAPRODLIKLEEVLTLEERTKNVMPFEGTVE 316
DB	246 NNMAFRLAQLGLVGMDEKDAVLEFLSKVSARQIAALDOVIMLDEVRSFLFAFGVIE 305
OY	317 PYQTADCVLPKHEWAKTAMGNSIPRMNGTSEGLEFSLIKOMPLKKELETQVNFV 376
DB	306 PYETDHCWVKRPRDILSEAMGNDIPYIVGNSFEGLEFSLQVLYKPDWALKNFH--NIL 362
OY	377 PSELDAERTAPETLEMGAKIKKAVTGETPTADNF--MDLCSHIYFWPMHRLDRLF 433
DB	363 PREVERETSLSEGOOL-LVRLRLKQLYFNNMEMQESMEMEALINFSHROIMWDTHTREILARQ 421
OY	434 NHSTGTPVLYLRFPFQSEDLINPRIRKSGGVKGVSHADLETYFENNQLAKRMPKESRE 493
DB	422 SYAKRTPIYLRFPFQSDPH-FNQKRLCYGDRIGVAHADLSLFLYNIISKIDKSSME 480
OY	494 YKTERMTGVIQFATGTGPNYSNEIEGMEVSWDPK-KSDVEYKCLNISDELKMIIDPE 552
DB	481 YKTERMTGVMGMTSFSSGNCPCPE---LGSAKWEAVOLKENAVEKCFNISDLEWRDLE 537
OY	553 MDKIKQWESMEFK 565
DB	538 SDCLAWMDTEYPR 550
RESULT 15	
09N161	PRELIMINARY: PRT; 564 AA.
AC	09N161:
DT	01-OCT-2000 (Tremblrel. 15, Created)
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE	Alpha-esterase 1a.
GN	AE1A.
OC	Drosophila buzzatii (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxId=7264;
RP	SEQUENCE FROM N.A.
RP	Robin C., Claudianos C., Russell R.J., Oakeshort J.G.;
RT	"The alpha-esterase cluster of Drosophila buzzatii.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -i- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL: AF216208; AAF26721.1; -.
 DR HSSP: P37967; I0E3.
 DR Lipase: FBgn0029453; Dnu2\AE1A.
 DR InterPro: IPR002018; Carbesteras.
 DR InterPro: IPR000379; Ser-estras_s1te.
 DR Pfam: PF00135; Coesterase; 1.
 DR Hydrolyse.
 SQ SEQUENCE 564 AA: 64540 MW: DB4A2E91038B9D12 CRC64:

Query Match	42.5%	Score 1306.5	DB 5	Length 564
Best Local Similarity	46.0%	Pred. No. 96-100		
Matches 262	Conservative 101	Mismatches 192	Indels 15	Gaps
QY	1	MNFNVSLMEKLKRIKICIKENKFLNRYLRTTNETVVAETEXKVKGVKRLTYVD-SYISFE	59	
DB	1	MNIQMSLGLKMGAKGLIGHRIEIQYMLAKITTVVDTGLGRGLKRLYLHDFLFAFE	60	
QY	60	GIPYAAPRGGLRFKAPQRTPTMDYQDRCOHNHDKSVQVDFIIGKVGSDCLYLSVYN	119	
DB	61	GIFAPARPLLELFRAPQSPDPEWEGIDCTHPRAKYQKHLVNHVLEGSDDLTVNVT	120	
QY	120	NLNPETRPALVYIHGGSGFTIIGENHRMDYGRDYFIKKDVLVLIQIYRLAGLFTLSND	179	
DB	121	TLKSESLPVMVIFPGSGFOTGEANRBYVSDPYFMQDYLVTNLNRLGALGFLSLSDRD	180	
QY	180	LNPNGNGLDDOYVALPWLKKNCAFCGNDNTIVFESAGASTHYMMLTEOTRGLFHR	239	
DB	181	LDPVGNGLDDOYVALKMWINDNLANGENENITIMLSAGASTOIMMTTEOTRGLFHR	240	
QY	240	GILMSGNAICPMWNTQCOHRAFTLAKYKGBDNKDYLLELMLKARPOLLIKLEKVLPT	299	
DB	241	AIIMGSSSLCDMAENPHNDMPYRLACHLGYGVSSNEKEVREFLORASAKDLIG-SALPS	299	
QY	300	LEERTNKVMPFEGTEVPEYQADCVLRLKHPREMKVKTAMGNSIPTMNCSTYEGLE-FTSI	358	
DB	300	LVESRDVILFPGGVIEEYVYASCVISOPREVLSEAMGNKLPLMIGASGEFTSYQFV	359	
QY	359	LKQPMALVKELETGVNVPSELAAERAPRTLPMGAKIKKAVHTGTGPTADNF--MDL	415	
DB	360	MRDATVHLSDEA--IIPREYREV-S-PTPLKHKIRLKYKFFDDATRGSMERKECLOL	415	
QY	416	CSHLYFMEPMHRLLOLRFNHTSGTRPVLYLRPDFSEDLINRYRLIMSRGSGKVSNHDEL	475	
DB	416	LSLKHFHWAIHRTVLAARAAYAPMTQTYLYRDFDS-PTENFHRIMLCGRHGVGCHADDF	474	
QY	476	TYFFENOLAKRRPKESREYKTIERTGTGIMIDFATGPNYSNEIBGEMVNSWDPIKSDDEV	535	
DB	475	FYLFPCIAFWKLKNSSEXYRTIERMIGMTFAENSQOCEB--LEPIQWEP-L-DSNAT	530	
QY	536	YKCLNISDELKMIIVPEMDKIKOMSMERK	565	
DB	531	AKCLNISQOLKIKLPERKOLKVMQSYTEK	560	

Search completed: April 4, 2003, 09:16:18
Job time : 59.8533 secs

OS Drosophila buzzatii (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7264;
RN [1]
RP SEQUENCE FROM N.A.
RT Robin C., Claudianos C., Russell R.J., Oakeshott J.G.:
RA "The alpha-esterase cluster of Drosophila buzzatii.";

Oy	1	MNFVSLMEKIKKWKIKCL	ENKFLVRLT	TNETVVA	EEFYGVKVKVRLTY	DSYSFEG	60		
Db	1	MNFVSLMEKIKKWKIKCL	ENKFLVRLT	TNETVVA	EEFYGVKVKVRLTY	DSYSFEG	60		
Oy	61	IPYAPRVGELRFKAPORPT	PMDSVROCCNFKD	SVQVDFIT	GVGCSDDLTY	LSVTNN	120		
Db	61	IPYAPRVGELRFKAPORPT	PMDSVROCCNFKD	SVQVDFIT	GVGCSDDLTY	LSVTNN	120		
Oy	121	LNPFTRPVLYIT	HGGGFTIGEN	HRDMYGPDY	FTKKDVLINIOY	RUGALGFLS	LNSEDL	180	
Db	121	LNPFTRPVLYIT	HGGGFTIGEN	HRDMYGPDY	FTKKDVLINIOY	RUGALGFLS	LNSEDL	180	
Oy	181	NVPNAGLKDQVYMLRWT	KNNCANGFNPD	ITVFGESAGA	ASHYMYLLE	FOOTGL	PHRG	240	
Db	181	NVPNAGLKDQVYMLRWT	KNNCANGFNPD	ITVFGESAGA	ASHYMYLLE	FOOTGL	PHRG	240	
Oy	241	ILMSGNALCPWANTQOCH	RAFTLAKLAGYK	GEDNDKVDLE	FLMKAKPOD	LILKEK	VLT	300	
Db	241	ILMSGNALCPWANTQOCH	RAFTLAKLAGYK	GEDNDKVDLE	FLMKAKPOD	LILKEK	VLT	300	
Oy	301	EEPRNKVAFPRGSPV	VERQTDVCLP	RHPRMVY	TANGNSIPT	MMGNTSY	EGLPFT	SIILK	360
Db	301	EEPRNKVAFPRGSPV	VERQTDVCLP	RHPRMVY	TANGNSIPT	MMGNTSY	EGLPFT	SIILK	360

QY 361 QMPMLVKELETCVNFVPSSELADEKTAPELLEMGAKIKKAHVTCGPTADNFMDCSHY 420
DB 361 QMPMLVKELETCVNFVPSSELADEKTAPELLEMGAKIKKAHVTCGPTADNFMDCSHY 420
QY 421 FWFPMHRLDOLRFNHTSGTPVLYLRFDFDSEDLINPYRIMSGRGVGVSHADELTYFFW 480
DB 421 FWFPMHRLDOLRFNHTSGTPVLYLRFDFDSEDLINPYRIMSGRGVGVSHADELTYFFW 480
QY 481 NOLAKRMPKESREYKTIERMGTGIMIOFATGPNYSNEIEGMEVSWDPKKSDEYKCLN 540
DB 481 NOLAKRMPKESREYKTIERMGTGIMIOFATGPNYSNEIEGMEVSWDPKKSDEYKCLN 540
QY 541 ISDELKMDVPEMDKIKOWESMEFEKHDLF 570
DB 541 ISDELKMDVPEMDKIKOWESMEFEKHDLF 570

RESULT 2
US-08-669-524-3
Sequence 3, Application US/08669524
Patent No. 5843758
GENERAL INFORMATION:
APPLICANT: RUSSELL, Robyn J.
APPLICANT: NEMCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPBELL, Peter M.
APPLICANT: PARKER, Anthony G.
APPLICANT: OAKSHOTT, John G.
APPLICANT: SMYTH, Keirle A.
TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe Price Leblanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669, 524
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-524-3

Query Match 99.8%; Score 3067; DB 2; Length 570;
Best Local Similarity 99.6%; Pred. No. 1.1e-312;
Matches 568; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFVSLMEKLMKIKICIKENKFLNRYLTNTNVAETEGYGVKGRVRLTYDDSYSEEG 60
DB 1 MNFVSLMEKLMKIKICIKENKFLNRYLTNTNVAETEGYGVKGRVRLTYDDSYSEEG 60
QY 61 IRYAOPPVGELRFRAPQRPPTMDGVRDCCNHRKDKSVQVDFITGKVGCSDEDCLYLSVTNN 120

DB 61 IRYAOPPVGELRFRAPQRPPTMDGVRDCCNHRKDKSVQVDFITGKVGCSDEDCLYLSVTNN 120
QY 121 LNPETKRPVLYIHHGGGFIIGENHRDMYGPDYFIKKQVVLINIOYRIGALGFLSLNSED 180
DB 121 LNPETKRPVLYIHHGGGFIIGENHRDMYGPDYFIKKQVVLINIOYRIGALGFLSLNSED 180
QY 181 NPGNAGLKDQYMALRWIKNNCANFGNPDITVGSAGASTHYMMLTEQTRGLFHRG 240
DB 181 NPGNAGLKDQYMALRWIKNNCANFGNPDITVGSAGASTHYMMLTEQTRGLFHRG 240
QY 241 IIMSGNAICPMANTOCORAFPLAKLAGYKGEDNDKDYLEFLMAKPODLIKLEEVLT 300
DB 241 IIMSGNAICPMANTOCORAFPLAKLAGYKGEDNDKDYLEFLMAKPODLIKLEEVLT 300
QY 301 EERTNKVMPFGPTVPRYOTADCVLPKHPREWKATGANSIPTMGNTSYGLFTSTLK 360
DB 301 EERTNKVMPFGPTVPRYOTADCVLPKHPREWKATGANSIPTMGNTSYGLFTSTLK 360
QY 361 QMPMLVKELETCVNFVPSSELADEKTAPELLEMGAKIKKAHVTCGPTADNFMDCSHY 420
DB 361 QMPMLVKELETCVNFVPSSELADEKTAPELLEMGAKIKKAHVTCGPTADNFMDCSHY 420
QY 421 FWFPMHRLDOLRFNHTSGTPVLYLRFDFDSEDLINPYRIMSGRGVGVSHADELTYFFW 480
DB 421 FWFPMHRLDOLRFNHTSGTPVLYLRFDFDSEDLINPYRIMSGRGVGVSHADELTYFFW 480
QY 481 NOLAKRMPKESREYKTIERMGTGIMIOFATGPNYSNEIEGMEVSWDPKKSDEYKCLN 540
DB 481 NOLAKRMPKESREYKTIERMGTGIMIOFATGPNYSNEIEGMEVSWDPKKSDEYKCLN 540
QY 541 ISDELKMDVPEMDKIKOWESMEFEKHDLF 570
DB 541 ISDELKMDVPEMDKIKOWESMEFEKHDLF 570

RESULT 3
US-09-068-960-2
Sequence 2, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Resrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068, 960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 570
TYPE: PRT
ORGANISM: Lucilia cuprina
US-09-068-960-2

Query Match 99.6%; Score 3060; DB 4; Length 570;
Best Local Similarity 99.8%; Pred. No. 5.9e-312;
Matches 569; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNFVSLMEKLMKIKICIKENKFLNRYLTNTNVAETEGYGVKGRVRLTYDDSYSEEG 60
DB 1 MNFVSLMEKLMKIKICIKENKFLNRYLTNTNVAETEGYGVKGRVRLTYDDSYSEEG 60
QY 61 IRYAOPPVGELRFRAPQRPPTMDGVRDCCNHRKDKSVQVDFITGKVGCSDEDCLYLSVTNN 120
DB 61 IRYAOPPVGELRFRAPQRPPTMDGVRDCCNHRKDKSVQVDFITGKVGCSDEDCLYLSVTNN 120
QY 121 LNPETKRPVLYIHHGGGFIIGENHRDMYGPDYFIKKQVVLINIOYRIGALGFLSLNSED 180
DB 121 LNPETKRPVLYIHHGGGFIIGENHRDMYGPDYFIKKQVVLINIOYRIGALGFLSLNSED 180

OY 181 NVPGNAGLKDOYMALRWIKNNCANFGNPDNTTVEGESAGASTHYMMLTEOTRGLFHRG 240
|||||
Db 181 NVPGNAGLKDOYMALRWIKNNCANFGNPDNTTVEGESAGASTHYMMLTEOTRGLFHRG 240
OY 241 ILMGNAICPMANTOCQHRAPFLAKLAGYKGEDNDKDVLEFLMKAKPOLLKLEEVLTU 300
|||||
Db 241 ILMGNAICPLANTOCQHRAPFLAKLAGYKGEDNDKDVLEFLMKAKPOLLKLEEVLTU 300
OY 301 EERTKKNVMPFGPTVEPYOTADCVLPKHPREKVTAMGNSIPTMMGNTSYEGLEFSTSILK 360
|||||
Db 301 EERTKKNVMPFGPTVEPYOTADCVLPKHPREKVTAMGNSIPTMMGNTSYEGLEFSTSILK 360
OY 361 OMPMLVKELETCVNFVPSLADERTAPETLEMGAKKIKAHYGTGPTADNMDLCSHLY 420
|||||
Db 361 OMPMLVKELETCVNFVPSLADERTAPETLEMGAKKIKAHYGTGPTADNMDLCSHLY 420
OY 421 FMFPHRLLOLRFNHTSGTPVLYRFDPSDDLINPYRIMRSGRGVKGVSADDELTYFFW 480
|||||
Db 421 FMFPHRLLOLRFNHTSGTPVLYRFDPSDDLINPYRIMRSGRGVKGVSADDELTYFFW 480
OY 481 NOLAKRMKESREKVTIERMTGIMTGFATGNPYSNEIEGMEVNSWDPKKSDEYVKCLN 540
|||||
Db 481 NOLAKRMKESREKVTIERMTGIMTGFATGNPYSNEIEGMEVNSWDPKKSDEYVKCLN 540
OY 541 ISDELKMTIDVPEMDKIKOMESMEFHRDLF 570
|||||
Db 541 ISDELKMTIDVPEMDKIKOMESMEFHRDLF 570

RESULT 4
US-09-068-960-4
; Sequence 4, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Lucilia cuprina
US-09-068-960-4

Query Match 99.6%; Score 3060; DB 4; Length 570;
Best Local Similarity 99.8%; Pred. No. 5.9e-312;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MNFNVSLEKLMKWKIKCIENKFLNRLTTNETVVAETEGYKGVKRLTYDDSYSEEG 60
|||||
Db 1 MNFNVSLEKLMKWKIKCIENKFLNRLTTNETVVAETEGYKGVKRLTYDDSYSEEG 60
OY 61 IPYADPPVGELEFKAPORPTPMDGVDRCCNHRDKSVQVDFITGKVGCSDDCLYLSYTN 120
|||||
Db 61 IPYADPPVGELEFKAPORPTPMDGVDRCCNHRDKSVQVDFITGKVGCSDDCLYLSYTN 120
OY 121 LNPETKRPVLYIHGGGFIIGENHRDMGPDYFIKKDVLINIOYRLGALGFLSLSNSED 180
|||||
Db 121 LNPETKRPVLYIHGGGFIIGENHRDMGPDYFIKKDVLINIOYRLGALGFLSLSNSED 180
OY 181 NVPGNAGLKDOYMALRWIKNNCANFGNPDNTTVEGESAGASTHYMMLTEOTRGLFHRG 240
|||||
Db 181 NVPGNAGLKDOYMALRWIKNNCANFGNPDNTTVEGESAGASTHYMMLTEOTRGLFHRG 240
OY 241 ILMGNAICPMANTOCQHRAPFLAKLAGYKGEDNDKDVLEFLMKAKPOLLKLEEVLTU 300
|||||

|||||
Db 241 ILMGNAICPLANTOCQHRAPFLAKLAGYKGEDNDKDVLEFLMKAKPOLLKLEEVLTU 300
OY 301 EERTKKNVMPFGPTVEPYOTADCVLPKHPREKVTAMGNSIPTMMGNTSYEGLEFSTSILK 360
|||||
Db 301 EERTKKNVMPFGPTVEPYOTADCVLPKHPREKVTAMGNSIPTMMGNTSYEGLEFSTSILK 360
OY 361 OMPMLVKELETCVNFVPSLADERTAPETLEMGAKKIKAHYGTGPTADNMDLCSHLY 420
|||||
Db 361 OMPMLVKELETCVNFVPSLADERTAPETLEMGAKKIKAHYGTGPTADNMDLCSHLY 420
OY 421 FMFPHRLLOLRFNHTSGTPVLYRFDPSDDLINPYRIMRSGRGVKGVSADDELTYFFW 480
|||||
Db 421 FMFPHRLLOLRFNHTSGTPVLYRFDPSDDLINPYRIMRSGRGVKGVSADDELTYFFW 480
OY 481 NOLAKRMKESREKVTIERMTGIMTGFATGNPYSNEIEGMEVNSWDPKKSDEYVKCLN 540
|||||
Db 481 NOLAKRMKESREKVTIERMTGIMTGFATGNPYSNEIEGMEVNSWDPKKSDEYVKCLN 540
OY 541 ISDELKMTIDVPEMDKIKOMESMEFHRDLF 570
|||||
Db 541 ISDELKMTIDVPEMDKIKOMESMEFHRDLF 570

RESULT 5
US-09-068-960-6
; Sequence 6, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
; TITLE OF INVENTION: MALATHION CARBOXYL ESTERASE
; FILE REFERENCE: Attorney Docket No. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Lucilia cuprina
US-09-068-960-6

Query Match 99.6%; Score 3060; DB 4; Length 570;
Best Local Similarity 99.8%; Pred. No. 5.9e-312;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MNFNVSLEKLMKWKIKCIENKFLNRLTTNETVVAETEGYKGVKRLTYDDSYSEEG 60
|||||
Db 1 MNFNVSLEKLMKWKIKCIENKFLNRLTTNETVVAETEGYKGVKRLTYDDSYSEEG 60
OY 61 IPYADPPVGELEFKAPORPTPMDGVDRCCNHRDKSVQVDFITGKVGCSDDCLYLSYTN 120
|||||
Db 61 IPYADPPVGELEFKAPORPTPMDGVDRCCNHRDKSVQVDFITGKVGCSDDCLYLSYTN 120
OY 121 LNPETKRPVLYIHGGGFIIGENHRDMGPDYFIKKDVLINIOYRLGALGFLSLSNSED 180
|||||
Db 121 LNPETKRPVLYIHGGGFIIGENHRDMGPDYFIKKDVLINIOYRLGALGFLSLSNSED 180
OY 181 NVPGNAGLKDOYMALRWIKNNCANFGNPDNTTVEGESAGASTHYMMLTEOTRGLFHRG 240
|||||
Db 181 NVPGNAGLKDOYMALRWIKNNCANFGNPDNTTVEGESAGASTHYMMLTEOTRGLFHRG 240
OY 241 ILMGNAICPMANTOCQHRAPFLAKLAGYKGEDNDKDVLEFLMKAKPOLLKLEEVLTU 300
|||||
Db 241 ILMGNAICPLANTOCQHRAPFLAKLAGYKGEDNDKDVLEFLMKAKPOLLKLEEVLTU 300
OY 301 EERTKKNVMPFGPTVEPYOTADCVLPKHPREKVTAMGNSIPTMMGNTSYEGLEFSTSILK 360
|||||
Db 301 EERTKKNVMPFGPTVEPYOTADCVLPKHPREKVTAMGNSIPTMMGNTSYEGLEFSTSILK 360

[illegible]

```

RESULT 6
US-09-068-960-10
; Sequence 10, Application US/09068960A
; Patent No. 6235515
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org
; TITLE OF INVENTION: MALATHION CARBOXYLSTERASE
; FILE REFERENCE: Attorney Docket NO. 6235515 50179-051
; CURRENT APPLICATION NUMBER: US/09/068,960A
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00746
; EARLIER FILING DATE: 1996-11-22
; EARLIER APPLICATION NUMBER: AU 6751
; EARLIER FILING DATE: 1995-11-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 10
; LENGTH: 570
; TYPE: PRF
; ORGANISM: Lucilia cuprina
US-09-068-960-10

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[illegible]

Db	421	FWPMRRLLQLEFNNHSTSGTPVYLKRPDEDEDDLINRYRLMRSGRGKGVSHADELLTYFCFW	480
	481	NOIAKMPRESSERYKTERMTGIMVIGATTTGNPNYSIEIGMEVNSMDPKKSDVEYKLN	540
Qy	481	NOIAKMPRESSERYKTERMTGIMVIGATTTGNPNYSIEIGMEVNSMDPKKSDVEYKLN	540
Db	481	NOIAKMPRESSERYKTERMTGIMVIGATTTGNPNYSIEIGMEVNSMDPKKSDVEYKLN	540
Qy	541	ISDELKKNIDVPEMDKIKQWESMEFKNRDLF	570
Db	541	ISDELKKNIDVPEMDKIKQWESMEFKNRDLF	570

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1  RESULT 7
2  US-08-669-524-4
3  ; Sequence 4, Application US/08669524
4  ; Patent No. 5843758
5  ; GENERAL INFORMATION:
6  ; APPLICANT: RUSSELL, Robyn J.
7  ; APPLICANT: NEWCOMB, Richard D.
8  ; APPLICANT: ROBIN, Geoffrey C.
9  ; APPLICANT: BOYCE, Thomas M.
10 ; APPLICANT: CAMPBELL, Peter M.
11 ; APPLICANT: PARKER, Anthony G.
12 ; APPLICANT: OAKSHOOT, John G.
13 ; APPLICANT: SMITH, Kerlie A.
14 ; TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
15 ; NUMBER OF SEQUENCES: 22
16 ; CORRESPONDENCE ADDRESS:
17 ; ADDRESSEE: Lowe Price Leblanc & Becker
18 ; STREET: 99 Canal Center Plaza, Suite 300
19 ; CITY: Alexandria
20 ; STATE: Virginia
21 ; COUNTRY: USA
22 ; ZIP: 22314
23 ; COMPUTER READABLE FORM:
24 ; MEDIUM TYPE: Floppy disk
25 ; COMPUTER: IBM PC compatible
26 ; OPERATING SYSTEM: PC-DOS/MS-DOS
27 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
28 ; CURRENT APPLICATION DATA:
29 ; APPLICATION NUMBER: US/08/669,524
30 ; FILING DATE:
31 ; CLASSIFICATION: 435
32 ; ATTORNEY/AGENT INFORMATION:
33 ; NAME: Price, Robert L.
34 ; REGISTRATION NUMBER: 22,685
35 ; REFERENCE/DOCKET NUMBER: 1451-021
36 ; TELECOMMUNICATION INFORMATION:
37 ; TELEPHONE: 703-684-1111
38 ; TELEFAX: 703-684-1124
39 ; INFORMATION FOR SEQ. ID NO.: 4:
40 ; SEQUENCE CHARACTERISTICS:
41 ; LENGTH: 570 amino acids
42 ; TYPE: amino acid
43 ; STRANDEDNESS: single
44 ; TOPOLOGY: linear
45 ; MOLECULE TYPE: peptide
46 ; US-08-669-524-4

```

Query Match	98.9%	Score 3040;	DB 2;	Length 570;
Best Local Similarity	98.8%	Pred. No. 7,4e-310;		
Matches	563;	Conservative	2;	Mismatches 5; Indels 0; Gaps 0
Qy	1	MNFNVSLMEKLEKWKIKCIENKFLNRLTNTNETVAELEFYGVKVKRRLTYDDSYSEFG	60	
Db	1	MNFNVSLMEKLMKWKIRCIENKFLNRLTNTNETVAELEFYGVKVKRRLTYDDSYSEFG	60	
Qy	61	IPYADPVGELERFKAPQRPPTMDGVGRDCCNKDKSVQDFTTGVCSESDCLYLSVYTN	120	
Db	61	IPYADPVGELERFKAPQRPPTMDGVGRDCCNKDKSVQDFTTGVCSESDCLYLSVYTN	120	
Qy	121	LNPEYKRPVLVYTHGGGFTIGENHBDMGDPYFIKKDVLINIQYRLGALGFLSNEDL	180	

Db 121 LNPTKRPVLYIHGGXFIIGENHRDMDYDPYFIKKDVLINIOYRLGALGFLSLNSEDL 180
QY 181 NVPAGAKDQVMAIRWIKNNCANPGNDITVGSAGASATHYMLTEOTGLFHRG 240
Db 181 NVPAGAKDQVMAIRWIKNNCANPGNDITVGSAGASATHYMLTEOTGLFHRG 240
QY 241 ILMGNAICPMANTOCQHRATFLAKLAGYKGEDNDKDVLEFLMAKPODLLKLEEKVLT 300
Db 241 ILMGNAICPMANTOCQHRATFLAKLAGYKGEDNDKDVLEFLMAKPODLLKLEEKVLT 300
QY 301 EERTNKVFPFGPYEPYOTADCVLPKHPREMYKAMGNSIPTMGNTSYEGLEFSTSLK 360
Db 301 EERTNKVFPFGPYEPYOTADCVLPKHPREMYKAMGNSIPTMGNTSYEGLEFSTSLK 360
QY 361 OPMPLVKELETCVNVSESLADAEETAPETLEMGAIRKAVTGPTPADNMDLCSHY 420
Db 361 OPMPLVKELETCVNVSESLADAEETAPETLEMGAIRKAVTGPTPADNMDLCSHY 420
QY 421 FMFPMHRLQLRFNHTSTGYLYRFDSEDLINPYRIMSGRGVKGVSADDELTFYFW 480
Db 421 FMFPMHRLQLRFNHTSTGYLYRFDSEDLINPYRIMSGRGVKGVSADDELTFYFW 480
QY 481 NOLAKRMPKESREKTYTIERMTGIWIOFATGPNPYSNEIEGMENSWDPRIKSDEYKCLN 540
Db 481 NOLAKRMPKESREKTYTIERMTGIWIOFATGPNPYSNEIEGMENSWDPRIKSDEYKCLN 540
QY 541 ISDELKMDVPEMDKIKOMESMEKHRDLF 570
Db 541 ISDELKMDVPEMDKIKOMESMEKHRDLF 570

RESULT 8

US-09-068-960-13
Sequence 13, Application US/09068960A
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYLSESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068, 960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 570
TYPE: PRT
ORGANISM: Musca domestica
US-09-068-960-13

Query Match

Best Local Similarity 74.2%; Pred. No. 2.9e-237;
Matches 423; Conservative 73; Mismatches 74; Indels 0; Gaps 0;

QY 1 MNEVSIAMEKIKKIKCIENKFLNRTLTNETVAETRYGAVKGRILTYVDSYSFEG 60
Db 1 MTFLEKOFIFRLKLCVCKVKNKTYNRLSTNETQIIDTEYGOIKGVKRTYVDDSYSES 60
QY 61 IPYOPPVGELRFRKAPQRPVWEGVRDCCGPANNSVQTFDLSGKPTGSDCLYLNWYND 120
Db 61 IPYAPPVGELRFRKAPQRPVWEGVRDCCGPANNSVQTFDLSGKPTGSDCLYLNWYND 120
QY 121 LNPTKRPVLYIHGGXFIIGENHRDMDYDPYFIKKDVLINIOYRLGALGFLSLNSEDL 180
Db 121 LNPTKRPVLYIHGGXFIIGENHRDMDYDPYFIKKDVLINIOYRLGALGFLSLNSEDL 180
QY 181 NVPAGAKDQVMAIRWIKNNCANPGNDITVGSAGASATHYMLTEOTGLFHRG 240
Db 181 NVPAGAKDQVMAIRWIKNNCANPGNDITVGSAGASATHYMLTEOTGLFHRG 240

QY 241 ILMGNAICPMANTOCQHRATFLAKLAGYKGEDNDKDVLEFLMAKPODLLKLEEKVLT 300
Db 241 ILMGNAICPMANTOCQHRATFLAKLAGYKGEDNDKDVLEFLMAKPODLLKLEEKVLT 300
QY 301 EERTNKVFPFGPYEPYOTADCVLPKHPREMYKAMGNSIPTMGNTSYEGLEFSTSLK 360
Db 301 ERTNKVFPFGPYEPYOTADCVLPKHPREMYKAMGNSIPTMGNTSYEGLEFSTSLK 360
QY 361 OPMPLVKELETCVNVSESLADAEETAPETLEMGAIRKAVTGPTPADNMDLCSHY 420
Db 361 OPMPLVKELETCVNVSESLADAEETAPETLEMGAIRKAVTGPTPADNMDLCSHY 420
QY 421 FMFPMHRLQLRFNHTSTGYLYRFDSEDLINPYRIMSGRGVKGVSADDELTFYFW 480
Db 421 FMFPMHRLQLRFNHTSTGYLYRFDSEDLINPYRIMSGRGVKGVSADDELTFYFW 480
QY 481 NOLAKRMPKESREKTYTIERMTGIWIOFATGPNPYSNEIEGMENSWDPRIKSDEYKCLN 540
Db 481 NOLAKRMPKESREKTYTIERMTGIWIOFATGPNPYSNEIEGMENSWDPRIKSDEYKCLN 540
QY 541 ISDELKMDVPEMDKIKOMESMEKHRDLF 570
Db 541 ISDELKMDVPEMDKIKOMESMEKHRDLF 570

RESULT 9

US-08-669-524-8
Sequence 8, Application US/08669524
Patent No. 5843758
GENERAL INFORMATION:
APPLICANT: RUSSELL, Robyn J.
APPLICANT: NEWCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPBELL, Peter M.
APPLICANT: PARKER, Anthony G.
APPLICANT: OAKSHOTT, John G.
TITLE OF INVENTION: ENZYME BASED BIOREMEDIATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: Lowe Price Leblanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669, 524
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-524-8

Query Match 64.9%; Score 1994.5; DB 2; Length 572;

[illegible]

Db 1 QDFTISGKPTGSEDLVYLVNTNDLNPDKRRVVFIIHGGEIFGEANRNVGPDYEMKK 60
QY 157 DVLINIOYRLGALGELINSEDLNVPNGNAGLKQDVALLRMKNNKANGCNPNTIYFG 216
Db 61 PVLIVVQYRLGVLGELSLKSENLNPGNAGLKQDVALLRMKNNKANGCNPNTIYFG 120
QY 217 ESAGASTHYMMLEETQRLGFLHRIHGLMGSNAICPMANPTQCHRAFTLAKLAGYKGEDNDK 276
Db 121 ESAGASTHYMMLEETQRLGFLHRIHGLMGSNAICPMANPTQCHRAFTLAKLAGYKGEDNDK 180
QY 277 DYLEFLMKAKPDOLIKLEEKVLTLE 301
Db 181 DLEFLMKAKPDOLIKLEEKVLTLE 205

RESULT 14
US-08-747-221B-53
Sequence 53, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-53

Query Match 25.6%; Score 785.5; DB 3; Length 530;
Best Local Similarity 34.3%; Pred. No. 2.1e-73;
Matches 182; Conservative 87; Mismatches 204; Indels 57; Gaps 15;

QY 55 YVSFEGIPYADPPVGELEFKAQRPPTPMQDGVBDCCNKHDSVOYDFTTGVGSESDCLYL 114
Db 25 YVSFEGIPYADPPVGELEFKAQRPPTPMQDGVBDCCNKHDSVOYDFTTGVGSESDCLYL 84
QY 115 SVYTNNLNEETRRPVLVYVYHGGFELIGENHDMYGPDIYFIKKDVLLINIOYRLGALGELS 174
Db 85 NVIAPKTTSDKKLPVFEVWVHGGFELIGENHDMYGPDIYFIKKDVLLINIOYRLGALGELS 144
QY 175 LNSEDLVNPGNAGLKQDVALLRMKNNKANGCNPNTIYFGESAGASTHYMMLEETQTR 234
Db 145 LELE--GARGNVGLLDQVALLRMKNNKANGCNPNTIYFGESAGASTHYMMLEETQTR 202

QY 235 GLPHRGLMGSNAICPMANPTQCHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPDOLIK- 292
Db 203 GLTKRAIAGSGALNPMFQRRHPVRSLSLAEILGHP-TNNTODALEFLQKAPYDSLKK 261
QY 293 --LEEKVLTLEERTNKVWPEPGTYEPYQTDVLPKHA-----PREMYTAWGNSIPT 343
Db 262 MPATEGEILEE-----FVFPASIEK-----VPSQPLLESPLARMKSGSFNKPVL 309
QY 344 MNGTSEYGEFFTSILKQMPVLVKELETCVNFPSLDAERTAP-----ETLEM 393
Db 310 LVGPNASAGELLYEFKPKERPEMLNQA-----ADFERLYPAEPELAGHSEESKTL 359
QY 394 GAKIKKAVTGETPTADN---FMDLCSHYFWFPMHRLLOLRENTSGTPYLYRFDEDS 450
Db 360 AEKIRKFF--DDKPVPENEQKFTLDLIDWFTFRGIDKHYKLSV-EKODEPYVYYEYFSFE 417
QY 451 EDLINPVRIMRSGVGVASHADELYTFPMNOLAKRMPRESREYKTIEMRGIVQFATF 510
Db 418 S--HPKGTGFDHNLGACHGEELVNLFEVEMKLEKDPVLLTKDVLAMMTNFTKN 474
QY 511 GNPSYNEIEGEMVSWDPIKSDVYKCLNISDELKMIIDVPEMDIKQWE 560
Db 475 GNP--TPVETELLPVKMBPATRKILNT--LNIDXTLTLGTNPETRYKWE 521

RESULT 15
US-09-005-051-53
Sequence 53, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-53

Query Match 25.6%; Score 785.5; DB 4; Length 530;
Best Local Similarity 34.3%; Pred. No. 2.1e-73;
Matches 182; Conservative 87; Mismatches 204; Indels 57; Gaps 15;

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 09:16:33 ; Search time 24.5753 Seconds
(without alignments)
1417.991 Million cell updates/sec

Title: US-09-776-910-8
Perfect score: 3073
Sequence: 1 MNFNVSIMELKWKIKICIN.....PEMDKIKQWSEKRDLP 570

Scoring table: BLOSUM62
Gapop 10.0 , gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	718	23.4	574	9 US-10-023-515-4	Sequence 4, Appl1
2	718	23.4	612	9 US-09-875-353-4	Sequence 4, Appl1
3	707.5	23.0	585	10 US-09-934-323-4	Sequence 4, Appl1
4	571.5	18.6	602	10 US-09-748-739A-2	Sequence 2, Appl1
5	365	18.4	574	10 US-09-748-739A-6	Sequence 6, Appl1
6	564	18.4	574	10 US-09-748-739A-18	Sequence 8, Appl1
7	563	18.3	574	10 US-09-748-739A-17	Sequence 17, Appl1
8	563	18.3	574	10 US-09-748-739A-20	Sequence 20, Appl1
9	561	18.3	574	10 US-09-748-739A-4	Sequence 4, Appl1
10	558	18.2	574	10 US-09-748-739A-19	Sequence 19, Appl1
11	558	18.2	574	10 US-09-748-739A-21	Sequence 21, Appl1
12	556	18.1	574	10 US-09-748-739A-18	Sequence 18, Appl1
13	554	18.0	574	10 US-09-748-739A-22	Sequence 22, Appl1
14	548	17.8	537	9 US-09-738-626-4754	Sequence 4754, Ap
15	526	17.1	574	10 US-09-748-739A-23	Sequence 23, Appl1
16	525.5	17.1	581	9 US-10-023-515-2	Sequence 2, Appl1
17	522	17.0	549	9 US-10-102-806-689	Sequence 689, App
18	507.5	16.5	565	10 US-09-895-860-5	Sequence 5, Appl1
19	495.5	16.1	554	10 US-09-895-860-4	Sequence 4, Appl1

20	486.5	15.8	583	10 US-09-925-301-1177	Sequence 1177, Ap
21	485	15.8	816	9 US-09-875-353-2	Sequence 2, Appl1
22	483.5	15.7	568	9 US-09-418-176-4	Sequence 4, Appl1
23	483.5	15.7	722	9 US-09-418-176-3	Sequence 3, Appl1
24	483.5	15.7	745	9 US-09-418-176-2	Sequence 2, Appl1
25	479	15.6	816	9 US-09-978-295A-375	Sequence 375, App
26	479	15.6	816	9 US-09-978-697-375	Sequence 375, App
27	479	15.6	816	9 US-09-978-192A-375	Sequence 375, App
28	479	15.6	816	9 US-09-999-832A-375	Sequence 375, App
29	479	15.6	816	9 US-09-978-189-375	Sequence 375, App
30	479	15.6	816	9 US-09-978-608A-375	Sequence 375, App
31	479	15.6	816	9 US-09-978-191A-375	Sequence 375, App
32	479	15.6	816	9 US-09-978-103A-375	Sequence 375, App
33	479	15.6	816	9 US-09-978-564A-375	Sequence 375, App
34	479	15.6	816	9 US-09-978-585A-375	Sequence 375, App
35	479	15.6	816	9 US-10-017-081A-375	Sequence 375, App
36	479	15.6	816	9 US-09-978-824-375	Sequence 375, App
37	479	15.6	816	9 US-09-981-915A-375	Sequence 375, App
38	479	15.6	816	9 US-09-999-833A-375	Sequence 375, App
39	479	15.6	816	9 US-10-167-749-375	Sequence 375, App
40	479	15.6	816	9 US-09-918-585A-375	Sequence 375, App
41	462	15.0	547	10 US-09-895-860-2	Sequence 2, Appl1
42	462	15.0	571	9 US-10-036-041-23	Sequence 23, Appl1
43	462	15.0	571	9 US-10-028-072-542	Sequence 542, App
44	462	15.0	571	9 US-10-035-855-23	Sequence 23, Appl1
45	462	15.0	571	9 US-10-121-049-542	Sequence 542, App

ALIGNMENTS

RESULT 1
US-10-023-515-4
Sequence 4, Application US/10023515
Publication No. US20020182636A1
GENERAL INFORMATION:
APPLICANT: Curtiss, Rory A. J.
TITLE OF INVENTION: Sllas-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYL ESTERASE
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 574
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence
US-10-023-515-4

Query Match 23.4%; Score 718; DB 9; Length 574;
Best Local Similarity 33.6%; Pred. No. 1.1e-57;
Matches 187; Conservative 83; Mismatches 223; Indels 64; Gaps 18;

QY	40	GKVVGVKRLTYV--DDSYVSFEIGIYVYAOPEVGELEKRAQ--RPTPDGVYRDCCNKHKDKVO 97	
DB	1	GKVVGVKRLTYV--DDSYVSFEIGIYVYAOPEVGELEKRAQ--RPTPDGVYRDCCNKHKDKVO 97	
QY	98	VDFI-----TKVVC--SEDCLYLSVY--NNLNPETKRPVLYIGG 136	
DB	61	DDDGGSLSDLKVALKMLSGMKNLVGLKLSDECLILNVYTPKTKRPVYVWIIIG 120	
QY	137	GTIIGENHR--DMYGPDYFIK--DVYLIINIQYRIGALGFLSLNSEDLVNPGNGLKDOV 192	
DB	121	GFMGSGSHSLPLSLYDGSGLARREGNIVYISINVRIGLPGFLSTGDDKLPJGSGNGLDOR 180	

[illegible]

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RESULT 2
US-09-875-353-4
Sequence 4, Application US/09875353
Patent No. US20020168713A1
GENERAL INFORMATION:
APPLICANT: CURTIS, ROY A. J.
TITLE OF INVENTION: 46580. A NOVEL HUMAN NEUROLOGIN FAMILY
TITLE OF INVENTION: MEMBER AND USES THEREOF
FILE REFERENCE: 10448-058001
CURRENT APPLICATION NUMBER: US/09/875,353
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/309,949
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO 4
LENGTH: 612
TYPE: prt
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus sequence
US-09-875-353-4

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Query Match	23.4%	Score 718:	DB 9:	Length 612:
Best Local Similarity	33.6%	Pred. NO. 1.3e-57:		
Matches 187: Conservative	83:	Mismatches 223:	Indels 64:	Gaps 18:

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Db      279  ALSPWALQSESNMARGKRELARLLGC-NEFSSSELLDCLRSKSAEBLLNATRSFLLEFV 337
QY      304  TNKMF-PFEGPTPEEYOTADCVLPKHBREKVTAMGNSIPTMGNTSYGLEFTSL--- 359
Db      338  PELPELFLAFGGVVDGDAEPAFLPEPDEBELIKGKPADVYLLGVKDCGGYFAMLLNA 397
QY      360  -----KQMPALYKELETCVNPVPS---LDAERTAPETE-MGAKIKKRAHVTOE 405
Db      398  SSKGEDELKKTENDVLELTKLYLLEFASALNLIKQMDLADLVKLYKFGVDVDESEER 457
QY      406  TPTADNEMDLCSHYFEMFPHRLQLTFNNTSGTPYLYKFDSESDLIINPYRIMSGRG 465
Db      458  KP---NIQDMITDLELFCSPRVADLHAKH-GSPYAYAYEFDHPASFGIOFLAKRVDEE 513
QY      466  VKGYSHADELTFFWNLQAKRM---PRESREYKTIEMTIGIWIQFMTGPNYSNEIEGRE 522
Db      514  FGGAVHGDELFEGVGNPLLEQLYKATEEBEKSSKTMNTMYANFNKATGNPNNGTNGSL- 572
QY      523  NVSWDPIKKSDEVYKCL 539
Db      573  -VVMFKYTSSEQKISLL 588

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RESULT 3
US-09-934-323-4
Sequence 4, Application US/09934323
Patent No. US20020150910A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYL ESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-081001
CURRENT APPLICATION NUMBER: US/09/934,323
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,774
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 585
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence
US-09-934-323-4

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Query Match	23.0%	Score 707.5;	DB 10;	Length 585;
Best Local Similarity	33.5%	Pred. NO. 1.1e-56;		
Matches 187;	Conservative	83;	Mismatches 223;	Indels 65;
				Caps 19

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Db 310 VPLPFLAEGPVYDGDADAEAFIPEDDEPEELIKEGKEFADVPYLLIGVTIKDEGGYFAAMLIN 369
Qy 360 -----KQMBMLVKELETCVNVPPSP-----LADAEKTAPELLE-MGAKIKKAHVTG 404
Db 370 ASSGEDELKKEINPDVWLELKYLLFYASALNIKMDLADLVADLYKPEDVDOSFVES 429
Qy 405 ETPADNFMDLCSHYEFWPMHRLLOLRFNHTSGTPVYLRFDPDSDDLINPYRIMSGR 464
Db 430 RKP---NLQDMLTDLLEKCPTRVAADLAHAKH-GGSPVYAVFDHPAPASFGIOFLAKRVDP 485
Qy 465 GVKGVSHADELTTFEWMOLAKRM---PKSREYKTIEMTGVIQFATGPNPYSNEIEGM 521
Db 486 EFGAGVAGHDEFFVEFGNPLLEKQLYKATBEESKSSKTMNMYANPAKTCGNPNNGTSGNL 545
Qy 522 ENVSMDDPKKSDEYKCL 539
Db 546 --VWPKYTSSEOKYSL 561

RESULT 4
US-09-748-739A-2
; Sequence 2, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748.739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-2

Query Match 18.6%; Score 571.5; DB 10; Length 602;
Best Local Similarity 29.0%; Pred. No. 4e-44;
Matches 176; Conservative 97; Mismatches 227; Indels 107; Gaps 25;

Qy 12 KWKIKCIENKFLNRYLT-----TNETVVAETEGYKVKVRLTVYDSDYSFEGIP 62
Db 4 KVTIICI-REFLFWFLMLCMILIGKSHTEDDIIATKNGKVGGM-NLWVFGGTVAFLGIP 60
Qy 63 YAOBPVELRKARORPTPMDCV-----RDCCNHNKDSV-----QVDFITGK 104
Db 61 YAOBPVLGRKPKPOSILTKWSDINNAIKYANSCQNDQSPFGHSEMMNPNTDL---- 116
Qy 105 VCGSEDLVLSVTNNINPETKRPVLVYIHGGFLIGENHNDMYGPDYFIKD-VVLINI 163
Db 117 ---SEDCILYNWVLPAPKPK-NATVLLIMWYGGFOTGSSSLAHVDDKFLAVERVIYVSM 172
Qy 164 QYRLGALGFLSL--NSEDLVNPNAGLKDQYALRWIKNNCANFGNPDNITVFESAGA 221
Db 173 NYRGALGFLALPGNPE---APGNMGLFDQDLALQWQKNIAGFGNPKSVTLFGESAGA 229
Qy 222 ASTHYMMLTETRGTLFHHGILMSGNATCPMANT---OCQNHAFPLAKLAGKGEDNDKDV 278
Db 230 ASVSLHLISPGSHLFTFALIIQSGSPNAPMAVTSLYEARNNTLMLAKLTGCSRE-NETEI 288
Qy 279 LEFLMKAKPODLIKLEEVLTLEERTNKVMPFGPTVEPYOTADCVLPKPHREMWKTAGM 338
Db 289 IKCLRNDDPOEILNLEAFVVPY---GTPLSVNPFGPTVDGDLTDM-----PDILLELQGF 340
Qy 339 NSIPTMGNTSYEGLEFSTSLKQMPMLVKELETCVNVPSLADAEKRT-APETLEMGAKI 397
Db 341 KKTQILVGVNDEGTWF--LVYGAAPGFSKDNNSII--TRKEFGGLKIFFGVSEFGKES 396

Qy 398 KKAHVTC--ETPTADNFMD-----LCSHIYF-----WPMHRLLOLRFNHTSG 438
Db 397 ILFHYTMDVDDQRENTREALGDVVGDNFICPALFETKRSKW-----G 441
Qy 439 TPVLYLRFPDESDLLINPYRIMSGRGVYSHADELTTFEWMOLAKRMPSREYKTI 498
Db 442 NNAFFYYFEHRSSKLPEWEM-----GYMHGYEIEFVGLPLERDNTKAEEILSR 493
Qy 499 RMTGIVQFATGTPNYSIEIGEMENVSMDPKKSDEYKCLKCNISDELKMDIVPEKDKIQ 558
Db 494 SIVRMANFAKYGNP--NETQN-NSTSWPKRSTEQKYLTLN-TESTRIKMLRAQOCRF 549
Qy 559 WESMEFEK 565
Db 550 WTSFEFPK 556

RESULT 5
US-09-748-739A-6
; Sequence 6, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748.739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-6

Query Match 18.4%; Score 565; DB 10; Length 574;
Best Local Similarity 29.0%; Pred. No. 1.5e-43;
Matches 168; Conservative 95; Mismatches 220; Indels 96; Gaps 23;

Qy 31 ETVVAETEGYKVKVRLTVYDSDYSFEGIPYAPQPRVGEILRFARQRPPTMDCV----- 85
Db 2 DDIIITATKNGKVGGM-NLWVFGGTVAFLGIPYAPQPRVGRKPKPOSILTKWSDIWNATK 60
Qy 86 --RDCCNHNKDSV-----QVDFITGKVGSEDCILVSYTNNINPETKRPVLVY 132
Db 61 YANSCQNDQSPFGHSEMMNPNTDL-----SEDCILYNWVLPAPKPK-NATVLLIM 112
Qy 133 IHGGFLIGENHNDMYGPDYFIKD-VVLINIQYRLGALGFLSL--NSEDLVNPNAGL 189
Db 113 IYGGFGFGTSSLYHVDGKFLAVERVIYVSMNRYVGAFLALPGNPE---APGNMGLF 169
Qy 190 DQWALNRIRKNNCANFGNPDNITVFESAGASHTHYMLLEBQTRGLFHHGILMSGNATC 249
Db 170 DQDLALQWQKNIAGFGNPKSVTLFGESAGAASVSLHLISPGSHLFTFALIIQSGSPNA 229
Qy 250 PMANT---OCQNHAFPLAKLAGYKGEDNDKDVLEFLMKAKPODLIKLEEVLTLEERTNK 306
Db 230 PMATVTSLEARNRNLNLAFLKLTGCSRE-NETELIKCLRNDDPOEILNLEAFVVPY---GTQ 285
Qy 307 VMPFGPTVEPYOTADCVLPKPHREMWKTAGNSIPTMGNTSYEGLEFSTSLKQMPMLV 366
Db 286 LSVNFGPTVDGDLTDM-----PDILLELQGFKKTQILVGVNDEGTAF--LVYGAAPGFS 338
Qy 367 KELETCVNVPSLADAEKRT-APETLEMGAKIKKAHVTG--ETPTADNFMD----- 414
Db 339 KDNNSII--TRKEFGGLKIFFGVSEFGKESILFHYDWDVDDQRENTREALGDVVG 396
Qy 415 --LCSHIYF-----WPMHRLLOLRFNHTSGTPVYLRFDPDSDDLINPYRIMSGRGV 466

Db 397 NFIGALEFTKKFSW-----GNNAFYFEHRSSKLPWEMM----- 434
Qy 467 KGVSHADELTYFFWNOQLAKRMPKESREKYTEIRMTGIMIOFATGPNYSNEIEGEMVSW 526
Db 435 -GVMHGEIEFVGLPLERRDNVTKAEILSRISYIKRRANFAKGNP--NETON-NSTSW 490
Qy 527 DPKKSDVEYKCLNISDELKMDVPEMDKIKOWESMEFK 565
Db 491 PVFKSTEQKYLTLN-TESTRIMTKLRAOCCRFWTSFEPK 528

RESULT 6
US-09-748-739A-8
Sequence 8, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Walkins, Jeffery D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 574
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-8

Query Match 18.48; Score 564; DB 10; Length 574;
Best Local Similarity 29.08; Pred. No. 1.8e-43;
Matches 168; Conservative 94; Mismatches 221; Indels 96; Gaps 23;
Qy 31 ETVVAETEGYKGVKRLTYVDSYSFEGIPYAPVGELEKRAQRPPTWDCV----- 85
Db 2 DDIITATKNGVRCGM-NLTVFGTGTAFGLIPYAPVGELEKRAQRPPTWDCV----- 60
Qy 86 --RDCNHRKDSV-----QVDFITGKVCSEDCLYLSYTNLNPETKRPVLY 132
Db 61 YANSCCOMIDSPFGHSEGMNPNITDL-----SEDCLYLNWITAPRPK-NATVLIW 112
Qy 133 IHGGFTIIGENHRDMYGPDYFIKRD-VVLINIOYRLGALGLSL--NSEDLNPGNGLK 189
Db 113 IYGGFTGTSTLHYDCKFLARVERIVVSMNRYVGLALPGNDE--ARGNGLF 169
Qy 190 DOVMALEWIKNNCANFGGNPDNITVEGSAAGASTHYMLTEQTRGLFHRGILMSGNAIC 249
Db 170 DOGLALOWQKNIAGFGKPSVTLFEGSAGASVSLHLSPGSHSLFTRAILDSSGFNA 229
Qy 250 PMAVT---OCORAFITLAKLAGYKGEDNDKYLEFLMKAKPODLIKLEKYLTEERTNK 306
Db 230 PMAVTSLYEARRNTLNALATGCSRE-NETETIKCLRKNKDOELILNFAFVVPY---GTS 285
Qy 367 KELETGVNFPSELDAERT-APETLEMGAKIKKAHVIG--ETPADNFM----- 414
Db 286 LSVNFGPTVDGFLIDM-----PDILLELGQFKKTOILLGVNKKDGTAF--LVYCAPGFS 338
Qy 307 VMEFPSPVEPYOTADCVLPKHREKVTAMGNSIPTMGNTSYEGLFSTILKOMPMLV 366
Db 397 NFIGALEFTKKFSW-----GNNAFYFEHRSSKLPWEMM----- 434
Qy 467 KGVSHADELTYFFWNOQLAKRMPKESREKYTEIRMTGIMIOFATGPNYSNEIEGEMVSW 526
Db 435 -GVMHGEIEFVGLPLERRDNVTKAEILSRISYIKRRANFAKGNP--NETON-NSTSW 490

Qy 527 DPKKSDVEYKCLNISDELKMDVPEMDKIKOWESMEFK 565
Db 491 PVFKSTEQKYLTLN-TESTRIMTKLRAOCCRFWTSFEPK 528

RESULT 7
US-09-748-739A-17
Sequence 17, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Walkins, Jeffery D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 574
TYPE: PR
ORGANISM: Homo sapiens
US-09-748-739A-17

Query Match 18.38; Score 563; DB 10; Length 574;
Best Local Similarity 29.08; Pred. No. 2.3e-43;
Matches 168; Conservative 94; Mismatches 221; Indels 96; Gaps 23;
Qy 31 ETVVAETEGYKGVKRLTYVDSYSFEGIPYAPVGELEKRAQRPPTWDCV----- 85
Db 2 DDIITATKNGVRCGM-NLTVFGTGTAFGLIPYAPVGELEKRAQRPPTWDCV----- 60
Qy 86 --RDCNHRKDSV-----QVDFITGKVCSEDCLYLSYTNLNPETKRPVLY 132
Db 61 YANSCCOMIDSPFGHSEGMNPNITDL-----SEDCLYLNWITAPRPK-NATVLIW 112
Qy 133 IHGGFTIIGENHRDMYGPDYFIKRD-VVLINIOYRLGALGLSL--NSEDLNPGNGLK 189
Db 113 IYGGFTGTSTLHYDCKFLARVERIVVSMNRYVGLALPGNDE--ARGNGLF 169
Qy 190 DOVMALEWIKNNCANFGGNPDNITVEGSAAGASTHYMLTEQTRGLFHRGILMSGNAIC 249
Db 170 DOGLALOWQKNIAGFGKPSVTLFEGSAGASVSLHLSPGSHSLFTRAILDSSGFNA 229
Qy 250 PMAVT---OCORAFITLAKLAGYKGEDNDKYLEFLMKAKPODLIKLEKYLTEERTNK 306
Db 230 PMAVTSLYEARRNTLNALATGCSRE-NETETIKCLRKNKDOELILNFAFVVPY---GTP 285
Qy 367 KELETGVNFPSELDAERT-APETLEMGAKIKKAHVIG--ETPADNFM----- 414
Db 286 LSVNFGPTVDGFLIDM-----PDILLELGQFKKTOILLGVNKKDGTAF--LVYCAPGFS 338
Qy 307 VMEFPSPVEPYOTADCVLPKHREKVTAMGNSIPTMGNTSYEGLFSTILKOMPMLV 366
Db 397 NFIGALEFTKKFSW-----GNNAFYFEHRSSKLPWEMM----- 434
Qy 467 KGVSHADELTYFFWNOQLAKRMPKESREKYTEIRMTGIMIOFATGPNYSNEIEGEMVSW 526
Db 435 -GVMHGEIEFVGLPLERRDNVTKAEILSRISYIKRRANFAKGNP--NETON-NSTSW 490
Qy 527 DPKKSDVEYKCLNISDELKMDVPEMDKIKOWESMEFK 565
Db 491 PVFKSTEQKYLTLN-TESTRIMTKLRAOCCRFWTSFEPK 528

RESULT 8
US-09-748-739A-20
Sequence 20, Application US/09748739A


```
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-748-739A-20

Query Match          18.3%; Score 563; DB 10; Length 574;
Best Local Similarity 29.0%; Pred. No. 2,3e-43;
Matches 168; Conservative 94; Mismatches 221; Indels 96; Gaps 23;

QY 31 ETVVAETEGYKVKVRLTVYDSDYSFEGIPYAPVGLERKAPQRPPTWGDV----- 85
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 DDIIATKNGKVRGM-NLTVFGGTVAFLGIPYAPGLRFRKPKQSLTKMSDIMNATK 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 86 --RCCNHKDKSV-----QVDFITGKVGSEDCLYLSYTNLNNETKRPVLVY 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YANSCCONIDSPFGFHGSEMMNPTDL-----SEDCLYLNWIPAPKPK-NATVLIW 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 133 IHGGFTIGENHRDMYGPDPYFIKRD-VVLINIOYRLGALGFLSL--NSEDLVNPGNAGLK 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 IYGGFGTGTSSLHYDGKFLARVERVIVSMNTRVAGLALPGNE---AAGNMGLEF 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 DQVALRMKKNKCNFGPNNTIVFGESAGASTHYMALTQETGRLEFHGILMSGNAIC 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 DQDALQWQVKNIAAFGPNPKSVTLFGESAGAAVSLLHSPGSHSLFTRAILLOGSFNA 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 250 PMAWT---QCOHRAFTLAKLAGYKGEDNDKDYLEFLMAKAKQDILKEEYVLTLEERTNK 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 PMAWTSLYEARNKRLNLAKLKGCSRE-NETETIKLRKRDQDELLINLAFVVPY---GTP 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 307 VMFPGPTVERUYQADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFTSILKOMPIV 366
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 286 LSVNFGPTVDGDFLDM-----PDLLELGQFKTKQLIVGNKDEGTAFL--LVYGARPGFS 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 367 KELETGVNVPVSELADEART-APETLEMGAKIKKANHVG--ETPTADNMD----- 414
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 339 KDNSIIT--TRKEPOEGKIFFPVSEFGKESILFHYTDWDDORPENYREALGDVVDY 396
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 415 --LCSHYF-----WFRMHRLLQLRFNHTSGTPVLYLRPDESDLLINPRIRMSGGV 466
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 397 NFICPALEFTKFKSEW-----GNNAFYFYEHRSSKLPWPEWM----- 434
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 467 KGVSHADELTFYFNNQALAKRMPKESREYKTIERTMTGIOWPATGNPYSNETEGMENYSW 526
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 435 -GVNHGYEIEFVGLPRLERRONYTKAEELISRSYVKRMANAKKYGNP--NETQN-NSTSW 490
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 527 DPIKSDDEVYKCLNISDELKMIIDVPEMDKIKOWESMEFK 565
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 491 PVFKSTQKYLTLN-TESTRIIMTKLRAOQCRRFTSFFPK 528
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-09-748-739A-4
; Sequence 4, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 574
; TYPE: PRT
```

```
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
; US-09-748-739A-4

Query Match          18.3%; Score 561; DB 10; Length 574;
Best Local Similarity 29.0%; Pred. No. 3,5e-43;
Matches 168; Conservative 94; Mismatches 221; Indels 96; Gaps 23;

QY 31 ETVVAETEGYKVKVRLTVYDSDYSFEGIPYAPVGLERKAPQRPPTWGDV----- 85
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 DDIIATKNGKVRGM-NLTVFGGTVAFLGIPYAPGLRFRKPKQSLTKMSDIMNATK 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 86 --RCCNHKDKSV-----QVDFITGKVGSEDCLYLSYTNLNNETKRPVLVY 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YANSCCONIDSPFGFHGSEMMNPTDL-----SEDCLYLNWIPAPKPK-NATVLIW 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 133 IHGGFTIGENHRDMYGPDPYFIKRD-VVLINIOYRLGALGFLSL--NSEDLVNPGNAGLK 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 IYGGFGTGTSSLHYDGKFLARVERVIVSMNTRVAGLALPGNE---AAGNMGLEF 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 DQVALRMKKNKCNFGPNNTIVFGESAGASTHYMALTQETGRLEFHGILMSGNAIC 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 DQDALQWQVKNIAAFGPNPKSVTLFGESAGAAVSLLHSPGSHSLFTRAILLOGSFNA 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 250 PMAWT---QCOHRAFTLAKLAGYKGEDNDKDYLEFLMAKAKQDILKEEYVLTLEERTNK 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 PMAWTSLYEARNKRLNLAKLKGCSRE-NETETIKLRKRDQDELLINLAFVVPY---GTP 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 307 VMFPGPTVERUYQADCVLPKHPREMYKTAMGNSIPTMGNTSYEGLEFTSILKOMPIV 366
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 286 LSVNFGPTVDGDFLDM-----PDLLELGQFKTKQLIVGNKDEGTAFL--LVYGARPGFS 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 367 KELETGVNVPVSELADEART-APETLEMGAKIKKANHVG--ETPTADNMD----- 414
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 339 KDNSIIT--TRKEPOEGKIFFPVSEFGKESILFHYTDWDDORPENYREALGDVVDY 396
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 415 --LCSHYF-----WFRMHRLLQLRFNHTSGTPVLYLRPDESDLLINPRIRMSGGV 466
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 397 NFICPALEFTKFKSEW-----GNNAFYFYEHRSSKLPWPEWM----- 434
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 467 KGVSHADELTFYFNNQALAKRMPKESREYKTIERTMTGIOWPATGNPYSNETEGMENYSW 526
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 435 -GVNHGYEIEFVGLPRLERRONYTKAEELISRSYVKRMANAKKYGNP--NETQN-NSTSW 490
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 527 DPIKSDDEVYKCLNISDELKMIIDVPEMDKIKOWESMEFK 565
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 491 PVFKSTQKYLTLN-TESTRIIMTKLRAOQCRRFTSFFPK 528
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-09-748-739A-19
; Sequence 19, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 574
; TYPE: PRT
```


ORGANISM: Homo sapiens
us-09-748-739A-19

18.2%: Score 558; DB 10; Length 574;

Query Match 29.0%: Pred. No. 6.5e-43;
Best Local Similarity 93; Mismatches 222; Indels 96; Gaps 23;
Matches 168; Conservative

31 ETVAETEGKVKGRKRLTYDDSYSEFGIPIYAPPGVGLRFAKAPQRTPMGV----- 85
2 DDIITATKNGKVRGM-NLIVFGGTVAFLGIPYAPPLGRKFKKQSLTKMSDWNATK 60
66 --RDCCNHKKDSV-----QVDFITGKVGSEDCLYLSTYNNLNPETRKRVLY 132
61 YANSCCQNTIDQSPFGFHGSEMNPNTDL-----SEDCLYLNVWIPAPKPK-NATVLIW 112
133 IHGGFTIGENHRDMYGPDIYFKKD-VVLINIQYRLGALGFLSL--NSEDLNVPGNAGLK 189
113 IYGGFQGTGTSILHYDGFARVERIVVSMNYRVGALGFALDGNPE--APGNMGIF 169
190 DOYVALRWIKNNCANFGNPDNIYFGESAGAASTHYMMLTEOTGTFPHRGILMSGNAIC 249
170 DQALALWQKNIATGAGNPKSVTLFGESAGAAVSALHLSFGSHSLFTRALLQSGSEFA 229
250 PAAANT---QOHRATFLAKYKKGEDNDKDVLEFLMAKAPDOLIKLEEKVLTLEERTNK 306
230 PMAVTSLYEARNRTMLAKLTGCSRE-NETETIKCLARNPOEILLNEAFVVPY--GTP 285
307 VMEPFQTEVPYOTADCVLPKHPREKVTAMGNSIPTMMGNTSYEGLEFTSLIKQMPMLV 366
286 LSNVFGTVDGFLTDM-----PDILLEQGFKKTOILVGNKDEGTAF--LVYGAPGFS 338
367 KELETGCVNPEPSLADAERT-APETLEMGAKIKKAHVIG--ETPPADNEMD----- 414
339 KDNNSIT--TRKEQOGLKIFPGVSEFGKESLIFHTBWDQORENREALGDVVGDY 396
415 --LCSHIYF-----WEPHRLQLRENTSGTPVYLYRDEPSEDLINPYRIMSGRGV 466
397 NEICPALEFKKSEW-----GNNAFFYFEHRSSKLPWPEWM----- 434
467 KGVSHADELYFFWNOAKRMKPKSEYKTIENGTGIMIOFATTGPNYSNEIGMENVS 526
435 -GVNHGEIEFEVGLPERRNDNTKAEELISRSIVKRWANFAKYGNP--NETON-NSTSW 450
527 DPKKSDVYKCLNISDELKMIIDVPEMDKIKOWESMEK 565
491 PVEKSTVOKYLTLN-TESTRINTMLRAQOCRFWTSFPPK 528

RESULT 11
US-09-748-739A-21
Sequence 21, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 21
LENGTH: 574
TYPE: PRT
ORGANISM: Equus caballus
US-09-748-739A-21

Query Match 18.2%: Score 558; DB 10; Length 574;
Best Local Similarity 29.2%: Pred. No. 6.5e-43;
Matches 167; Conservative 100; Mismatches 232; Indels 72; Gaps 21;

31 ETVAETEGKVKGRKRLTYDDSYSEFGIPIYAPPGVGLRFAKAPQRTPMGV----- 85

DB 2 EDIITTKNGKVRGM-NLIVFGGTVAFLGIPYAPPLGRKFKKQSLTKMSDWNATK 60
86 --RDCCNHKKDSVQVDFITGKVG-----SEDCLYLSTYNNLNPETRKRVLYIHGGF 138
61 YANSCCQNTIDQSPF-GFLGSEMNPNTLSEDCLYLNVWIPAPKPK-NATVIMIIYGGGF 118
139 IIGENHRDMYGPDIYFKKD-VVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDOYVALRW 197
119 QGTGSSLPYVDFARVERIVVSMNYRVGALGFAL--SENDEAGNGLDQDQALW 177
198 IKNNCANFGNPDNIYFGESAGAASTHYMMLTEOTGTFPHRGILMSGNAICPAAANT--- 254
178 VQKNIAAFGKNPSVTLFGESAGAAVSALHLSFSPROPLFTRAILQSGSSMAPWATSLY 237
255 QOHRATFLAKYKKGEDNDKDVLEFLMAKAPDOLIKLEEKVLTLEERTNKVMEPFQ 314
238 EARNRTITLAKRMCC-SRDNETEMIKLRDKDPOEILLNEAFVVPY--TLLSVNGFP 293
315 VEPYOTADCVLPKHPREKVTAMGNSIPTMMGNTSYEGLEFTSLIKQMPMLVKELETCVN 374
294 VDGEFLTDM-----PDTLLQGFKKRTQILVGNKDEGTAF--LVYGAPGFSKDNNSIT- 345
375 FVPSLADAERT-APETLEMGAKIKKAHVIG--ETPPADNEMD-----LCSHIY 420
346 -TRKEFOGLKIFPRVSEFGRESILFHYMDQDQARENREALDQVVDYNNICPALE 404
421 WEPHRLQLRENTSGTPVYLYRDEPSEDLINPYRIMSGRGVGVSHADELYFEW 480
405 FTRKSEL-----GNDAFFYFEHRSTKLWPEWM-----GVNHGEIEFEVFG 447
481 NOLAKRMKPKSEYKTIENGTGIMIOFATTGPNYSNEIGMENVS--WDPKKSDEYK 538
448 IPLERRVNTTRAEEILSSIMKRWANFAKYGNP-----NGTQNNSTIRPKVSEQKYL 502
539 LNISDELKMIIDVPEMDKIKOWESMEKRD 569
503 LN-TESPKVYTLRAQOCRFWTLFPPKVL 532

RESULT 12
US-09-748-739A-18
Sequence 18, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 18
LENGTH: 574
TYPE: PRT
ORGANISM: Homo sapiens
US-09-748-739A-18

Query Match 18.1%: Score 556; DB 10; Length 574;
Best Local Similarity 28.8%: Pred. No. 1e-42;
Matches 167; Conservative 94; Mismatches 222; Indels 96; Gaps 23;

31 ETVAETEGKVKGRKRLTYDDSYSEFGIPIYAPPGVGLRFAKAPQRTPMGV----- 85
2 DDIITATKNGKVRGM-NLIVFGGTVAFLGIPYAPPLGRKFKKQSLTKMSDWNATK 60
86 --RDCCNHKKDSV-----QVDFITGKVGSEDCLYLSTYNNLNPETRKRVLY 132
61 YANSCCQNTIDQSPFGFHGSEMNPNTDL-----SEDCLYLNVWIPAPKPK-NATVLIW 112
133 IHGGFTIGENHRDMYGPDIYFKKD-VVLINIQYRLGALGFLSL--NSEDLNVPGNAGLK 189


```

Db 113 IYGGFQGTGSSSLHVGKFLARVERIVVSMNRVAGALGFLAPGPE---AGNMGLE 169
QY 190 DQVVALRMKNNKNCANFGNPDNITVEGSEAGASTHYMTLEOTRGLFHRGILMSGNAIC 249
Db 170 DQALALWQVOKNIAAFGKNPKSVTLFEGSAGASVSLHLSFGSHSLFTRAILQSGSFNA 229
QY 250 PWMT---QOCHRAFTLAKLAGYKGEDNDKDVLEFLKAKAQODIKLEEKVLTLEERTNK 306
Db 230 PMAVTSLEYEARNRTLNAKLKLGCSRE-NETETIKCLRNDQOELLWEAFVVPY---GTP 285
QY 307 VMFPGPTVEPYQADCVLPKHPREMYKTANGNSIPTMNGTSYGLFETSILOMPALV 366
Db 286 LSVAFGPTVDDFLTDM-----PDILLEGOFKTOILVGNKDEGTAFA--LVYGAPGFS 338
QY 367 KELETCAVNPVELADERT-APETLEMGAKIKRAHVYG--ETPTADNEMD----- 414
Db 339 KDNNSIIT--TRKEFOEGKIFFPGVSEFGKESILFHYTDWVDQDRPENYREALGDVYGDY 396
QY 415 --LCSHIYF-----WPMHRLLOLRFNHSGTVPVLYLRFPDSEDDLINPYRIRSGRGV 466
Db 397 NFICPALEFKKESSEW-----GNNAFYFYEHRSSKLPWPEWM----- 434
QY 467 KGVSHADELTYFFMNOLAKRMPKESREXYKTIERMTGIMIOFATTGNPYSNEIEGEMENYSV 526
Db 435 -GVHGYEIEFVGLPLERRRNYTKAEILSRSTYVKRANAKYGNP--NETQN--NSTSW 490
QY 527 DPKSKDEYVKCLNISDELKMIIDVPEMDKIKOMESMEK 565
Db 491 PVFKSTOKYLTLLN-TESTRIMTKLRAOOCRFWTSPFPK 528

```

RESULT 13

```

US-09-748-739A-22
; Sequence 22, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748, 739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Felis catus
US-09-748-739A-22

```

```

Query Match 18.0%; Score 554; DB 10; Length 574;
Best Local Similarity 28.1%; Pred. No. 1,Se-42;
Matches 167; Conservative 100; Mismatches 201; Indels 126; Gaps 24;

```

```

QY 31 ETVAAEPFEGYKVGKRLTYVDDSYSPGPIYAPQPRGELRFRAPQPTWMDGV----- 85
Db 2 EDIITITKNGKVRGM-NLPVLDGTVAFGLIPYAPPLGRKRPQPLTKWMSDWMATK 60
QY 86 --RDCSNHKDSV-----QVDFITGKVCSEDCILSYTYNNLNPEETKRPVLVY 132
Db 61 YANSCYQNAODSFGPFQSESEMMNNTDL-----SEDCILTNWIPRPKRP-KATYWIW 112
QY 133 IHGGFIIIGENHRDMYGPDYFIKRD-VVLINIOYRLAGLGLSL--NSEDLVNPGNAGL 189
Db 113 IYGGFQGTGSSSLPYDQKFLARVERIVVSMNRVAGALGFLAPGPE---VPGNMGLE 169
QY 190 DQVVALRMKNNKNCANFGNPDNITVEGSEAGASTHYMTLEOTRGLFHRGILMSGNAIC 249
Db 170 DQALALWQVOKNIAAFGKNPKSVTLFEGSAGASVSLHLSFGSHSLFTRAILQSGSFNA 229
QY 250 PWMT---QOCHRAFTLAKLAGYKGEDNDKDVLEFLKAKAQODIKLEEKVLTLEERTNK 306

```

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Db 230 PMAVMSDEAKNRRLTLAKLFGC--SKENDTEIICLRKNDQOELL-LNELLVVSDDTLLS 287
QY 307 VMFPGPTVEPYQADCVLPKHPREMYKTANGNSIPTMNGTSYGLFETSILOMPALV 366
Db 288 V--NFGPVDDDFLTD-----PDTLLQGOFKTOILVGNKDEGTAFA--LVYGAPGFS 338
QY 367 KELETCAV-----FVPSLADERTAPETLEMGAKIKRA-- 400
Db 339 KDNNSIITRKEFOEGKIFFPGVSEFGREALLFYVVDLDDQR-----AEKYREALD 390
QY 401 HVTEG---PPTAD---NEMDLSHIYFPMHRLLOLRFNHSGTVPVLYLRFPDSEDDL 453
Db 391 DVLGDYNICALLETTKFSELGNNAFYFYEHRSSQLPW-----PEWM----- 434
QY 454 INPYRIRSGRGVGVSHADELTYFFMNOLAKRMPKESREXYKTIERMTGIMIOFATTGNP 513
Db 435 -----GVHGYEIEFVGLPLERRRNYTKAEILSRSTYVKRANAKYGNP 480
QY 514 YSNEIEGEMENYS--WDPKSKDEYVKCLNISDELKMIIDVPEMDKIKOMESMEK 565
Db 481 -----NETQNNSTWPAERSTQRYLTLLN-AESPKVYTKLRAOOCRFWTLPFPK 528

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RESULT 14

```

US-09-738-626-4754
; Sequence 4754, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, MAKOTO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4754
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4754

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Query Match 17.8%; Score 548; DB 9; Length 537;
Best Local Similarity 29.2%; Pred. No. 4,9e-42;
Matches 169; Conservative 97; Mismatches 220; Indels 92; Gaps 22;

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QY 91 HKDSVQVDFI-TGKVCSEDCILSYTYNNLNPEETKRPVLVYIYHGGFIIIG-ENHRDMY 148
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GenCore version 5.1.4.p5_4578
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Title: US-09-776-910-9

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Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Database :

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1713	100.0	1713	6	ARI53442 Sequence
2	1711.4	99.9	1713	6	ARI53438 Sequence
3	1711.4	99.9	1713	6	ARI53439 Sequence
4	1708.2	99.7	1713	6	ARI53440 Sequence
5	1703.4	99.4	1713	6	AR062837 Sequence
6	1703.4	99.4	1713	6	ARI53441 Sequence
7	1703.4	99.4	2240	3	ICU56636
8	1678.2	98.0	1713	6	AR062838
9	987.2	57.6	2160	3	AF133341
10	959.4	56.0	2175	3	AF139082
11	958.6	55.8	1710	6	ARI53445
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13	378.6	22.1	2660	3	AY121675
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RESULT 1
LOCUS   ARI53442
DEFINITION Sequence 9 from patent US 6235515.
ACCESSION ARI53442
VERSION   ARI53442.1 GI:15120974
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS   Russell,R.Joyce., Newcomb,R.David., Campbell,L.P.Malcolm.,
          Robin,G.Charlesde,Quetleville., Claudianos,C., Smyth,K.-A.,
          Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
TITLE     Malathion carboxylesterase

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JOURNAL Patent: US 6235515-A 9-22-MAY-2001;
FEATURES Location/Qualifiers
Source 1.1713
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BASE COUNT 515 a 305 c 370 g 523 t
ORIGIN

Query Match 100.0%; Score 1713; DB 6; Length 1713;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 GGTGAAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
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DB 481 ATTAACATACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 AATGCGCGGATATGCGGCGCTTAAAGATCAATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 AATGCGCGGATATGCGGCGCTTAAAGATCAATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 AATGCGCGCACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 AATGCGCGCACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 GGTGCTTACCCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 GGTGCTTACCCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
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DB 1381 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
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DB 1441 AATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
QY 1501 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1501 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1561 ATGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 ATGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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LOCUS AR153438
DEFINITION Sequence 1 from patent US 6235515.
ACCESSION AR153438
VERSION AR153438.1 GI:15120970
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
Robin, G. Charles., Queteville., Claudianos, C., Smyth, K. A.,
Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Collin.
Malachon carboxylesterase
JOURNAL Patent: US 6235515-A 9-22-MAY-2001;
FEATURES Location/Qualifiers
Source 1.1713
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Db	61	AAATTTTAAACATCTCGTTTAACCTACCAATGAACAGGTGGTACGTGAACATGAAATATGCG	120
OY	121	AAAGTGAAGGCGTTTAAACGTTTAACTGTGTACAGATGATTCCTACTACAGTTTGTAGGGT	180
Db	121	AAAGTGAAGGCGTTTAAACGTTTAACTGTGTACAGATGATTCCTACTACAGTTTGTAGGGT	180
OY	181	ATACCGTAGCGCCCAACCGCCAGTGGGTGAGGAGTTTAAAGCACCCACGAGCACACA	240
Db	181	ATACCGTAGCGCCCAACCGCCAGTGGGTGAGGAGTTTAAAGCACCCACGAGCACACA	240
OY	241	CCCTGGATGGTGTGCGTGTATTTGTGCATATCAATCAATGAAGATTAAGTCAAGTCAATTTT	300
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OY	361	CTAATGCCGAACATAAGCTCCCGTTTAGTATACATACATAGTGGGTATTTATATTC	420
Db	361	CTAATGCCGAACATAAGCTCCCGTTTAGTATACATACATAGTGGGTATTTATATTC	420
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Db	421	GGTGAATAATCATCGTGTATGTATGTGTCCGATTTATTTATTTAAAGAGATGTGGTGTG	480
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Db	481	ATTAAACATACATATTCGTTTGGAGCTTAAGTTTTCTAAGTTTAAATTCAGAGACCTT	540
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OY	841	TTTTCTTATGAAGCCAAAGCCACAGGATTTATATAAACTTTAGGAAAAAGTTTTAATCTTA	900
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OY	901	GAAGAGCGTACAAATTAAGTCAATGTTCCGTTTGGTCCCACTGTTGAGCAATATACAGCC	960
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VERSION	ARI53439.1	
KEYWORDS	GI:15120971	
SOURCE	Unknown.	
ORGANISM	Unknown.	
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AUTHORS	Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm., Roblin,G.Charlesde.QUetleville., Claudiolos,C., Smyth,K.A., Boyce,T.Mark., Oakesholt,J.Graham, and Brownlie,J.Colin.	
TITLE	Malathion carboxylesterase	
JOURNAL	Patent: US 6235515-A 3 22-MAY-2001;	
FEATURES	Location/Qualifiers	
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BASE COUNT	515 a 306 c 370 g 522 t	
ORIGIN		

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Best Local Similarity	99.9%	Pred. No. 0			
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DB	121	AAAGTGAAGGCGTTAAACGTTTAACTGCTGATGATGATGATGATGATGATG	180		
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DB	301	ATAACGGGCAAGTGTGCTGAGAGATGCTATACCTAAGTGTCTATACCAAT	360		
QY	361	CTAAATCCCGAACTAAACGTCCTGTTTAACTATACATACATGATGATGATG	420		
DB	361	CTAAATCCCGAACTAAACGTCCTGTTTAACTATACATACATGATGATGATG	420		
QY	421	GGTGAATATCATGATGATGATGATGATGATGATGATGATGATGATGATG	480		
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DB	1141	GCTGATGCTGAACGACCGCCCAAGACCTGTGAAATGAGTGTGATTAATTA	1200		
QY	1201	CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATGATGATGATG	1260		
DB	1201	CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATGATGATGATG	1260		
QY	1261	TTCTGCTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATG	1320		
DB	1261	TTCTGCTTCCCATGATGATGATGATGATGATGATGATGATGATGATGATG	1320		
QY	1321	GCTACTTGTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATG	1380		
DB	1321	GCTACTTGTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATG	1380		
QY	1381	CGTACTGAGCTGTGTTTAAAGGTTAGTCAATGATGATGATGATGATGATG	1440		
DB	1381	CGTACTGAGCTGTGTTTAAAGGTTAGTCAATGATGATGATGATGATGATG	1440		
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DB	1441	AATCAATGGCCAAACGATGATGATGATGATGATGATGATGATGATGATGATG	1500		
QY	1501	ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1560		
DB	1501	ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1560		
QY	1561	ATGGAATATGTTCTGCGATGATGATGATGATGATGATGATGATGATGATG	1620		
DB	1561	ATGGAATATGTTCTGCGATGATGATGATGATGATGATGATGATGATGATG	1620		
QY	1621	ATTAAGTGAATGAAATGATGATGATGATGATGATGATGATGATGATGATG	1680		
DB	1621	ATTAAGTGAATGAAATGATGATGATGATGATGATGATGATGATGATGATG	1680		
QY	1681	TCGATGTTGAAAACATGATGATGATGATGATGATGATGATGATGATGATG	1713		
DB	1681	TCGATGTTGAAAACATGATGATGATGATGATGATGATGATGATGATGATG	1713		

RESULT 4	AR153440	1713 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR153440				
DEFINITION	Sequence 5 from patent US 6235515.				
ACCESSION	AR153440				
VERSION	AR153440.1	GI:15120972			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1713)				
AUTHORS	Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm., Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Collin.				
TITLE	Malathion carboxylesterase				
JOURNAL	Patent: US 6235515-A 5 22-MAY-2001.				
FEATURES	Location/Qualifiers				
source	1..1713				
BASE COUNT	516 a 305 c 369 g 523 t				
ORIGIN					
Query Match	99.7%	Score 1708.2	DB 6	Length 1713	
Best Local Similarity	99.8%	Pred. No. 0			

Matches 1710: Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
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Db	1	ATGAATTTCAACGTTAGTTTGATGAGAAATTAATAAGAGATTAAATGCAATGAAAT	60	
Qy	61	AAATTTTAACTATCTTTAACTACCAATGAAGCGTGTAGCTGAAGCTGATATGTC	120	
Db	61	AAATTTTAACTATCTTTAACTACCAATGAAGCGTGTAGCTGAAGCTGATATGTC	120	
Qy	121	AAAGTGAAGCGCTTAAAGCTTTAACTGTACGATGATCTTAACTACAGTTTGAAGGT	180	
Db	121	AAAGTGAAGCGCTTAAAGCTTTAACTGTACGATGATCTTAACTACAGTTTGAAGGT	180	
Qy	181	ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCCCCAGGACCA	240	
Db	181	ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCCCCAGGACCA	240	
Qy	241	CCCTGGATGGTGTGCGATGTTGCAATCATTAAGATTAAGTCAAGTTGATTTT	300	
Db	241	CCCTGGATGGTGTGCGATGTTGCAATCATTAAGATTAAGTCAAGTTGATTTT	300	
Qy	301	ATACGGGCAAGTGTGTGCTCAGAGATTTGTCTATACCTAAGTGTCTATACGAATAT	360	
Db	301	ATACGGGCAAGTGTGTGCTCAGAGATTTGTCTATACCTAAGTGTCTATACGAATAT	360	
Qy	361	CTAAATCCCGAACTAAGCGCCGTTTAACTATACATACATGCTGGTGTATATATC	420	
Db	361	CTAAATCCCGAACTAAGCGCCGTTTAACTATACATACATGCTGGTGTATATATC	420	
Qy	421	GGTGAATATCATCTGATATGATGCTGCTGATTTTCAATTAAGAGATGCTGTG	480	
Db	421	GGTGAATATCATCTGATATGATGCTGCTGATTTTCAATTAAGAGATGCTGTG	480	
Qy	481	ATTAACATACATATCTGTTGGAGCTCTAGCTTTCTAAGTTTAAATTCAGAACCTT	540	
Db	481	ATTAACATACATATCTGTTGGAGCTCTAGCTTTCTAAGTTTAAATTCAGAACCTT	540	
Qy	541	AATGCGCCGGTAAATGCGGCTTAAAGATCAATGATGCTGCTGCTGATTTAAAT	600	
Db	541	AATGCGCCGGTAAATGCGGCTTAAAGATCAATGATGCTGCTGCTGATTTAAAT	600	
Qy	601	AATGCGGCAACTTTGGTGGCAATCCGATATATTTACAGTCTTTGGTGAAGTCCGGT	660	
Db	601	AATGCGGCAACTTTGGTGGCAATCCGATATATTTACAGTCTTTGGTGAAGTCCGGT	660	
Qy	661	GCTGCTCTACCCACTACATGATGTTAACGAACTCGCGTCTTTCCATCGTGT	720	
Db	661	GCTGCTCTACCCACTACATGATGTTAACGAACTCGCGTCTTTCCATCGTGT	720	
Qy	721	ATACAAATGCTGGGTAATGCTATTTGCTATGCTATACCAATGTCACATGCTGC	780	
Db	721	ATACAAATGCTGGGTAATGCTATTTGCTATGCTATACCAATGTCACATGCTGC	780	
Qy	781	TTTCACTTACGCAAAATTTGGCGCTATTAAGGTGAGATTAATGATTAAGATTTTGA	840	
Db	781	TTTCACTTACGCAAAATTTGGCGCTATTAAGGTGAGATTAATGATTAAGATTTTGA	840	
Qy	841	TTTCTTATGAAGCCACGACAGATTTAATAAATCTTGAGGAAAAAGTTTAACTCTA	900	
Db	841	TTTCTTATGAAGCCACGACAGATTTAATAAATCTTGAGGAAAAAGTTTAACTCTA	900	
Qy	901	GAGAGGCTACAAATTAAGTATGTTCTTTGCTTGTCCACGCTGACCATATAGACC	960	
Db	901	GAGAGGCTACAAATTAAGTATGTTCTTTGCTTGTCCACGCTGACCATATAGACC	960	
Qy	961	GCTGATTTGCTTACCCAAATCTCGGGAATGTTAAATGCTTTGGGTAAATCG	1020	
Db	961	GCTGATTTGCTTACCCAAATCTCGGGAATGTTAAATGCTTTGGGTAAATCG	1020	
Qy	1021	ATACCACTATGATGGGTAAACATCTCATATGAGGGTCTATTTTCACTCAATCTTAAG	1080	
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Qy	1081	CAATGCCATCTCTGTTAAGGAATTTGAAGAACTGTGTCATTTTGTCCAGTGAATG	1140	
Db	1081	CAATGCCATCTCTGTTAAGGAATTTGAAGAACTGTGTCATTTTGTCCAGTGAATG	1140	
Qy	1141	GCTGATGCTGAACGCGACCGCCCGACAGACCTTGAAGTGGTCTAAATTTAAAAAGCT	1200	
Db	1141	GCTGATGCTGAACGCGACCGCCCGACAGACCTTGAAGTGGTCTAAATTTAAAAAGCT	1200	
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Db	1201	CATGTTACAGGAGAAACACCAACAGCTGATTAATTTTATGATCTTGTCTCACATCTAT	1260	
Qy	1261	TTCTGGTCCCATGATGATGCTTTGTTGAATACCTTTCAACACACCTCGGTACACC	1320	
Db	1261	TTCTGGTCCCATGATGATGCTTTGTTGAATACCTTTCAACACACCTCGGTACACC	1320	
Qy	1321	GCTACTTGTATGCTGCTGACCTTCGATTCGGAAGATCTTATCAATCCATGCTATATG	1380	
Db	1321	GCTACTTGTATGCTGCTGACCTTCGATTCGGAAGATCTTATCAATCCATGCTATATG	1380	
Qy	1381	GCTAGTGACGTGTGTTAAGGTTTATGCTATGCTGATGAATTAACCTATTTCTTGG	1440	
Db	1381	GCTAGTGACGTGTGTTAAGGTTTATGCTATGCTGATGAATTAACCTATTTCTTGG	1440	
Qy	1441	ATCAATTTGCCCAACGATGCTTAAAGATGCGTGAAATACAAACATTTGAACGTATG	1500	
Db	1441	ATCAATTTGCCCAACGATGCTTAAAGATGCGTGAAATACAAACATTTGAACGTATG	1500	
Qy	1501	ACTGCTATATGATGATCAATTTTCCACACCTGCTAATCTTATAGCAATGAATGAAGT	1560	
Db	1501	ACTGCTATATGATGATCAATTTTCCACACCTGCTAATCTTATAGCAATGAATGAAGT	1560	
Qy	1561	ATGGAATATGTTTCTGCGATCCAAATTAAGAAATCCGATGAAGTATCAAGTGTGAAAT	1620	
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Qy	1621	ATTAGTATGATTTGAATGAATGATGATGCTGCTGAAGTGAATGAATGAATGAAGGAG	1680	
Db	1621	ATTAGTATGATTTGAATGAATGATGATGCTGCTGAAGTGAATGAATGAATGAAGGAG	1680	
Qy	1681	TGCATGTTTGAAGAAACATAGATATTTATTTTGG	1713	
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RESULT 5				
AR062837				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
BASE COUNT				
ORIGIN				
Query Match				
Best Local Similarity				
Matches 1707: Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
Qy	1	ATGAATTTCAACGTTAGTTTGATGAGAAATTAATAAGAGATTAAATGCAATGAAAT	60	

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RESULT 7
 LCUS5636
 LOCUS
 DEFINITION
 Lucilia cuprina alpha esterase (lcaet) mRNA, implicated in
 organophosphate resistance, complete cds.
 ACCESSION
 U5636
 VERSION
 U5636.1
 KEYWORDS
 Lucilia cuprina.
 Lucilia cuprina.
 ORGANISM
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Oestroidea; Calliphoridae; Lucilia.
 REFERENCE
 1 (bases 1 to 2240)
 Newcomb,R.D., East,P.D., Russell,R.J. and Oakeshott,J.G.
 Isolation of alpha cluster esterase genes associated with
 organophosphate resistance in *Lucilia cuprina*
 Insect Mol. Biol. 5 (3), 211-216 (1996)
 JOURNAL
 MEDLINE
 PUBMED
 8799740
 REFERENCE
 2 (bases 1 to 2240)
 Newcomb,R.D., Campbell,P.M., Russell,R.J. and Oakeshott,J.G.
 cDNA cloning, baculovirus expression and kinetic properties of the
 esterase, E3, involved in organophosphorus resistance in *Lucilia*
cuprina
 Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997)
 JOURNAL
 MEDLINE
 PUBMED
 9061925
 REFERENCE
 3 (bases 1 to 2240)
 Newcomb,R.D., Campbell,P.M., Ollis,D.L., Cheah,E., Russell,R.J. and
 Oakeshott,J.G.
 A single amino acid substitution converts a carboxylesterase to an
 organophosphorus hydrolase and confers insecticide resistance on a

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997)
MEDLINE
97352821
PUBMED
9207114
4 (bases 1 to 2240)
Campbell, P.M., Newcomb, R.D., Russell, R.J. and Oakeshott, J.G.
Two different amino acid substitutions in the all-esterase, E3,
confer alternative types of organophosphorus insecticide resistance
in the sheep blowfly

JOURNAL
Unpublished
5 (bases 1 to 2240)
Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
Direct Submission
Submitted (24-Apr-1996) Richard D. Newcomb, Molecular Genetics,
HortResearch, Private Bag 92 169, Auckland, New Zealand
JOURNAL
Location/Qualifiers

FEATURES

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exon
BASE COUNT
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Query Match 99.4%; Score 1703.4; DB 3; Length 2240;
Best Local Similarity 99.6%; Fred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1501 ACTGATATGATGATATCAATTTTGCCACCTGCTATACCTTATGCAATGAATGAACGT 1560
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QY 1621 ATTAGTATGATTAAGAAATGATGATGCTGCTGAATGATGAATGAATGAATGAGAG 1680
Db 1918 ATTAGTATGATTAAGAAATGATGATGCTGCTGAATGATGAATGAATGAATGAGAG 1977
QY 1681 TCGATGTTTGAATAACATAGAGATTTATTTAG 1713
Db 1978 TCGATGTTTGAATAACATAGAGATTTATTTAG 2010

RESULT 8
AR062838 1713 bp DNA Linear PAT 29-SEP-1999
LOCUS AR062838
DEFINITION Sequence 2 from patent US 5843758.
ACCESSION AR062838
VERSION AR062838.1 GI:5990529
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Russell,R.Joyce., Newcomb,R.David., Robin,G.Charlesde,Quetleville.,
Boyce,J.Mark., Campbell,P.Malcolm., Parker,A.Gerard.,
Oakeshott,J.Graham, and Smyth,K.-A.
TITLE Enzyme based bioremediation
JOURNAL Patent: US 5843758-A 2 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..1713
BASE COUNT 506 a 299 c 363 g 515 t 30 others
ORIGIN

Query Match 98.0%; Score 1678.2; DB 6; Length 1713;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1680; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGAATTTCAACGTTAGTTTATGAGAAATTAATGAAGTGAATGAATGAATGAATGAATGAAT 60
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QY 61 AAGTTTTAACTATCGTTTAACATCAATGAAGAAAGGTGTAGTGAAGTGAATGAATGAC 120
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[illegible]

FEATURES	source
DEFINITION	AF139082 2175 bp mRNA linear INV 20-OCT-2000
LOCUS	AF139082
ACCESSION	AF139082
KEYWORDS	Haematobia irritans irritans alpha E7 esterase (ae7) mRNA, complete cds.
ORGANISM	AF139082.1 GI:6502938
SOURCE	Haematobia irritans irritans.
REFERENCE	Guerrero, F.D. Cloning of a horn fly CDNA, H1alphaE7, encoding an esterase whose transcript concentration is elevated in diazinon-resistant flies Insect Biochem. Mol. Biol. 30 (11), 1107-1115 (2000)
REFERENCE	Guerrero, F.D. Direct Submission Submitted (30-MAR-1999) USDA-ARS, Knipling-Bushland U.S. Livestock Insects Research Laboratory, 2700 Fredericksburg Rd., Kerrville, TX 78028, USA
gene	1. .2175 /organism="Haematobia irritans irritans" /strain="Camp Cooley 4/97" /sub_species="irritans" /db_xref="taxon:75445" /clone="HF41CC" /note="Hyethroid and diazinon-resistant" 1. .2175 /gene="ae7" 282. .1994 /gene="ae7" /note="similar to Lucilia cuprina and Drosophila melanogaster alpha E7 esterases" /codon_start=1 /product="alpha E7 esterase" /protein_id="AF14517.1" /db_xref="GI:6502938" /translating="MNFNVSEFLERKIKCVENKILNLTINETHIVDEYKIKG VKRLTYVDSPSEGIPIYAKPYGELFRAPORPWPMDVCKOCHCAASVOTDFIS ITNVSQEDICLYINVTNNLTNDPRPVLVPEHGGFICGEANRYCAADYFIKDYVF ITVYRLGVLTGELSLNSENLNVENAGLKVQWALRIKNNKCSFGCDPCLTFGES AGASTYRMMITEQARGLFHRVAVLMSGTAC IAAHTQCQRHGYTIARIYKGENND DVEDFLMKANPYDLAREHNVLTNEELRDVMAFGTPEYTPDCVLKPRNEMIK TAMVNSIPLTILGNTSYEGLFLISYVGNPKPLIKELTEFEYVGEIVEDRSSSELT IASTLKLIVRGETPTLESFTELCSDPEFWYPMHRLTOLRPNHTVGSPIYLYRPDS EELINPRIMRYGKVGCAHDTDELTYLFTMTLSIKMPKRSREKTEIRMGITMPTA TTGMPYSEPEINGENMTTWDSLSKSDVEYKCMNIGDELFTDLPEMKLAWQSVFNK RELF"
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ORIGIN	
Query Match	56.0%; Score 959.4; DB 3; Length 2175;
Best Local Similarity	72.5%; Pred. No. 3e-204;
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61	AAGTTTAAACATGTTTAACTACCAATGAACGCGTGTAGCTGAAATGATATGCG 120
342	AAAATTTAACTACGCGCTTATTACCAATGAACGCAATATTGTGCAATCGAATATGA 401
121	AAAGCAAGGCGTTAAACGTTTAACTGTGACATGATGTTCTCTACTACAGTTTGAGGCT 180
402	AAAATTTAAAGGCGTTTAAACGTTTGAACATGTGACATGATGATCTCATCTACAGCTTTGAAGCT 461

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 DB 522 CTTTGGATGAGATTAAGATTTGTTGCTGCTGCCCTCCGTGCTCAACACGATTTTC 581
 QY 301 ATACGGGCAAGTGTGTGCTCAGAGATTTGCTATACCTAAGTCTATACGATTAAT 360
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 QY 481 ATTAACATACAAATATGCTTTGGAGCTTAGGTTTCTAAGTTTAAATTCAGAGACCTT 540
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 DB 1122 TTTCTTAAAGAAAGCAAGCAAGATTTTAAACCTTGAGGAAAGATTTTAACTCTA 1181
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 DB 1182 GAGGAACTTCTGATTAAGTATGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1241
 QY 961 GCTGATGCTGCTTACCCAAACATCTGCGGGAATGTTTAAACGCTTGGGATTTG 1020
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 DB 1962 AGTGTTCATTAAGAGCGGATTTGTTAG 1994
 RESULT 11
 AR153445 1710 bp DNA linear PART 08-AUG-2001
 LOCUS AR153445
 DEFINITION Sequence 14 from patent US 6235515.
 ACCESSION AR153445
 VERSION AR153445.1 GI:15120977
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1710)
 AUTHORS Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm., Robin,G.Charlesde,Quetleville., Claudinos,C., Smyth,K.-A., Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
 TITLE Malathion carboxylesterase
 JOURNAL Patent: US 6235515-A 14 22-MAY-2001;
 FEATURES
 source location/Qualifiers
 1..1710
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 Best Local Similarity 73.4%; Pred.No.1.3e-203;
 Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;
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 DB 104 CTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 163
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 DB 164 ACTACGTTTGAAGATATACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 223
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RESULT 12
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 AY051473
 ACCESSION
 AY051473.1 GI:15291256
 VERSION
 KEYWORDS
 FLI.CDNA.
 SOURCE
 ORGANISM
 Drosophila melanogaster.
 Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1017)

REFERENCE
 AUTHORS
 Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
 Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,
 Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J.,
 Nuno, J., Pacleb, J., Paragas, V., Park, S., Phouenavong, S., Wan, K.,
 Yu, C., Lewis, S.E., Rubin, G.M. and Celisner, S.
 Direct Submission
 Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA
 Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory

TITLE
 JOURNAL
 COMMENT
 This clone was sequenced as part of a high-throughput process to
 sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
 Science 2000). The sequence has been subjected to integrity checks
 for sequence accuracy, presence of a polyA tail and contiguity
 within 100 kb in the genome. Thus we believe the sequence to
 reflect accurately this particular cDNA clone. However, there are
 artifacts associated with the generation of cDNA clones that may
 have not been detected in our initial analyses such as internal
 priming, priming from contaminating genomic DNA, retained introns
 due to reverse transcription of unspliced precursor RNAs, and
 reverse transcriptase errors that result in single base changes.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our Web site
 (<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.

FEATURES
 source
 location/Qualifiers
 1..2017
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NKDLLE"
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Best Local Similarity 62.7%: Pred. No. 1.8e-141;
Matches 1074; Conservative 0; Mismatches 637; Indels 3; Gaps 1;

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DB 151 AAGTCCACGATATCGCCAGTCGACCATGAACAGTTGCGCGACACGAGTACGGC 210
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QY 121 AAGTGAAGGCGTTAAACGTTTAACTGTGATGATGATCTCTACAGTTTGAGAGGT 180
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DB 211 CAGGTGAGGGGTATCAAGGCTATCTCTGATGATGATGATGATGATGATGATGAT 270
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 ATACCGTAGCCCAACGCCGACGAGGTGATGATGATGATGATGATGATGATGATGAT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 271 ATCCCGTACGCCGACGCTCGGTGGGAGAGTGGGTTAAAGGCCCTCAGAGGCCCAT 330
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QY 241 CCCGTGATGTGTGCGTATGTTGATGATGATGATGATGATGATGATGATGATGAT 300
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DB 331 CCCGAGGAGGAGTTCGCGACTGACGCCAGCCGAGAGATGAAGCCGCTCCAGGTGCA 390
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QY 301 ATACGGGCAAAAGTGTGTGCTCAGAGGATGTTCTATACCTAAGTGTCTATACGATAT 360
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DB 391 GTCTTGATAGTAGAGGAGGCTCGAGAGACTGCTCTATCTCAATGTATACCAACAAT 450
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QY 361 CTAAATCCCGAACTAAACGTCGGTTTATGATACATACATGCTGTGTTTATATATC 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 451 GTGAAGCCCGCAAGGCTCGCCGTTATGTTGATGATGATGATGATGATGATGATGAT 510
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 GGTGAATAATCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 511 GCGGAGGCCAATCGGGAATGATGATGATGATGATGATGATGATGATGATGATGAT 570
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 481 ATTAACATACAAATATGTTGGAGCTCTAGTTTCTAGATTAAATTAAGAAGACTT 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 571 GTACAGATACAGTACGCACTTGGGCTTGGGATTTATGATTTTAAATCCCGAGCTA 630
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 541 AATGTGCCGTAATCCGCGCTTAAAGATGAAGTGAAGGCTGCGTGGATTAATAAAT 600
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DB 631 AATGTACAGAAATGCTGGCTCAAGATCAAGTGTGCGCCCTCAAGTGAATCAAGAC 690
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QY 601 AATGTGCCAATGTTGGTGAATCCGATATATTAAGTCTTGTGTGAATGCGCGGT 660
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DB 691 AATGTGCTAGTTTGGGAGAGATCCCAATGATCACTGTTTGTGAGAGAGTGTGGA 750
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QY 661 GCTGCTTACCCACTACATGATGTTAAACCAACACTGCGGCTCTTTCATCGTGGT 720
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DB 751 GCGCGCTCCACCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 810
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QY 721 ATACTAATGTGCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 770
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DB 811 ATCTTGCACTGCGGAGCGCATTTGTCTTGGGCTCAACAGGCGCATTAACCATAT 870
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QY 778 GCGTTCACCTTACGCCAATTTGGCGCGCTATTAAGGATGATGATGATGATGATGAT 837
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DB 871 CCTACAGGATAGCCAAAGCTGTTGCTACAGAGATCTTATTCGCGAGAGAAATGCT 930
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QY 838 GAATTTCTATGAAGCAACGACAGCATTTTAATAAATCTGAGAGAAAGTTTAACT 897
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 958 ACCGCTATGTTGCTTACCAACATCTCTCGGAAATGTTAAATGCTTGGGGTAAT 1017
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DB 1051 ACGCCGAATGTGATATCAAGCTCCAAAGAGATGATGATGATGATGATGATGAT 1110
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QY 1018 TCGATACCCACTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
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DB 1111 TCGATACCCACTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1078 AAGCAATGCTTATGTTTGAAGAAATGGAACCTTGTCTCAATTTTGGCAAGTGA 1137
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QY 1138 TTGCGTATGCTGAACGACACCGCCCGAGAGACCTTGAATGAGTGTGAATTA 1197
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DB 1291 GTTCAATGCACTGCTCAGAAAGACCCAGATATTAATGATGATGATGATGATGAT 1350
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QY 1258 TATTTGCTGCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
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DB 1351 TACTTGTGTTCCGCGCTGAGGGTGTTCATTTCCGACACGGGTACGGGCTGAG 1410
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QY 1318 CCGCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1411 CCGATATATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470
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QY 1378 ATGCGTAGTGACGCTGCTTAAAGGCTGTTAGTCAATGATGATGATGATGATGAT 1437
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DB 1471 ATGCGTGTGGAGCGGTGTCAAGGGGTCAGCAGTCCGAGATTTGAGTACCAATTC 1530
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QY 1438 TGAATCAATGTTGCCAACAAGTATGCTTAAGAAATGCGGTGAATTAACAAATTA 1497
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QY 1498 ATGAGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
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DB 1591 ACCGTGGCATCTGACACCGATTTGCGCACGGGTATATCCACAGCAAGAAATCA 1650
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DB 1651 GGTATGACACTCTGACCATGATGATGATGATGATGATGATGATGATGATGATGAT 1710
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QY 1618 AATATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
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DB 1711 AATCATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1770
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QY 1678 GAGTGAATGTTGAAGAAACATGATGATGATGATGATGATGATGATGATGATGAT 1737
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DB 1771 GAGAGCTCTATGACGACACAAAGATTTATGTT 1804
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	RESULT	13
	LOCUS	AV121675 2660 bp mRNA linear INV 18-JUN-2002 AV121675
	DEFINITION	Drosophila melanogaster R24825 full insert cDNA.
	ACCESSION	AY121675
	VERSION	AY121675.1 GI:21464397
	KEYWORDS	FLI;CDNA.
	SOURCE	Fruit fly. Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Empidoidea; Drosophilidae; Drosophila. 1 (bases 1 to 2660)
	REFERENCE	Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J., Champe,M., Chavez,C., Dorset,L.V., Dresnek,D., Farfan,D., Flise,E., George,R., Gonzalez,M., Guarin,H., Krommler,B., Li,P., Liao,G., Miranda,A., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Patel,S., Phoumenavong,S., Wan,K., Yu,C., Lewis,S.E., Rubin,G.M., and Celinker,S. Direct Submission Submitted (13-JUN-2002) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA
	COMMENT	Sequence submitted by: Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory
TITLE	JOURNAL	This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to cdaef@fruitfly.berkeley.edu .
FEATURES	Source	location/qualifiers 1..2660 /oranism=Drosophila melanogaster" /strain=y; cn bw sp" /db_xref=taxon:7227"
gene	CDS	1..2660 /gene=alpha-Fst8" /db_xref=FLYBASE:FBN015576" 462..2186 /gene=alpha-Bst8" /note=Longest ORF" /codon_start=1 /product=R24825p" /protein_id=AAMS2002.1" /db_xref=GI:21464398" /db_xref=FLYBASE:FBN015576" translation="MSFDIAVADMDRIALNIVKFTNQORLSNDKVITADVYGKVGKVKMSISANNYSFEQIPPAKPVPGLRFPAPVRPEHSDVRCRTHTARPCOVNIYLKYONGSEDCLLNTYTRELHHRRLPYLVMTYGGGFPMGEASRDLYSPDYIMHEHYLVVISIRGALGFLSLADELDLPGNAGIKDVAMLRWKRKCOPFGDDPNNIVTIGSSAGGSATHTYMLLTDAKGFLFKTIIMSSTALA.PMAQTPLTIMVPRILAQAAGTYGDANDRIDIAHLKKRASVMLEVAEDIIIMEERHORLIWFSEGTIEPLTPHCVI.PKSLEMMDWGNS.IPIVIGNSFEGLIMPVEKNMKELICODGCENLAPOAHDEOORAK.FGKRVLEYLGDRPTGRKTILEYDLGYKKFWHGITHETILSRHAHALAPLETYPREEFSKHFNMRITTCGCRKRYCTHADDES.YLFYNAAKLTKRTAEFKTRILSYNVHFAISGDPNTMVCODEKEPPRAAMLPSISKDVFQCLINHSHVHIIDLP.EARKLKLMDCIYDELly"
BASE COUNT		724 a 632 C 650 G 654 T
ORIGIN		

Query Match	Similarity	Score	DB 3	Length	Best Local	Conservative	Indels	Gaps
Matches	877;	877;	877;	877;	877;	877;	877;	877;
QY	ACCAATGGAACGGTGGTGGTGAACCTGAATATGTCGAAGTGAAGAGCGCTTAACGTTTA	144						
DB	546	AGCATGACAAAGTCATCGCCGACACACGGCTGACGAAAGTGAAGGGGTGAAGTGGCAG	605					
QY	145	ACTGTGTACGATGATTCCTACTACAGTTTGGAGGTATACCGTACGCCAACCGCAGTG	204					
DB	606	TCCATCTACAGCAACACTACTACAGCTTCGAGGGCATCCCGTTCGCCAAGCGCGCGTG	665					
QY	205	GGTGTGCGAGATTTTAAAGCACCCGAGGACCAACACCTGGGATGTTGGCTATGTT	264					
DB	666	GCGGAGCTCCGCTTAAGAGCGCCGTTGAGGCCGACGACTGGTCAAGATGCAAGCGTGC	725					
QY	265	TGCAATTCATTAAGATTAAGTCACTGCAAGTTGATTTTATTAACGGGCAAAAGTGTGGCTCA	324					
DB	726	ACACATGTTTCGGCCGAAGCCCGCCAGGTCACATCTGTTCTGAACAGAGTGAAGGACAC	785					
QY	325	GAGGATTTGCTATACCTTAAGTCTATACGATATATCTAAATCCGGAACCTAAAGTCCC	384					
DB	786	GAGGATCTGCTGTACCTCAATGTCTACACCGAGGAGTTACATCCACACGACTTTTGC	845					
QY	385	GTTTACTATACATACATCATGTGTGTTTATATTCGCGAAATCATCGTATATGAT	444					
DB	846	GTTCTGTTTGGATCTATGCGCGGTGATTCGAATGGGGAAGCATCGGGGATCTGTAC	905					
QY	445	GCTCCTGATTTATTCATTAATAAAGATGCTGTTGATTAACATACATATCTTTGGGA	504					
DB	906	ACCCGCGCATACATTAATGATGGAACATCTCGTACGTCGTATATCTATCGTTAAGA	965					
QY	505	GCTTACGTTTCTTAAGTTTAAATTCAGAAAGCTTAAATGTCGCCGTTATCCGGCCTT	564					
DB	966	GCCCTGGGATTCCTATGCTTGCACAGCAAGAACTGTGCTCTGTGAAGACCGCGACTA	1025					
QY	565	AAAGATCAAGTCATGGCTTGGCTTGATTTAAATTAATTTGGCCAACTTTGGTGGCAAT	624					
DB	1026	AAGGATCAAGTTATGGCTTGGCTTGATTTAAATTAATTTGGCCAACTTTGGTGGCAAT	1085					
QY	625	CCCGATTAATTAATACAGTCTTGTGAAGGTGGCGGCTGCTCAACCCATCAATGATG	684					
DB	1086	CCCGATTAATTAATACAGTCTTGTGAAGGTGGCGGCTGCTCAACCCATCAATGATG	1145					
QY	685	TTAACCGAACAACCTCGCGGCTTTTCCATCGTGATTAATGATGCGGGTAAATGCTATT	744					
DB	1146	CTGACGGATCAAGCCCAAGGGCTTATTTCAACAGACTATTAATTCGCGGATCCGACATG	1205					
QY	745	TGTCATTTGCTTAATTAACCAATGTCA--ACATCGTCTTACCTTAACCAATTTGGCC	801					
DB	1206	GCACCTCGGCGCAACCCCAACCCACATTAATTTGGCCCTATCGCTGGCACAGGCCACT	1265					
QY	802	GGCTTAAAGGGTGAAGGATTAATGATTAAGATGTTTGGATTTCTTAATGAACCAAGCA	861					
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QY	862	CAGGATTTAATAAACCCTTGAGAAAAAGTTTAACTCTGAAGAGCGTACAAATAAGGT-	920					
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QY	921	--CATGTTTCCCTTTGGTGGCCCATCTGTGAGCCATTAACAAGCGGTATGTGCTTAACC	978					
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QY	1039	AACACTTCAATGAGAGGCTATTTTCACTTCAATTTCTTAAGCAAAATGCGCTATGTTT	1098					
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[illegible]

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 AC015272
 AC015272
 AC015272.1 GI:6436063
 VERSION HTG; HTGS_PHASE2.
 KEYWORDS Drosophila melanogaster.
 SOURCE Drosophila melanogaster
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 57335)
 AUTHORS Adams, M. and Venter, J. C.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
 Rockville, MD, USA
 COMMENT This sequence was identified as CDM-10213452 by the submitter.
 For further information on this sequence e-mail to fly@celera.com.
 * NOTE: This is a working draft sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
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 /db_xref="taxon:7227"
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 Best Local Similarity 54.5%; Pred. No. 1.le-72;
 Matches 1052; Conservative 0; Mismatches 614; Indels 263; Gaps 5;
 Qy 46 AATGCAATTAAGTATTAATTTTAACTATGCTTAACTACCAATGAACGGTGTAGCT 105
 Db 36481 AGAACATGAGACATTAAGTCCAGCAGATATGCCAGTGCACCAATGAACATTTGCGC 36422
 Qy 106 GAACTGATATGCGAAGTGAAGAGCGTTAAACCTTTAACTGTATGATGATTTCTTAC 165
 Db 36421 GACACGAGATACGGCAGTGAAGAGGATTCACAGCTTATCTCTAGATGTGCGCTAC 36362
 Qy 166 TACATTTTGAAGGTATACCGTACGCCCAACCGCAGTGTGATGATGATTTAAAGCA 225
 Db 36361 TTCACCTTGAAGGTATCCCGTACGCCCAACCGCTGCGTGGAGAGTGTGATTAAGGC 36302
 Qy 226 CCCGACGACCAACACCGCTGGATGTGTGATTTGTTGAATCAATTAAGTATAGTCA 285
 Db 36301 CCTCAGAGGCCATTTCCCTGGAGGAGATTCGCGACTGAGCCGACCGAAGGATTAAGGC 36242
 Qy 286 GTCAAGTTGATTTTATTAACGGCAAGTGTGCTGCTGAGAGATTTGCTATACCTAAGT 345
 Db 36241 GTCCAGGTGACAGTGTCTGCTGATTAAGTGAAGAGGCTCGAGAGATGCTCTATCTCAT 36182
 Qy 346 GTCTATACGAATAT----- 360
 Db 36181 GTGTACACCAACAAATGTAGTATTTCTATTAATTTGATGATTAACATCGTTAAACCC 36122


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OY 563 TTAAGATCAAGTATGCGCTTGCCTTGGATTTAAATAATATGCGCACTTTGGTGCA 622
Db 35821 TCAAGATCAAGTATGCGCTTGCCTTGGATTTAAATAATATGCGCACTTTGGTGCA 35762
OY 623 ATCCGATTAATTTACAGTCTTTGTGTAAGTGGCGGTGCTGCTTACCCACTATATGA 682
Db 35761 ATCCGATTAATTTACAGTCTTTGTGTAAGTGGCGGTGCTGCTTACCCACTATATGA 35702
OY 683 TGTAAACCGAACAATCGCGCTTTTCCATGCTGTGTATTAATGCTGCGTAATGCTA 742
Db 35701 TGTAAACCGAACAATCGCGCTTTTCCATGCTGTGTATTAATGCTGCGTAATGCTA 35642
OY 743 TTTGTCTCATTTGGC---TAATACCCAATGTCAACATCGTCCCTTACCTTGAACCAATG 799
Db 35641 TTTGTCTCATTTGGC---TAATACCCAATGTCAACATCGTCCCTTACCTTGAACCAATG 35582
OY 800 CCGGCTAATAGGTAAGATATGATTAAGGATTTTGAATTTCTTATGAACCAAGC 859
Db 35581 TTTGTCTCATTTGGC---TAATACCCAATGTCAACATCGTCCCTTACCTTGAACCAATG 35522
OY 860 CACAGGATTTAATAAACTTGAGAAAGATTTAATCTGAGAGGCTACAATAAGG 919
Db 35521 CACAGGATTTAATAAACTTGAGAAAGATTTAATCTGAGAGGCTACAATAAGG 35462
OY 920 TCATGTTCTTTTGTGCTCCACTGTGAGCAATATCAGACGCTGATTTGCTTACCA 979
Db 35461 TCATGTTCTTTTGTGCTCCACTGTGAGCAATATCAGACGCTGATTTGCTTACCA 35402
OY 980 AACATCCTCGGAATGTTAAAGTCTTGGGTAATTCGATACCCACTATGATGGTA 1039
Db 35401 AACATCCTCGGAATGTTAAAGTCTTGGGTAATTCGATACCCACTATGATGGTA 35342
OY 1040 ACACCTTCATGAGGCTCT----- 1058
Db 35341 ACACCTTCATGAGGCTCT----- 35282
OY 1059 -----ATTTTCACTTCAATTTCTTAAGCAATGCGTATGCTTGT 1097
Db 35281 TTTCTTCAATTAAGTAATTTAATTTTATTTTACAGAGGTAAAGCTTATGCGCAGGTGCT 35222
OY 1098 TAAGGAATTTGAACTTTGTGCAATTTTGTGCAAGTAAAGTATGCTGTAAGCGCAC 1157
Db 35221 GCAGAGCTTATGATGCTGCAACCTTTCATTTCCAAAGAAATTTGCTGCGCAGAGCGCAC 35162
OY 1158 CGCGCCAGAGACTTGGAAATGTTGCTAAATAATTAAGGCTCATGTTACAGAGAAAC 1217
Db 35161 TAAGGAATTTGAACTTTGTGCAATTTTGTGCAAGTAAAGTATGCTGTAAGCGCAC 35102
OY 1218 ACCAAGCTGATAATTTTATGAT----- 1242
Db 35101 AACGACCCAGATTAATTTACATGATGTAAGTGTGCTCAATTTAGGCTTACATATCAT 35042
OY 1243 -----CTTTGCTCTCACATCTAATTTCTGTTCCCATGATCGTT 1282

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Db 35041 AAGCTGTATTTATTTTACAGCTCTGTGATTTTACTACTGTCTTCCGCGCTGAGG 34982
OY 1283 TGTTCATTTACGTTTCAATACACCTCGGATACACCGCTCTACTGTGATGCGTTCGACT 1342
Db 34981 TGTTCATTTACGTTTCAATACACCTCGGATACACCGCTCTACTGTGATGCGTTCGACT 34922
OY 1343 TCGATTTGGAAGATCTTATCAATCCCTTATCGTATATGAGTGAAGTGAAGG 1402
Db 34921 TCGATTTGGAAGATCTTATCAATCCCTTATCGTATATGAGTGAAGTGAAGG 34862
OY 1403 GTGTAGTCAATGCTGATGTAATTAACCTATTCTTGTGAATCAATTTGCGCAAGGTATG 1462
Db 34861 GTGTAGTCAATGCTGATGTAATTAACCTATTCTTGTGAATCAATTTGCGCAAGGTATG 34802
OY 1463 CTAAAGATCGCTGATTAACAAATGAAGCTGTGACTGTATATGATACAAATTTG 1522
Db 34801 CTAAAGATCGCTGATTAACAAATGAAGCTGTGACTGTATATGATACAAATTTG 34742
OY 1523 CCACCACTGTAAATCTTATAGCAATGAATTAAGTATGAAATCTTTCTGCGATC 1582
Db 34741 CTGACAGGATTAATCCCTTACAGGAGATCAACGTAATGACACTGTGACCAATTTGATC 34682
OY 1583 CAATTAAGAAATCCGATGAAGTATACAGAGTGTGATATATGATGATGAATGA 1642
Db 34681 CAATTAAGAAATCCGATGAAGTATACAGAGTGTGATATATGATGATGAATGA 34622
OY 1643 TTGATGTCCCTGAATAGATTAAGATTAACAAATGAGTGTGATGTTGAAAAATGATAG 1702
Db 34621 TTGATGTCCCTGAATAGATTAAGATTAACAAATGAGTGTGATGTTGAAAAATGATAG 34562
OY 1703 ATTTATTTT 1711
Db 34561 ATTTATTTT 34553

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Search completed: April 11, 2003, 06:06:59
 Job time : 3016.03 secs

PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG,
 Barker AC, Robin CC, Russell DT, Smith V.

XX
DR WPI: 1995-263870/34.
DR P-PSDB: AAR78142.
PT Pure E3 esterase from *Lucilia cuprina* and related DNA - used to
PT eliminate residues of organo:phosphate and carbamate pesticides from
PT water, meat etc.
XX
PS Claim 5: Page 12-17: 38pp; English.
XX cDNA from organophosphate (OP)-sensitive *L. cuprina* pupa cDNA
XX library was amplified using cluster-specific esterase primers.
CC Isolated clone Lc743, a probable full-length cDNA, was expressed
CC using a baculovirus vector in insect cells and shown to encode
CC an OP-susceptible E3 esterase, useful in bioremediation.
XX
SQ Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other:
Query Match 99.4%; Score 1703.4; DB 16; Length 1713;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGAATTTCAACCTTACTTTGATGAGAAATTAATGCAAGATTAAATGCAATTTGAAAT 60
DB 1 ATGAATTTCAACCTTACTTTGATGAGAAATTAATGCAAGATTAAATGCAATTTGAAAT 60
QY 61 AAGTTTTAACTATCGTTTAACTAATGAAACGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 AAGTTTTAACTATCGTTTAACTAATGAAACGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 AAGTGAAGCGTTAAACGTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 AAGTGAAGCGTTAAACGTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 ATACCGTACCGCCACCGCCAGTGGTGAAGATTAAAGCCAGCCAGCCAGCCAGCCAGCC 240
DB 181 ATACCGTACCGCCACCGCCAGTGGTGAAGATTAAAGCCAGCCAGCCAGCCAGCCAGCC 240
QY 241 CCTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 CCTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 ATAAAGGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 ATAAAGGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 CTAAATCCGAAACTAAGCTCCCTTTTAACTAATGCAATGCTGCTGCTGCTGCTGCTGCT 420
DB 361 CTAAATCCGAAACTAAGCTCCCTTTTAACTAATGCAATGCTGCTGCTGCTGCTGCTGCT 420
QY 421 GGTGAANAATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 GGTGAANAATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 ATTAACATACAAATATCGTTTGGAGCTCTAGCTTCTAAGTTTAAATTCAGAAAGCCTT 540
DB 481 ATTAACATACAAATATCGTTTGGAGCTCTAGCTTCTAAGTTTAAATTCAGAAAGCCTT 540
QY 541 AATGCGCCGCTATGCGCGCTTAAAGATCAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 AATGCGCCGCTATGCGCGCTTAAAGATCAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 AATGCGCCGCTATGCGCGCTTAAAGATCAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 AATGCGCCGCTATGCGCGCTTAAAGATCAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GCTGCTTACCCACTACATGATGTTAAACGAAACAACTCCGCTTTTCCATCGTGTG 720
DB 661 GCTGCTTACCCACTACATGATGTTAAACGAAACAACTCCGCTTTTCCATCGTGTG 720
QY 721 ATACTAATGCGGCTAATGCTATTTGCTCAATGGCTAATACCAATGCTCAATGCTGCT 780
DB 721 ATACTAATGCGGCTAATGCTATTTGCTCAATGGCTAATACCAATGCTCAATGCTGCT 780

QY 781 TTCACCTTAGCCAAATTTGCGCGCTATAGCGTGAAGATTAATGATGATGTTTGGAA 840
DB 781 TTCACCTTAGCCAAATTTGCGCGCTATAGCGTGAAGATTAATGATGATGTTTGGAA 840
QY 841 TTTCTTATGAAGCCAGCCAGCAGATTTAATAAATCTTGAGAAATTTAACTCTTA 900
DB 841 TTTCTTATGAAGCCAGCCAGCAGATTTAATAAATCTTGAGAAATTTAACTCTTA 900
QY 901 GAAGAGCGTACCAATTAAGTCAATGCTTCTTGGTCCACTGTTGAGCCATATCAGACC 960
DB 901 GAAGAGCGTACCAATTAAGTCAATGCTTCTTGGTCCACTGTTGAGCCATATCAGACC 960
QY 961 GCTGATGCTTACCCCAATCCTGCGGAAATGTTAAATGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 GCTGATGCTTACCCCAATCCTGCGGAAATGTTAAATGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 ATACCCATATGATGCTGCTTAAAGATTTGAATGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 ATACCCATATGATGCTGCTTAAAGATTTGAATGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 CAATGCTTATGCTTGTAAAGATTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 CAATGCTTATGCTTGTAAAGATTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTTGCTTCAATCTAT 1260
DB 1201 CATGTTACAGAGAAACACCAACAGCTGATTAATTTATGATCTTTGCTTCAATCTAT 1260
QY 1261 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 AATCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 AATCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 ACTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
DB 1501 ACTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 ATGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 ATTAATGATTAATTTGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 ATTAATGATTAATTTGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 TCGATGCTTGAATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
DB 1681 TCGATGCTTGAATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
RESULT 2
AAT68596
ID AAT68596 standard; DNA: 1713 BP.
XX
AC AAT68596;
XX
DT 08-AUG-1997 (first entry)

XX LC-alpha-E7 malathion susceptible esterase clone Lc743.
 XX Melathion carboxylesterase; organophosphate; insecticide;
 KM pesticide; remediation; bioremediation; decontamination; esterase;
 KM ss.
 XX Lucilia cuprina.
 XX
 PH Key Location/Qualifiers
 FT primer_bind complement (1..26)
 FT /tag- a
 FT /note- "Lc743 5' primer"
 FT primer_bind 1686..1713
 FT /tag- b
 FT /note- "Lc743 3' primer"
 FT mutation 752
 FT /tag- c
 FT /note- "base 752 is T in resistant clones
 (Trp to Leu mutation)"
 FT mutation 1344
 FT /tag- d
 FT /note- "base 1344 is C in resistant clones
 (silent mutation)"
 FT mutation 1362
 FT /tag- e
 FT /note- "base 1362 is C in resistant clones
 (silent mutation)"
 FT mutation 1599
 FT /tag- f
 FT /note- "base 1599 is T in resistant clones
 (silent mutation)"
 FT mutation 1629
 FT /tag- g
 FT /note- "base 1629 is T in resistant clones
 (silent mutation)"
 MO9719176-A1.
 XX 29-MAY-1997.
 XX 22-NOV-1996; 96MO-AU00746.
 XX 23-NOV-1995; 95AU-0006751.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PI Boyce T, Brownlie JC, Campbell PM, Claudianos C;
 PI Newcomb RD, Oakeshott JG, Roblin GC, Russell RJ, Smyth K;
 DR WPI: 1997-298113/27.
 DR P-PSDB; AAM17765.
 PT DNA encoding enzyme that degrades organophosphate pesticides -
 PT useful for decontamination of soil, water, food etc
 XX
 PS Claim 4; Fig 1; 52pp; English.
 XX DNA molecule Lc743 (AAT68596) codes for an esterase (AAM17765) from
 CC a malathion susceptible strain of Lucilia cuprina. Comparison
 CC with a consensus sequence from derived from clones of the
 CC Lc-alpha-E7 resistant allele (see also AAM17768) indicated only one
 CC replacement site difference, a Trp to Leu substitution at amino
 CC acid position 251 (nucleotide position 752). This mutation is an
 CC excellent candidate for the malathion resistance mutation. The
 CC resistant enzyme acts as a malathion carboxylesterase and can be
 CC formulated for use in degrading environmental carboxylester or
 CC dimethyl general organophosphates.
 SQ Sequence 1713 BP; 516 A; 305 C; 370 G; 522 T; 0 other;
 Query Match 99.4%; Score 1703.4; DB 18; Length 1713;
 Best Local Similarity 99.6%; Pred. No. 0;

Matches 1707; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ATGAATTCACGCTTACGTTGATGAGAAATTTAAATGAGATTAAATGCAATTAAT 60
 DB 1 ATGAATTCACGCTTACGTTGATGAGAAATTTAAATGAGATTAAATGCAATTAAT 60
 QY 61 AAGTTTAACTATCGTTTAACTACCAATGAACGGGTGAGTGAACGTAATATGAC 120
 DB 61 AAGTTTAACTATCGTTTAACTACCAATGAACGGGTGAGTGAACGTAATATGAC 120
 QY 121 AAGTGAAGGCGTTAAACGTTTAACTGTCAGATGATTCCTACTACAGTTTGAGGGT 180
 DB 121 AAGTGAAGGCGTTAAACGTTTAACTGTCAGATGATTCCTACTACAGTTTGAGGGT 180
 QY 181 ATACCGTACCGCCCAACCGCCGAGGTGAGTGAATTTAAAGCAACCCAGCAGCA 240
 DB 181 ATACCGTACCGCCCAACCGCCGAGGTGAGTGAATTTAAAGCAACCCAGCAGCA 240
 QY 241 CCTGGGATGCTGTCGATTTGTCATATGAAGATTAAGTCAGTCAAGTTGATTTT 300
 DB 241 CCTGGGATGCTGTCGATTTGTCATATGAAGATTAAGTCAGTCAAGTTGATTTT 300
 QY 301 ATACGGGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTGTCTATACGAATAT 360
 DB 301 ATACGGGCAAGTGTGTGCTCAGAGATTTCTATACCTAAGTGTCTATACGAATAT 360
 QY 361 CTAAATCCGCAACTAAACGTCCTGTTTACTATACATACATGATGATGTTTATATC 420
 DB 361 CTAAATCCGCAACTAAACGTCCTGTTTACTATACATACATGATGATGTTTATATC 420
 QY 421 GGTGAATATCATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 DB 421 GGTGAATATCATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 QY 481 ATTAACATACATATATGCTTTGGAGCTCTAGTTTCTAAGTTTAAATTCAGAACCTT 540
 DB 481 ATTAACATACATATATGCTTTGGAGCTCTAGTTTCTAAGTTTAAATTCAGAACCTT 540
 QY 541 AATGTCGCCGCTAATGCCGCTTAAAGATCAAGTCATGCGCTTGATTTAAAT 600
 DB 541 AATGTCGCCGCTAATGCCGCTTAAAGATCAAGTCATGCGCTTGATTTAAAT 600
 QY 601 AATGCGCCCACTTTGGTGGCAATCCGATATATATATATATATATATATATATAT 660
 DB 601 AATGCGCCCACTTTGGTGGCAATCCGATATATATATATATATATATATATATAT 660
 QY 661 GCTGCTCTACCCACTACATGATGTTAACCGAACCAACTCGCGCTTTCCATCGTGT 720
 DB 661 GCTGCTCTACCCACTACATGATGTTAACCGAACCAACTCGCGCTTTCCATCGTGT 720
 QY 721 ATACTAATGTCGGGTAATGCTATTTGTCATTTGGCTATACCAATGTCACATGCTGC 780
 DB 721 ATACTAATGTCGGGTAATGCTATTTGTCATTTGGCTATACCAATGTCACATGCTGC 780
 QY 781 TTCACTTAGCCAAATTTGGCGGCTATAGGTTAGGATTAATGATTAAGATGTTTGA 840
 DB 781 TTCACTTAGCCAAATTTGGCGGCTATAGGTTAGGATTAATGATTAAGATGTTTGA 840
 QY 841 TTCTTATGAAGCCACAGAGATTTAAATTAATTAATTAATTAATTAATTAATTA 900
 DB 841 TTCTTATGAAGCCACAGAGATTTAAATTAATTAATTAATTAATTAATTAATTA 900
 QY 901 GAAGAGCTACAAATTAAGTATGTTTCTTTTGTCCCACTGTTGACCATATAGAC 960
 DB 901 GAAGAGCTACAAATTAAGTATGTTTCTTTTGTCCCACTGTTGACCATATAGAC 960
 QY 961 GGTGATTTGCTTACCAACATCTCGGGAATGTTTAAACGCTTGGGTAATTCG 1020
 DB 961 GGTGATTTGCTTACCAACATCTCGGGAATGTTTAAACGCTTGGGTAATTCG 1020
 QY 1021 ATACCACTATGATGAGTGAACATCTCATATGAGGCTATATTTTCACTCAATTTTAAG 1080
 DB 1021 ATACCACTATGATGAGTGAACATCTCATATGAGGCTATATTTTCACTCAATTTTAAG 1080


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OY 1081 CAATGCGCTATGCTTTAGGAATTTGGAACCTGTGTCAATTTTGTGCCAAGTGAATG 1140
    |||||||
DB 1081 CAATGCGCTATGCTTTAGGAATTTGGAACCTGTGTCAATTTTGTGCCAAGTGAATG 1140
OY 1141 GCTGATGCTGAACGACCGCCCGCAGACGCTTTGGAATGSGTGTAAATTTAAAAAGGCT 1200
    |||||||
DB 1141 GCTGATGCTGAACGACCGCCCGCAGACGCTTTGGAATGSGTGTAAATTTAAAAAGGCT 1200
OY 1201 CATGTTACGAGGAACACCAACAGCTGATTAATTTTATGATCTTTGCTGCACATCTAT 1260
    |||||||
DB 1201 CATGTTACGAGGAACACCAACAGCTGATTAATTTTATGATCTTTGCTGCACATCTAT 1260
OY 1261 TTCTGTTGTTCCCATGACGCTTTGTTGCAATTAAGTTCAATCACACCGCGGTACACC 1320
    |||||||
DB 1261 TTCTGTTGTTCCCATGACGCTTTGTTGCAATTAAGTTCAATCACACCGCGGTACACC 1320
OY 1321 GTCTACTGTATGCTGCTTCGACTTCGATTCGAGAGATCTTATCAATCCCTATGCTATATG 1380
    |||||||
DB 1321 GTCTACTGTATGCTGCTTCGACTTCGATTCGAGAGATCTTATCAATCCCTATGCTATATG 1380
OY 1381 CGTAGTGAGCGTGTGTTAAGGCTGTTAGTCATGCTGATGAATTAACCTATTCTCTGG 1440
    |||||||
DB 1381 CGTAGTGAGCGTGTGTTAAGGCTGTTAGTCATGCTGATGAATTAACCTATTCTCTGG 1440
OY 1441 AATCAATTGGCCAAACGATTCCTTAAGAAATCGCGTGAATACAAACAAATTTGAAGCTATG 1500
    |||||||
DB 1441 AATCAATTGGCCAAACGATTCCTTAAGAAATCGCGTGAATACAAACAAATTTGAAGCTATG 1500
OY 1501 ACTGCTATATGATGATCAATTTTGGCCACGACGCTGATTAATCTTATGCAATTTGAAGCT 1560
    |||||||
DB 1501 ACTGCTATATGATGATCAATTTTGGCCACGACGCTGATTAATCTTATGCAATTTGAAGCT 1560
OY 1561 ATGGAATGTTTCTGCGATCAATTTAAGAAATCCGATGAATTAAGCTATGCTTTGAAT 1620
    |||||||
DB 1561 ATGGAATGTTTCTGCGATCAATTTAAGAAATCCGATGAATTAAGCTATGCTTTGAAT 1620
OY 1621 ATTAGTATGATTAATTAATGATGATGCTGCTGAATTAAGCTATTAACATTTGAAGCT 1680
    |||||||
DB 1621 ATTAGTATGATTAATTAATGATGATGCTGCTGAATTAAGCTATTAACATTTGAAGCT 1680
OY 1681 TCGATGTTTGAATTAATGATGATGCTGCTGAATTAAGCTATTAATTTAG 1713
    |||||||
DB 1681 TCGATGTTTGAATTAATGATGATGCTGCTGAATTAAGCTATTAATTTAG 1713

RESULT 3
ID AA091566 standard: cDNA: 1713 BP.
XX
AC AA091566:
XX
DT 22-DEC-1995 (first entry)
XX
DE Op-resistant esterase Lc7L103con.
XX
KW Esterase; E3: bioremediation; organophosphate; carbamate;
    insecticide; pesticide; water decontamination; meat decontamination;
    ss.
XX
OS Lucilia cuprina.
XX
XX Key location/Qualifiers
    FT 1..1713
    FT CDS /*tag= a
XX
PN WO9519440-A1.
XX
PD 20-JUL-1995.
XX
PF 13-JAN-1995; 95WO-AU00016.
XX
PR 13-JAN-1994; 94AU-0003347.

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XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX Parker AG, Robin GC, Russell RJ, Smyth K;
PI WPI: 1995-263870/34.
XX
DR Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX eliminate residues of organo-phosphate and carbamate pesticides from
XX water, meat etc.
XX
PS Example 4; Page 12-17; 38pp; English.
XX
XX RT-PCR was used to clone a cDNA allele of Lc-alpha-E3 (encoding
XX OP-susceptible esterase E3 of L. cuprina) from a diazinon
XX resistant strain, Dlandillo 103. 4 isolated clones were
XX sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
XX esterases; a consensus sequence is given in AA091566.
XX
SO Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0.other:

Query Match 98.2%; Score 1682.6; DB 16; Length 1713;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 ATGAATTTCAACGTTAGTTGATGAGAGAAATTAATGAAGATTAATGCAATTTGAAT 60
    |||||||
DB 1 ATGAATTTCAACGTTAGTTGATGAGAGAAATTAATGAAGATTAATGCAATTTGAAT 60
OY 61 AAGTTTAACTATGCTTTACTACCAATGAACGCTGTAGCTGAACCTGAATATGGC 120
    |||||||
DB 61 AAGTTTAACTATGCTTTACTACCAATGAACGCTGTAGCTGAACCTGAATATGGC 120
OY 121 AAAGTGAAGGCGTTAAACGTTTAACTGTACGATGATTCCTACATTTTGAAGGT 180
    |||||||
DB 121 AAAGTGAAGGCGTTAAACGTTTAACTGTACGATGATTCCTACATTTTGAAGGT 180
OY 181 ATACCGTACGCCCAACCGCCAGTGGTGAAGCTTAAAGCAACCCACGCCACACA 240
    |||||||
DB 181 ATACCGTACGCCCAACCGCCAGTGGTGAAGCTTAAAGCAACCCACGCCACACA 240
OY 241 CCCTGGGATGATGTCGCTGATTTGTCATATCAATTAAGTACAGTCAAGTATTTT 300
    |||||||
DB 241 CCCTGGGATGATGTCGCTGATTTGTCATATCAATTAAGTACAGTCAAGTATTTT 300
OY 301 ATACCGGCAAGTGTGTCAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
    |||||||
DB 301 ATACCGGCAAGTGTGTCAGAGATGCTATACCTAAGTGTCTATACGAATAT 360
OY 361 CTAAATCCCGAACTAAAGCTCCGTTTATGATATCATGATGAGTGTATATTC 420
    |||||||
DB 361 CTAAATCCCGAACTAAAGCTCCGTTTATGATATCATGATGAGTGTATATTC 420
OY 421 GGTGAAATATCATGCTATGATGATGCTGATTTATTAATAAGAGATGCTGTG 480
    |||||||
DB 421 GGTGAAATATCATGCTATGATGATGCTGATTTATTAATAAGAGATGCTGTG 480
OY 481 ATTAACATACAAATATGCTTTGGAGCTTAGCTTTCTAAGTTTAATTCAGAACCT 540
    |||||||
DB 481 ATTAACATACAAATATGCTTTGGAGCTTAGCTTTCTAAGTTTAATTCAGAACCT 540
OY 541 AATGTCGCGGTATATGCGGCTTAAGATCAAGTCAAGTCCCTGCTGATTAAT 600
    |||||||
DB 541 AATGTCGCGGTATATGCGGCTTAAGATCAAGTCAAGTCCCTGCTGATTAAT 600
OY 601 AATTGCGCAACTTTGATGCAATCCGATTAATATTTACATCTTTGATGAAGTCCGCT 660
    |||||||
DB 601 AATTGCGCAACTTTGATGCAATCCGATTAATATTTACATCTTTGATGAAGTCCGCT 660
OY 661 GCTGCTTACCCACTATGATGTTAAGCGAACAACTCCGGTCTTTTCATCGGTG 720
    |||||||
DB 661 GCTGCTTACCCACTATGATGTTAAGCGAACAACTCCGGTCTTTTCATCGGTG 720

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QY 721 ATACAAATGTCGGGAATGCTATTGTCATTGGCTAATACCAATGTCACATCGTGC 780
    |||||||
Db 721 ATACTAATGTCGGGAATGCTATTGTCATTGGCTAATACCAATGTCACATCGTGC 780
QY 781 TTCACCTTAGCCAAATTTGGCCGGCTATTAAGGCTAGAGTAATGATTAAGATGTTTGGAA 840
    |||||||
Db 781 TTCACCTTAGCCAAATTTGGCTATTAAGGCTAGAGTAATGATTAAGATGTTTGGAG 840
QY 841 TTTCTTATGAAAAGCCAGCCACAGATTTAATAAACTTGAGGAAAAAGTTTAACCTTA 900
    |||||||
Db 841 TTTCTTATGAAAAGCCAGCCACAGATTTAATAAACTTGAGGAAAAAGTTTAACCTTA 900
QY 901 GAAGAGCGTACAAATTAAGGCTATGTTCCCTTTGGTCCACTGTTGACCATATCAGACC 960
    |||||||
Db 901 GAAGAGCGTACAAATTAAGGCTATGTTCCCTTTGGTCCACTGTTGACCATATCAGACC 960
QY 961 GCTGATGTCCTTACCACCAATCCTCGGAAATGTTAAACCTGCTGGGTAATTG 1020
    |||||||
Db 961 GCTGATGTCCTTACCACCAATCCTCGGAAATGTTAAACCTGCTGGGTAATTG 1020
QY 1021 ATACCCACTATGATGGGTACACACTTCATATAGGGCTATTTTTCACCTTCAATTCCTTAAG 1080
    |||||||
Db 1021 ATACCCACTATGATGGGTACACACTTCATATAGGGCTATTTTTCACCTTCAATTCCTTAAG 1080
QY 1081 CAAATGCCCTATGCTTGTAAAGGAATGGAACCTGTGCATTTTGTGCGCAAGTGAATTG 1140
    |||||||
Db 1081 CAAATGCCCTATGCTTGTAAAGGAATGGAACCTGTGTCAATTTGTGCCAAGTGAATTG 1140
QY 1141 GCTGATGCTGAACGACCGCCCGCAGAGACCTTGGAAATGGTGTCTAAATTAATAAGGCT 1200
    |||||||
Db 1141 GCTGATGCTGAACGACCGCCCGCAGAGACCTTGGAAATGGTGTCTAAATTAATAAGGCT 1200
QY 1201 CATGTTACAGAGAAACCAACAGCTATATTTTATGATCTTTTGTCTTCACATCTAT 1260
    |||||||
Db 1201 CATGTTACAGAGAAACCAACAGCTATATTTTATGATCTTTTGTCTTCACATCTAT 1260
QY 1261 TTTCTGTTCCCATGATCGTTTGTGCAATTAGCTTTCATTCACACCTCGGTAACCC 1320
    |||||||
Db 1261 TTTCTGTTCCCATGATCGTTTGTGCAATTAGCTTTCATTCACACCTCGGTAACCC 1320
QY 1321 GTCTACTGTATCGCTTGCCTGACTTCGATTCGGAAGATCTTATCAATCCCTATCGATTATG 1380
    |||||||
Db 1321 GTCTACTGTATCGCTTGCCTGACTTCGATTCGGAAGATCTTATCAATCCCTATCGATTATG 1380
QY 1381 CGTAGTGCAGCTGCTGTTAAGGCTTGTAGTGTGATGATGATTAACCTATTTCTTCTGG 1440
    |||||||
Db 1381 CGTAGTGCAGCTGCTGTTAAGGCTTGTAGTGTGATGATGATTAACCTATTTCTTCTGG 1440
QY 1441 AATCAATTTGGCCAAACGATATGCTTAAAGATCGCTGAATCAAAACCAATTTGAACGTATG 1500
    |||||||
Db 1441 AATCAATTTGGCCAAACGATATGCTTAAAGATCGCTGAATCAAAACCAATTTGAACGTATG 1500
QY 1501 ACTGCTATATGGAATCAAAATTTGCCACACTGTAATCCTTATAGCAATGAATTTGAAGGT 1560
    |||||||
Db 1501 ACTGCTATATGGAATCAAAATTTGCCACACTGTAATCCTTATAGCAATGAATTTGAAGGT 1560
QY 1561 ATGGAATATGTTTCTCTGGGATCCAAATTAAGAAATCCGATGAAGTATACAAGTGTGTAAT 1620
    |||||||
Db 1561 ATGGAATATGTTTCTCTGGGATCCAAATTAAGAAATCCGATGAAGTATACAAGTGTGTAAT 1620
QY 1621 ATTAGTATGATTAAGAAATGATTTGATGCTGGAATGATTAAGATTAACAATGGAG 1680
    |||||||
Db 1621 ATTAGTATGATTAAGAAATGATTTGATGCTGGAATGATTAAGATTAACAATGGAG 1680
QY 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713
    |||||||
Db 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713

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RESULT 4
AA091564
ID AA091564 standard; cdna; 1713 bp.

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XX AC AA091564;
XX XX 22-DEC-1995 (first entry)
XX XX
XX XX OP-resistant esterase Lc7L103C allele.
DE XX Esterase; E3; bioremediation; organophosphate; carbamate;
XX XX insecticide; pesticide; water decontamination; meat decontamination;
XX XX ss.
XX XX Lucilia cuprina.
XX XX
XX XX Key Location/Qualifiers
XX FT CDS 1..1713
XX FT /*tag= a
XX XX
XX XX M09519440-A1.
XX XX
XX XX 20-JUL-1995.
XX XX
XX XX 13-JAN-1995; 95WO-AU00016.
XX XX
XX XX 13-JAN-1994; 94AU-0003347.
XX XX
XX XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX XX Parker AG, Robin GC, Russell RJ, Smyth K;
XX XX
XX XX WPI: 1995-263870/34.
XX XX
XX XX Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX XX eliminate residues of organo:phosphate and carbamate pesticides from
XX XX water, meat etc.
XX XX
XX XX Example 4; Page 12-17; 38pp; English.
XX XX
XX XX RT-PCR was used to clone a cdna allele of Lc-alpha-E7 (encoding
XX XX OP-susceptible esterase E3 of L. cuprina) from a diazinon
XX XX resistant strain, Llandillo 103. 4 Isolated clones were
XX XX sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
XX XX esterases. The esterases, or cells expressing them, are used
XX XX in bioremediation.
XX XX
XX XX Sequence 1713 bp; 512 A; 308 C; 368 G; 525 T; 0 other;
XX XX
XX XX Query Match 98.0%; Score 1679.4; DB 16; Length 1713;
XX XX Best Local Similarity 98.8%; Pred. No. 0;
XX XX Matches 1692; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
XX XX
QY 1 ATGAATTTCAACGTTAGTTTGTGAGAGAAATTAATGAGATTAATGCAATTAAT 60
    |||||||
Db 1 ATGAATTTCAACGTTAGTTTGTGAGAGAAATTAATGAGATTAATGCAATTAAT 60
QY 61 AAGTTTAACTATCGTTTAACTACCAATGAAGCGGTGTGCTGAACGTAATATGCG 120
    |||||||
Db 61 AAGTTTAACTATCGTTTAACTACCAATGAAGCGGTGTGCTGAACGTAATATGCG 120
QY 121 AAAGTGAAGGCGTTAAAGCTTTAACTGTGACATGATTTCTTACTACAGTTTGAAGGT 180
    |||||||
Db 121 AAAGTGAAGGCGTTAAAGCTTTAACTGTGACATGATTTCTTACTACAGTTTGAAGGT 180
QY 181 AAAGTGAAGGCGTTAAAGCTTTAACTGTGACATGATTTCTTACTACAGTTTGAAGGT 240
    |||||||
Db 181 AAAGTGAAGGCGTTAAAGCTTTAACTGTGACATGATTTCTTACTACAGTTTGAAGGT 240
QY 241 CCCTGGATGCTGCTGATTTGTGCAATCTTAAGATTAAGTCAAGTCAAGTTGATTTT 300
    |||||||
Db 241 CCCTGGATGCTGCTGATTTGTGCAATCTTAAGATTAAGTCAAGTCAAGTTGATTTT 300
QY 301 ATACGGGCAAAAGTGTGCTCAGAGATTTGCTATACCTTAAGTGTCTATACGAATAT 360
    |||||||

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Db 301 ATTACAGCAAGTGTGTGGCTCAGAGATTTGCTATACCTAAGCGTCTATACGATAT 360
Qy 361 CTAAATCCGGAAGTAACGTCCTCTTTAGTATACATACATGCGTGCTTTATATATC 420
Db 361 CTAAATCCGGAAGTAACGTCCTCTTTAGTATACATACATGCGTGCTTTATATATC 420
Qy 421 GGTGAAATCATCGTATGTATGTATGCTGATTTATTTATTTAAAGATGTGCTTG 480
Db 421 GGTGAAATCATCGTATGTATGTATGCTGATTTATTTATTTAAAGATGTGCTTG 480
Qy 481 ATTACATACATATGCTTTGGAGCTCTAGGTTTCTAAGTTTAATTCAGAGACCTT 540
Db 481 ATTACATACATATGCTTTGGAGCTCTAGGTTTCTAAGTTTAATTCAGAGACCTT 540
Qy 541 AATGTCGCCGTAATCCGCGCTTAAAGATCAAGTATGCGCTTGGTGATTAATAAT 600
Db 541 AATGTCGCCGTAATCCGCGCTTAAAGATCAAGTATGCGCTTGGTGATTAATAAT 600
Qy 601 AATGTCGCCGTAATCCGCGCTTAAAGATCAAGTATGCGCTTGGTGATTAATAAT 660
Db 601 AATGTCGCCGTAATCCGCGCTTAAAGATCAAGTATGCGCTTGGTGATTAATAAT 660
Qy 661 GCTGCTTACCCATCATATGATGTTACCGAACAACCTCGCGCTTTTCATGCTGT 720
Db 661 GCTGCTTACCCATCATATGATGTTACCGAACAACCTCGCGCTTTTCATGCTGT 720
Qy 721 ATACTAATGTCGGGTATGCTATTTGCTCATGCTGCTAATACCAATGCTGCTGCC 780
Db 721 ATACTAATGTCGGGTATGCTATTTGCTCATGCTGCTAATACCAATGCTGCTGCC 780
Qy 781 TTGACCTTACCAAAATTTGCGCGCTTAAAGGTGAGATTAATGATGTTTGGAA 840
Db 781 TTGACCTTACCAAAATTTGCGCGCTTAAAGGTGAGATTAATGATGTTTGGAA 840
Qy 841 TTTCTTATGAAGCCAGCCACAGATTTAATAAAGTTAGAGAAAAGTTTAACTCTA 900
Db 841 TTTCTTATGAAGCCAGCCACAGATTTAATAAAGTTAGAGAAAAGTTTAACTCTA 900
Qy 901 GAAGAGCGTCAATATAGTATGTTCTTTGCTCCACTGCTGAGCCATATACAGACC 960
Db 901 GAAGAGCGTCAATATAGTATGTTCTTTGCTCCACTGCTGAGCCATATACAGACC 960
Qy 961 GCTGATTTGTCTTTACCAAAACATCTCGGGAATGTTTAAACTGCTTGGGTAATTG 1020
Db 961 GCTGATTTGTCTTTACCAAAACATCTCGGGAATGTTTAAACTGCTTGGGTAATTG 1020
Qy 1021 ATACCCACTATGATGGGTACACTTCAATGAGGGTCTAATTTTTCACCTGCTTCTTAAG 1080
Db 1021 ATACCCACTATGATGGGTACACTTCAATGAGGGTCTAATTTTTCACCTGCTTCTTAAG 1080
Qy 1081 CAATATGCTATGCTTTTGAAGATTTGGAACCTTGTCAATTTTGTGCCAAGTGAATTG 1140
Db 1081 CAATATGCTATGCTTTTGAAGATTTGGAACCTTGTCAATTTTGTGCCAAGTGAATTG 1140
Qy 1141 GCTGATGCTGAAGCCACCGCCAGAGACCTTGAATGGGTGCTAATAATTAAGAGCT 1200
Db 1141 GCTGATGCTGAAGCCACCGCCAGAGACCTTGAATGGGTGCTAATAATTAAGAGCT 1200
Qy 1201 CATGTTACAGAGAAACCAACCAAGCTGATTAATTTATGATCTTCTGCTCACATCTAT 1260
Db 1201 CATGTTACAGAGAAACCAACCAAGCTGATTAATTTATGATCTTCTGCTCACATCTAT 1260
Qy 1261 TTTCTGTTCCCATGATGCTTTGTGCAATTTACCTTCAATCAACCTCCGCTACACC 1320
Db 1261 TTTCTGTTCCCATGATGCTTTGTGCAATTTACCTTCAATCAACCTCCGCTACACC 1320
Qy 1321 GTCTACTTGTATGCTTGTGATGCTGAGAGATCTTATTAATCCCTAATGATTAATG 1380
Db 1321 GTCTACTTGTATGCTTGTGATGCTGAGAGATCTTATTAATCCCTAATGATTAATG 1380
Qy 1381 CGTAGTGAGCGTGTGTTAAGGTTAGTATGCTGATGATTAACCTATTTCTTCTGG 1440
Db 1381 CGTAGTGAGCGTGTGTTAAGGTTAGTATGCTGATGATTAACCTATTTCTTCTGG 1440

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Qy 1441 AATCATTTGGCCAAACGTATGCTTAAAGATCGCGTGAATACAAACATTTGAACGTATG 1500
Db 1441 AATCATTTGGCCAAACGTATGCTTAAAGATCGCGTGAATACAAACATTTGAACGTATG 1500
Qy 1501 ACTGATATGATGATCAATTTTGGCCACCTGCTGATATCTTATACCATTAATGAAGGT 1560
Db 1501 ACTGATATGATGATCAATTTTGGCCACCTGCTGATATCTTATACCATTAATGAAGGT 1560
Qy 1561 ATGGAATATGTTTCTGCGATCAATTTAAGAAATCCGATGATATACAGTGTGTAAT 1620
Db 1561 ATGGAATATGTTTCTGCGATCAATTTAAGAAATCCGATGATATACAGTGTGTAAT 1620
Qy 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Db 1621 ATTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Qy 1681 TCGATGTTGAAAAACATGAGATTTATTTAG 1713
Db 1681 TCGATGTTGAAAAACATGAGATTTATTTAG 1713

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RESULT 5
AAQ91565
ID AAQ91565 standard; cDNA; 1713 BP.
XX
AC AAQ91565;
XX
DT 22-DEC-1995 (first entry)
XX
DE OP-resistant esterase Lc7L103D allele.
XX
KW Esterase; E3; bioremediation; organophosphate; carbamate;
KW insecticide; pesticide; water decontamination; meat decontamination;
KW ss.
XX
OS Lucilia cuprina.
XX
FH Key
FT Location/Qualifiers
FT CDS 1..1713
FT /tag= a
XX
PN WO9519440-A1.
XX
PD 20-JUL-1995.
XX
PF 13-JAN-1995; 95WO-AU00016.
XX
PR 13-JAN-1994; 94AU-0003347.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX Parker AG, Robin GC, Russell RJ, Smyth K;
XX WPI; 1995-263870/34.
XX
PT Pure E3 esterase from Lucilia cuprina and related DNA - used to
PT eliminate residues of organo-phosphate and carbamate pesticides from
PT water, meat etc.
XX
PS Example 4; Page 12-17; 38pp; English.
XX
CC R1-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
CC OP-susceptible esterase E3 of L. cuprina) from a diazinon
CC resistant strain, Llandillo 103. 4 isolated clones were
CC sequenced (Lc7L103 A-D, AAQ91562-65) that encoded diazinon-resistant
CC esterases. The esterases, or cells expressing them, are used
CC in bioremediation.
XX
SQ Sequence 1713 BP; 513 A; 307 C; 369 G; 524 T; 0 other;
Query Match 98.0%; Score 1679.4; DB 16; Length 1713;

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Db	1021	ATACCCCACTGATGATGGGTAAACACTTCATATATGAGGGTCTATATTTTCACTTGCTTTCTTAAG	10
Qy	1081	CAATGCGCATGCTGTGTAAAGAAATTTGGAACCTTGCTGTCAATTTTGTGCCAAGTAATG	11
Db	1081	CAATGCGCATGCTGTGTAAAGAAATTTGGAACCTTGCTGTCAATTTTGTGCCAAGTAATG	11
Qy	1141	GCTGATGCTGAACGCACCCGCCCAAGACCTTGGAAATGGGTGCTAAATTTAAAGGCT	12
Db	1141	GCTGATGCTGAACGCACCCGCCCAAGACCTTGGAAATGGGTGCTAAATTTAAAGGCT	12
Qy	1201	CATGTTACAGAGAAACACCAACACGCTGATATTTATGATCTTTGCTGTCACATCTAT	12
Db	1201	CATGTTACAGAGAAACACCAACCGCCGATATTTATGATCTTTGCTGTCACATCTAT	12
Qy	1261	TTCTGATTTCCCATGCGATGCTTTGTTGGCAATATACCTTTCATTCACACTCCGGTACACC	13
Db	1261	TTCTGATTTCCCATGCGATGCTTTATTTGCAATTTAGCTTTCAATTCACACTCCGGTACACC	13
Qy	1321	GCTACTGTTATGCGTTGCGACTTCGATTTGGAGAGATCTTATCAATCCCTATCGTATTATG	13
Db	1321	GCTACTGTTATGCGTTGCGACTTCGATTTGGAGAGATCTTATTAATCCCTATCGTATTATG	13
Qy	1381	CGTATGTCGACGTCGTATTAAGGGTGTATGTCATGCTGATGATTAACCTATTTCTCTCG	14
Db	1381	CGTATGTCGACGTCGTATTAAGGGTGTATGTCATGCTGATGATTAACCTATTTCTCTCG	14
Qy	1441	AATCAATTTGGCCAAACGTAATGCTTAAGAAATCGCTGAATACAAACAAATTTGAACGTATG	15
Db	1441	AATCAATTTGGCCAAACGTAATGCTTAAGAAATCGCTGAATACAAACAAATTTGAACGTATG	15
Qy	1501	ACTGTGATATGATACAAATTTTGGCACACACTGTAATCCTTTATGCAATGAATTTGAAGGT	15
Db	1501	ACTGTGATATGATACAAATTTTGGCACACACTGTAATCCTTTATGCAATGAATTTGAAGGT	15
Qy	1561	ATGGAATAATTTTCTGCGGATCCCAATTAAGAAATCCGATGAATTCAGTGTGTTGAAT	16
Db	1561	ATGGAATAATTTTCTGCGGATCCCAATTAAGAAATCCGATGAATTCAGTGTGTTGAAT	16
Qy	1621	ATTAGTGATGAATTTGAATTTGATGATGTCCTGTAATGATTAAGATTAAACAATGGGAG	16
Db	1621	ATTAGTGATGAATTTGAATTTGATGATGTCCTGTAATGATTAAGATTAAACAATGGGAG	16
Qy	1681	TCGATGTTTAAAAACATGACATTTATTTTAG 1713	
Db	1681	TCGATGTTTAAAAACATGACATTTATTTTAG 1713	
RESULT 6			
AAQ91563			
ID	AAQ91563 standard; cDNA; 1713 BP.		
XX	AAQ91563:		
AC			
XX			
DT	22-DEC-1995 (first entry)		
XX			
DE	OP-resistant esterase Lc7LI03B allele.		
XX			
KW	Esterase; E3: bioremediation; organophosphate; carbamate;		
KW	insecticide; pesticide; water decontamination; meat decontamination.		
KW	ss.		
XX			
OS	Lucilia cuprina.		
XX			
FT	Key	Location/Qualifiers	
FT	CDS	1..1713	
XX			
XX	W09519440-A1.		
XX			
PD	20-JUL-1995.		
XX			
PF	13-JAN-1995; 95WO-AU00016.		
XX			

ID	AA091562	standard; cDNA, 1713 BP.
XX	AA091562;	
XX	22-DEC-1995	(first entry)
XX	DE	OP-resistant esterase Lc7L103A allele.
XX	KW	Esterase; E3; bioremediation; organophosphate; carbamate;
XX	KM	Insecticide; pesticide; water decontamination; meat decontamination;
XX	ss.	
XX	OS	Lucilia cuprina.
XX	FT	Key
XX	FT	Location/Qualifiers
XX	CDS	1..1713
XX	FT	/*tag= a
XX	PN	MO9519440-A1.
XX	PD	20-JUL-1995.
XX	PE	13-JAN-1995; 95WO-AU00016.
XX	PR	13-JAN-1994; 94AU-0003347.
XX	PA	(CSIR) COMMONWEALTH SCT & IND RES ORG.
XX	PI	Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG;
XX	PI	Parker AG, Robin GC, Russell RJ, Smyth K;
XX	DR	WPI. 1995-263870/34.
XX	PT	Pure E3 esterase from Lucilia cuprina and related DNA - used to
XX	PT	eliminate residues of organo:phosphate and carbamate pesticides from
XX	XX	water, meat etc.
XX	PS	Example 4; Page 12-17; 38pp; English.
XX	CC	RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding
XX	CC	OP-susceptible esterase E3 of L. cuprina) from a diazinon
XX	CC	resistant strain, Llandillo 103. 4 isolated clones were
XX	CC	sequenced (Lc7L103 A-D, AA091562-65) that encoded diazinon-resistant
XX	CC	esterases. The esterases, or cells expressing them, are used
XX	CC	in bioremediation.
XX	SO	Sequence 1713 BP; 512 A; 307 C; 369 G; 525 T; 0 other;
XX	Query Match	97.9%; Score 1676.2; DB 16; Length 1713;
XX	Best Local Similarity	98.7%; Pred. No. 0;
XX	Matches 1690; Conservative	0; Mismatches 23; Indels 0; Gaps 0
QY	1	ATGAATTCACAGTTAGTTGATGAGAAATTAATAATGGAAGATTAAATGATTGAAAAAT 60
DB	1	ATGAATTCACAGTTAGTTGATGAGAAATTAATAATGGAAGATTAAATGATTGAAAAAT 60
QY	61	AAAGTTTAAACTATCGTTTAACTACCAATGAACGGTGTAGCTGAAACTGAATATGGC 120
DB	61	AAAGTTTAAACTATCGTTTAACTACCAATGAACGGTGTAGCTGAAACTGAATATGGC 120
QY	121	AAAGTGAAGAGCGTTAAAGCTTTAACTGTCAGATGATTCCTACTACAGTTTGAAGGT 180
DB	121	AAAGTGAAGAGCGTTAAAGCTTTAACTGTCAGATGATTCCTACTACAGTTTGAAGGT 180
QY	181	ATACCGTACGCCAACCCGCACTGGGTGAGTGAAGATTTAAAGCACCCGACGACCAACA 240
DB	181	ATACCGTACGCCAACCCGCACTGGGTGAGTGAAGATTTAAAGCACCCGACGACCAACA 240
QY	241	CCCTGGGATGCGTGGCTGATGTTGCAATTAAGATTAAGTCAAGTGTGATTTT 300
DB	241	CCCTGGGATGCGTGGCTGATGTTGCAATTAAGATTAAGTCAAGTGTGATTTT 300

OY	301	ATFACGGGCAAAAGTGTGGCTACAGAGATGTGCTATACCTAAGTGTCTATACGAATAT	360
Db	301	ATFACAGGCAAAAGTGTGGCTACAGAGATGTGCTATACCTAAGGCTCTATACGAATAT	360
OY	361	CTAATGCCGAATTAACGTCCCGTTTAAAGTATACATCAATGAGTGGTGTATATATC	420
Db	361	CTAATGCCGAACCTAAAGCTCCCGTTTAAAGTATACATCAATGAGTGGTGTATATC	420
OY	421	GGTGAATAATCATGCTGATGTATGTATGGTCTGATTAATTTCAATAAAGATGTGGTGTG	480
Db	421	GGTGAATAATCATGCTGATGTATGTATGGTCTGATTAATTTCAATAAAGATGTGGTGTG	480
OY	481	ATTAACTACAAATATTCGTTTGGGAGCTCTAAGTTTTCTAAGTTTAAATTACAGACCTT	540
Db	481	ATTAACTACAAATATTCGTTTGGGAGCTCTAAGTTTTCTAAGTTTAAATTCAACAAACCTT	540
OY	541	AATGTGCCGGTAAATGCGGCGCTTAAAGATCAAGTCATAGCGCTGGTGGATTTAAAT	600
Db	541	AATGTGCCGGTAAATGCGGCGCTTAAAGATCAAGTCATAGCGCTGGTGGATTTAAAT	600
OY	601	AATTGGCGCAACTTTGGTGGCAATCCCGATATATTTACAGTCTTTGGTGAAGTCCGGT	660
Db	601	AATTGGCGCAACTTTGGTGGCAATCCCGATATATTTACAGTCTTTGGTGAAGTCCGGT	660
OY	661	GCTGCTCTACCCACTCAATGATGTATACCGAAACAATCGGGCTTTTTCATGTGTGT	720
Db	661	GCTGCTCTCTACCCACTCAATGATGTATACCGAAACAATCGGGCTTTTTCATGTGTGT	720
OY	721	ATACAAATGTCGGGTATTCGTTATTTGCCATTTGGCTAAATACCAATGTCACATGTGCC	780
Db	721	ATACAAATGTCGGGTATTCGTTATTTGCCATTTGGCTAAATACCAATGTCACATGTGCC	780
OY	781	TTTCACTTACGCAAAATTTGGCGGCTATAAAGGTGAGAGATATGATTAAGATGTTTTGAA	840
Db	781	TTTCACTTACGCAAAATTTGGCGGCTATAAAGGTGAGAGATATGATTAAGATGTTTTGAG	840
OY	841	TTTCTTATGAAGCCAGCACAGATTTATATAAATTGAGAGAAAAGTTTTAACTCTA	900
Db	841	TTTCTTATGAAGCCAGCACAGATTTATATAAATTGAGAGAAAAGTTTTAACTCTA	900
OY	901	GAGAGGGTACAAATTAAGTATCATGTTTCCTTTGGTCCAGCTGTGAGCATATACAGCC	960
Db	901	GAGAGGGTACAAATTAAGTATCATGTTTCCTTTGGTCCAGCTGTGAGCATATACAGCC	960
OY	961	GCTATTTGTCTTACCCCAACATCTCTCGGGAATGTTTAAACTGCTGGGGTAATTCG	1020
Db	961	GCTATTTGTCTTACCCCAACATCTCTCGGGAATGTTTAAACTGCTGGGGTAATTCG	1020
OY	1021	ATPACCCATATGATGGTAAACACTTCAATATAGAGGCTCTATTTTTCACCTTCAATCTTAAG	1080
Db	1021	ATPACCCATATGATGGTAAACACTTCAATATAGAGGCTCTATTTTTCACCTTCTTAAG	1080
OY	1081	CAAAATGCTATGCTTTTAAAGAAATTTGGAACCTGTGTAAATTTGTGTGCAAGTAATTG	1140
Db	1081	CAAAATGCTATGCTTTTAAAGAAATTTGGAACCTGTGTAAATTTGTGTGCAAGTAATTG	1140
OY	1141	GCTATGCTGAAGCACACCGGCCCAAGAGACCTTGGAAATGGTGTCTAAATTTAAAAAGCT	1200
Db	1141	GCTATGCTGAAGCACACCGGCCCAAGAGACCTTGGAAATGGTGTCTAAATTTAAAAAGCT	1200
OY	1201	CATGTTACAGAGAAACACACAGCTGATTAATTTATGATCTTGTGCTCACATCTAT	1260
Db	1201	CATGTTACAGAGAAACACACAGCTGATTAATTTATGATCTTGTGCTCACATCTAT	1260
OY	1261	TTTGGTTCGCCATGATGCTTTGTGGCAATTAAGTTCATACACACCTCGGTCACACC	1320
Db	1261	TTTGGTTCGCCATGATGCTTTGTGGCAATTAAGTTCATACACACCTCGGTCACACC	1320
OY	1321	GTTCTACTTGTATCGCTTCGACTTCGATTTGGAAGATCTTATCAATCCCATGATTTATG	1380
Db	1321	GTTCTACTTGTATCGCTTCGACTTCGATTTGGAAGATCTTATTAATCCCATGATTTATG	1380
OY	1381	CGTATGAGACGTGTGTTAAAGGCTGTTATGTCATGCTGATGAATTAACCTAATTTCTTGG	1440


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Db 1381 CCGTAGGACGCTGCTTAAAGGCTTGTGTCATGCTGATTAACCTATTCTCTGG 1440
QY 1441 AATCAATGGCCAAACGATGCTTAAGATCGCTGAATCAAAACATTAACGATG 1500
Db 1441 AATCAATGGCCAAACGATGCTTAAGATCGCTGAATCAAAACATTAACGATG 1500
QY 1501 ACTGCTATGATGATCAATTTGCGACACGCTGATCCTTATAGCAATGAATGAAGT 1560
Db 1501 ACTGCTATGATGATCAATTTGCGACACGCTGATCCTTATAGCAATGAATGAAGT 1560
QY 1561 ATGGAATATGTTCTCGGATCAATTAAGAAATCCGATGAAGTATCAAGCTTTGAT 1620
Db 1561 ATGGAATATGTTCTCGGATCAATTAAGAAATCCGATGAAGTATCAAGCTTTGAT 1620
QY 1621 ATTAGTATGATGATGAATGATGATGCTGCTGAATGATGAATGAATGAAGT 1680
Db 1621 ATTAGTATGATGATGAATGATGATGCTGCTGAATGATGAATGAATGAAGT 1680
QY 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713
Db 1681 TCGATGTTGAAAAACATAGAGATTTATTTAG 1713

RESULT 8
AAT68597 standard; DNA; 1710 BP.
XX AAT68597;
AC 08-AUG-1997 (first entry)
DT
DE Md-alpha-E7 gene.
XX Malathion carboxylesterase; organophosphate; insecticide;
KW pesticide; remediation; bioremediation; decontamination; ds.
XX Musca domestica Rutgers strain.
OS
FH Key Location/Qualifiers
FT mutation 752
FT /*tag a "TTP-251 TGG codon is altered to a Ser
FT /note- codon in resistant mutants"
XX W09719176-A1.
XX 29-MAY-1997.
XX 22-NOV-1996; 96WO-AU00746.
XX 23-NOV-1995; 95AU-0006751.
PA (CSTR ) COMMONWEALTH SCI & IND RES ORG.
PI Boyce T, Brownlie JC, Campbell PM, Claudianos C,
PI Newcomb RD, Oakeshott JG, Robin GC, Russell KJ, Smyth K;
XX MPI: 1997-298113/27.
DR P-PSDB: AAM17767.
XX DNA encoding enzyme that degrades organophosphate pesticides -
PT useful for decontamination of soil, water, food etc
XX
PS Claim 6: Fig 3: 52pp: English.
XX A 1710 bp DNA molecule (AAT68597) comprises the Md-alpha-E7
XX coding sequence of the Musca domestica Rutgers strain. It was
XX isolated by amplification of genomic DNA using alpha-esterase
XX consensus primers (see also AAT68598-99) and use of a 534 bp
XX amplicon to screen a genomic library of M. domestica. A
XX mutation of the gene, resulting in substn. of serine for tryptophan
XX at amino acid position 251 (see also AAM17767), confers malathion

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CC resistance. The resistant enzyme acts as a malathion
CC carboxylesterase and can be formulated for use in degrading
CC environmental carboxylester or dimethyl general organophosphates.
XX
SQ Sequence 1710 BP; 498 A; 369 C; 394 G; 449 T; 0 other:
Query Match 55.8%; Score 956.6; DB 18; Length 1710;
Best Local Similarity 73.4%; Pred. No. 6e-253;
Matches 1223; Conservative 0; Mismatches 444; Indels 0; Gaps 0;
44 TTAATGATGTAATAATAGTATTTTAACTATGCTTAACTACCAATGAAGAGTGTAG 103
Db TTAATGATGTAATAATAGTATTTTAACTATGCTTAACTACCAATGAAGAGTGTAG 103
QY 104 CTGAATGATGTAATAATAGTATTTTAACTATGCTTAACTACCAATGAAGAGTGTAG 163
Db 104 TCGATGATGTAATAATAGTATTTTAACTATGCTTAACTACCAATGAAGAGTGTAG 163
QY 164 ACTACAGTATGAGGATATACCGTACGACCAACCGGAGGAGTGTAGTGTAGTAAAG 223
Db 164 ACTACAGTATGAGGATATACCGTACGACCAACCGGAGGAGTGTAGTGTAGTAAAG 223
QY 224 CACCCAGCGCAGCAACACCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 283
Db 224 CACCCAGCGCAGCAACACCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 283
QY 284 CAGTGCAGATGATTTATTAACGGCAAGTGTGCTGATGCTGATGCTGATGCTGATGCT 343
Db 284 CAGTGCAGATGATTTATTAACGGCAAGTGTGCTGATGCTGATGCTGATGCTGATGCT 343
QY 344 GTGCTATACGATTAATGATTAATGCTGATTAATGCTGATTAATGCTGATTAATGCT 403
Db 344 GTGCTATACGATTAATGATTAATGCTGATTAATGCTGATTAATGCTGATTAATGCT 403
QY 404 GTGCTGATTTATTAATGCTGATTAATGCTGATTAATGCTGATTAATGCTGATTAAT 463
Db 404 GTGCTGATTTATTAATGCTGATTAATGCTGATTAATGCTGATTAATGCTGATTAAT 463
QY 464 AAAAGATGCTGCTGATTAATGCTGATTAATGCTGATTAATGCTGATTAATGCTGAT 523
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QY 524 TGAATTCAGAAACCTTAATGCTGATTAATGCTGATTAATGCTGATTAATGCTGAT 583
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QY 584 TGCCTGATTAATGCTGATTAATGCTGATTAATGCTGATTAATGCTGATTAATGCT 643
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QY 704 GTCTTTTCCATGCTGATTAATGCTGATTAATGCTGATTAATGCTGATTAATGCT 763
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QY 764 AATGTCACATGCTGCTTACCTACCTACCTACCTACCTACCTACCTACCTACCT 823
Db 764 AATGTCACATGCTGCTTACCTACCTACCTACCTACCTACCTACCTACCTACCT 823
QY 824 ATAGGATGTTTGAATTTCTTATGAAGCCAGCCAGCAAGATTAATGAAGATTTAGG 883
Db 824 ATAGGATGTTTGAATTTCTTATGAAGCCAGCCAGCAAGATTAATGAAGATTTAGG 883
QY 884 AAAAGTTTTAACTCTGAGAGAGCGTAAACATTAAGGATGTTTCTTCTTCTCCACTG 943
Db 884 CACAGTTTTGAACCCGCAAGAGATTAAGATTAAGTATGTTCTTCTTCTCCACTG 943
QY 944 TTGAGCATATCAACCGCTGATTTGCTTACCAACATCTCTGAGGAATGTTTAA 1003
Db 944 TAGAACCATACAGACCGGAGCTGTGTACCAACATCAAGAAATGTTGAG 1003

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QY 325 GAGATGTTCTATACCTAAGTGTCTATACGAATAATCTAATCCCGAATAACGTCC 384
 DB 304 GAGAGCTGTCTGTAACCTCAATGTCTACACGAGGAGTTTCACTCCACACAGACCTTTGGCG 363
 QY 385 GTTTTAGTATACATACATGCTGTGTGTTTATATCGGTGAATAATCATCGATATGAT 444
 DB 364 GTTCTGTTTGATCTATGAGGGGTGATTCGAATGGAGAGATCCGGGATCTGTAC 423
 QY 445 GGTCTGATTAATTTCAATTAAGAGATGTGTGTTGATTAACTATCAATATCGTTTGGGA 504
 DB 424 AGCCCGGACTATATATGATGAAATGTCTACTGCTGTAATATCTTATCGTTAGGA 483
 QY 505 GCTTAGTGTTCCTAAGTTTAAATTCAGAAACCTTATGTGCCCCGTAATCCGGCTT 564
 DB 484 GCGCTGGATTCCTTAGCTTGACAGACGAAACGTGTTCTGTGAACGCGGACTTA 543
 QY 565 AAGATCAAGTCAATGCGCTTGCTGTGATTAATAATATTCGCGCAACTTGTGTGCAT 624
 DB 544 AAGATCAAGTTATGCGCTTGCGGTGATCAACGGAATTCAGATTCTTTGTGTGCAT 603
 QY 625 CCCGATTAATATACAGTCTTTGTGAAGTCCGCTGCTCTACCCACTACATGATG 684
 DB 604 CCCGATTAATATACGCTTTTGTGTGAGAGTCTGTGAGGTGCATCATTAATATGATG 663
 QY 685 TTAACCGAACAACGCGGCTTTTCCATGCTGTGTATACATAAGTGTGTAATGCTATT 744
 DB 664 CTGACGATGTCAGGCCAAGGCGCTTATTTACAAAGACTATTATATGTGCGGATCCGACTG 723
 QY 745 TGTCATTTGGCTTAATACCAATGTCA--ACATGCTGCTTACCTTATGCGCAATTTGGCC 801
 DB 724 GCACCTTGCGGCGACAGCCCAACCAACCAATTAATTTGCGCTTATGCGGACAGCCACT 783
 QY 802 GCGTATAGGGTGAGATGATGATAGAGATGTTTGGAAATTTCTTATAAAGCCAGCCA 861
 DB 784 GCGTACAGGAGATGCTACAGATCGGACATTTTGGCCATCTCAAAATAATGTAAGCC 843
 QY 862 CAGATTTAATAAATCTGAGAAAAAGTTTAACTCTAGAAAGCCGTAATAATAGT- 920
 DB 844 AGTAGCATGCTGAAGGTGCGGAGATATCATCACATGAGAGACGACACCGGTTG 903
 QY 921 --CATGTTCTTGTGTCACAGTGTGAGCCATATCAGACCGCTGATTTGTCTTACC 978
 DB 904 ACCATGTTCACTTGTGACCCACCATCGAGCCCTATTGACTCCATTTGTGTATGCC 963
 QY 979 AAATCTCTCGGGAATGTGTAATACTGTGGGTAACTGTATGCCCATATGATGGGT 1038
 DB 964 AAGTCCGACATGAAATATGATCGGACTGTTGGGCAACACGATTCCTGATTCGA 1023
 QY 1039 AACCTTCATTTGAGGCTCTATTTTCTACTCAATTTTAAAGCAATGCCATGCTGTT 1098
 DB 1024 GGAACCTCTCGAAGGCTCTCTCATGTTTCCCAAGTGAACAGTGGCCGGAATGCTT 1083
 QY 1099 AAGCAATTTGAAACTGTGTCAATTTTGTGCAAGTGAATTTGGCTGATGTAAGCCACC 1158
 DB 1084 TGCCAGCTGGGTGACTGCGAAGACCTGCGCCCTCAAGATGCCCAGATGAGAGACAA 1143
 QY 1159 GCCCAGAGACTTGGAAATGTGTCTAAATTAATAAGGCTCATGTATACAGAGAACAA 1218
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 QY 1219 CCAACAGCTGATTAATTTATGATTTTGTCTCATATTTTGTGTTGCCCATGAT 1278
 DB 1204 AAGACATATTTGAGATACAGGATCTTCTGTGTAATATTTTGTGCAATGACATTTAT 1263
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 DB 1264 AGGACTTTGCTGCTGCTGCTACACGCGCCATTTGCGCCCAACATTCCTGTACGATTC 1323
 QY 1339 GACTTCGATTTGGAGATCTTATCAATCCCTATGCTATTAATGCGTAGTGGAGTGT 1398
 DB 1324 GATTTGCACTG--AACCTTCAATATCATGCAATTAATACCTGTGGCGCAAGGTG 1380

QY 1399 AAGGCTTAGTCATGCTGATGAATTAACCTATTCTTCTGGAATCAATTTGGCAAGCT 1458
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 QY 1459 ATGCTTAAGAATCGCTGTAATACAAACAATTTGAACGTATGCTGTAATGATACAA 1518
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 QY 1519 TTTGCCACCTGCTGTAATCTTATA-----GCATGAATAATGAAGTATGGA 1566
 DB 1501 TTTGCCATTTCCGGGGATCCCAACATACGATGTCTGCTCAGATGAGAAAGAACGCG 1560
 QY 1567 AATGTTCTGCGGATCCATTAAGAATCCCATGAAGTATCAATGTTTGAATTTACT 1626
 DB 1561 CGTGCGCTGCTGCTGCCATTTTCGAAGACGATTAAGTGTTCACAGTCCCTGAATATTCG 1620
 QY 1627 GATGAATGAATAATGATGATGCTGCTGAATGATGATTAATTAACAATGAGATGATG 1686
 DB 1621 CACGATGTCATGATGATGATTTTGGCCGAGCGCAAGCGAAAGCTGAGACTTGGGACTGCATC 1680
 QY 1687 TTTGAAA 1693
 DB 1681 TACGACA 1687
 RESULT 11
 ABL02066
 ID ABL02066 standard; cDNA; 6175 BP.
 XX
 AC ABL02066;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 680.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 OS Drosophila melanogaster.
 XX
 OS
 XX WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US09231.
 PF 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR P-PSDB; ABB57963.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS
 PS Claim 1; SEQ ID NO 680; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (ABB5737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.


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Db      846 ATATACCTACCGAGACACACTGTGTGCTTAACACCCGATGACTGATGCAAGTACGTC 905
      1011 GGGTATTCGATACCCACATATGATGGTAAACCTTCATATGAGGGTCTTATTTTCACTTC 1070
      906 GACTCAGACGATACCCATGATGTTTGAGAGCCAGAGCTTCGAGGGATGATGCTTATCC 965
      1071 AATTCTTAAGCAATAGCCATATGCTTTTAAAGAAATTTGCAATTTTGTGCC 1130
      966 AGAGGTTTCAAGCGCCGACCAACCCCTCGATGAGTGGGTACTGACAGAAATCTGCTACC 1025
      1131 AAGTGATTTGGCTGATGTCGAAACGACCCGCCAGAGACCTTGAATGGGTGCTAAAT 1190
      1026 GACGCAATCTCGT-----CTTAACCTAGATCCAAACTGCGTAGAACTAGGCTTGCAAC 1081
      1191 TAAAGGCTCATGTTACAGAGAAACACCAACAGCTGATAT-----TTTATGG 1240
      1082 TGAAGAGGCGGTATTTCCGGAGCAACCCCTGTAACAGGCAACATGATGAAGTTTCTCG 1141
      1241 ATCTTTGCTCTACATCTATTTCTGGTCCCATGCAATGCTTGTGTAATACGTTCA 1300
      1142 AGCATCTCATATCGAGATTTCTGGACCCCTATATACAGGCGAGCTTTGAACCGGTGCC 1201
      1301 ATCACACCTCCGGTACACCCGCTACTTGTATGCTTCGACTTCGATTCGGAAGATCTTA 1360
      1202 GGCATATCCAGCG---CACCCACGATCTGTATGATGATTCGATCCAGATTCGAA---CTGT 1255
      1361 TCATACCCCTATCTATATGATGATGATGAGTGTGTTAAGGTTTATGATGCTGATG 1420
      1256 GCACGCCATTAAGATGTTGTAATTTGCGGCCATCGATGCGAGGTTTGTTCATGATGACG 1315
      1421 AATTAACTATTTCTTCTGGAATCAATTTGGCCAAACGTAATGCGTAAGATTCGGTAAT 1480
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      1541 ATAGCAATGAATTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1600
      1436 ACTGCGAAAGTATTAATCACTCAAGTTTGCACCCATGCAAAACGTAACCACTTT---- 1491
      1601 AAGTATACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1660
      1492 -----AAGTGTCTCATATTTGGGATGATGATGATGATGATGATGATGATGATGATG 1543
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RESULT 15

ABL01859 ID ABL01859 standard; cDNA: 1863 BP.

XX ABL01859;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SHQ ID NO 59.

XX Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical; gene; ss.

XX Drosophila melanogaster.

OS WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

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PR      23-MAR-2000; 2000US-191637P.
PR      11-JUL-2000; 2000US-0614150.
PA      (PEKE ) PE CORP NY.
XX      Venter JC, Adams M, LJ PMD, Myers EW;
XX      WPI; 2001-656860/75.
XX      P-SDB; ABB57756.
PT      New isolated nucleic acid detection reagent for detecting 1000 or more
PT      genes from Drosophila and for elucidating cell signalling and cell-cell
PT      interactions -
PS      Claim 1; SEQ ID NO 59; 21bp + Sequence Listing; English.
XX      The invention relates to an isolated nucleic acid detection reagent
XX      capable of detecting 1000 or more genes from drosophila. The invention is
XX      useful in developmental biology and in elucidating cell signalling and
XX      cell-cell interactions in higher eukaryotes for the development of
XX      insecticides, therapeutics and pharmaceutical drugs. The invention
XX      discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins
XX      sequences (ABL01840-ABL16175).
CC      (ABB57737-ABB72072).
CC      The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pcl_sequences.
XX      Sequence 1863 BP; 425 A; 493 C; 523 G; 422 T; 0 other:
SO
Query Match      18.9%; Score 323; DB 23; Length 1863;
Best Local Similarity 51.5%; Pred. No. 1,7e-78;
Matches 796; Conservative 0; Mismatches 745; Indels 6; Gaps 2;
      1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGAAAGATTAATGATGAAT 60
      166 ATGAGATCCGAGTGGAGTGGCGATGCTGGAATGGCACCAAGCTATTTGGCCAC 225
      61 AAGTTTAACTATGCTTAACTACCAATGAACGTTGATGTAAGTGAATATGCG 120
      226 AAGATGTCACATGATGCTTGGCAAAAGCAGAGGATGCTGCACCGAGGATGCG 285
      121 AAGTGAAGGCGTTAAACGTTTAACTGTGT---ACGATGATTCCTACTACAGTTTGG 177
      286 CAGTGGCGGACATGCGCGAAGGACACTCTACGAGGAGATGATGCTGCTTGAG 345
      178 GGTATACCGGACCGCCACGCGAGTGGTGAAGTGAATTAAGCAACCCAGGACCA 237
      346 GAATCCCTTTGCACAGCGCGCGGTGGGAGCTGCGCTTCGAGCCCGCCAGCACA 405
      238 ACACCTGGAGTGTGCGTGTGTTGCAATCATTAAGATTAAGTCAAGTGTGAT 297
      406 CATTCCCTGTTGGGGGCGGATGACCTATCCCGGGCCAGACCGCATGAAGACAC 465
      298 TTTATTAACGGCAAGTGTGCTGAGAGATTTGCTATTAAGTGTCTATACGAT 357
      466 TTTGCTCTCAGCATGCTGCAAGGACGAGAGATTTGCTGATGATTAATTCGAAG 525
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      526 CGCTGAGATCGACAGCCGCGCTGATGCTGTGATCTATGCGGTGATTCGAG 585
      418 ATCGGTGAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
      586 TTGGCGAGGCTGTGAGATTTCTAAGTCAAGACTACTTATGACAGCAAGACGTAAG 645
      478 TTGATTAACATACATATGCTTTGGAGCTCTGAGCTTTCTAAGTTTAAATTCAGAC 537
      646 GTTGACATTCATTAATTAAGGTGGGCAATTTGGGCTTCTCAGCCCGGATTCGAC 705
      538 CTATATGCCCCGATATGCGGCTTAAGATCAATGATGATGATGATGATGATGATGAT 597
      706 TTGATGTGCGCGAAGATGCTGATCTCAAGACCAAGTGAATGATGATGATGATGAT 765

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QY 598 AATAATTGCGCAACTTGTGGCAATCCGATATATTACAGTCTTGTGTAAGTCC 657
DB 766 CAGAAACATAGGCCAATTCATGAGATGCCAAATATATACCGTATGGGAGAGTCCG 825
QY 658 GGTGCTGCTCTACCCACTACATGATGTTAACGACAAACCTCGGCTCTTTCCATCGT 717
DB 826 GGACACAGCTCCGTTACGCGGTGATGACACGACGAAACCCGAGGCTGTCACAG 885
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DB 886 GCCATCATGCAATGGATTCATGTCGAGTGGCCATGAGCCAAATGAGTGGCAGTGG 945
QY 778 GCCCTTCACTTACCAATTTGGCGGCTATAGGGTGAGTAAATGATAGATGTTTG 837
DB 946 GCATACCGACTGGCTGCAATTTGGGACTCGGGCAGTGAAGAGAAAGTGT 1005
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QY 898 CTAGAAGAGCTACAAATAGGATGTTTCTTTGGTCCACTGTTGAGCAATTCAG 957
DB 1066 CAAAGAGACGGCGCAGTACGCTCTTCTTACTCCGTTGAGAACATATATC 1125
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QY 1018 TCGATACCCACTATGATGAGTACATTCATATGAGGCTATTTTCACTTCAATTCY 1077
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DB 1246 CTGCACGACGAGAACACATGCTGATGCTTTGAGTCTTAATTCCTCGGAGATCAG 1305
QY 1138 TTGCTGTGCTGAACGACCGCCCGACAGACTTGGAAATGGGCTAAATTAAG 1197
DB 1306 GAGAAAGATACCCAGTGCATCTTAAGATCTGCTACGTCATTTAAGTGATTAATCTC 1365
QY 1198 GCTCATGTTACAGAGAAACACACAGCTGATATTTTATGATCTTGTCTCACATC 1257
DB 1366 GATGATGGAGCTCGAGGGCGAATGAGTTCAATGATGCTCGCAATPACTGCGTTAA 1425
QY 1258 TATTTCTGTTCCCATGATGCTTTGTGCAATTAGCTTCAATCACACCTCCGTTACA 1317
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QY 1318 CCCGCTACTGTATMGCTTGCAGTTCGGAAGATCTTATCAATCCCTATCGTAT 1377
DB 1486 CCCACCTTACCTGTACCGCTTGATGTGACTCG--CCCAATTCATACCTTCCGGCAG 1542
QY 1378 ATGCGTAGTGACGTGTGTAGGGGTGTAGTATGCTGATGATTAACCTATTTCTTC 1437
DB 1543 GTGATGCGCGGAAACAGGTTCCGGGAGTGTATGTCAGACGATCTCTCTACCTTTC 1602
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Search completed: April 11, 2003, 01:06:53
Job time : 263.905 secs

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 00:24:12 ; Search time 1663.49 Seconds
(without alignments) 16677.553 Million cell updates/sec

Title: US-09-776-910-9
Perfect score: 1713
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estov:*
5: em_estpl:*
6: em_estro:*
7: em_estro:*
8: em_estro:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est5:*
15: em_estfun:*
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17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_othr:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	313.6	18.3	778	9	AI062034 GH01076.5
2	282.4	16.5	649	9	AI388926 GH19977.5
3	265.2	15.5	688	9	AI403569 GH23036.5
4	256.6	15.0	671	9	AI517692 GH28740.5
5	254.4	14.9	569	13	BI609541 RH14337.5
6	250	14.6	674	13	BI628316 RH56682.5

7	249.4	14.6	676	13	BI635372 SD16705.5
8	248.6	14.5	660	13	BI639486 SD22067.5
9	248.4	14.5	673	13	BI614181 RH43493.5
10	246.8	14.4	672	13	BI614443 RH43812.5
11	246.4	14.4	670	13	BI233202 RE29491.5
12	245	14.3	648	9	AI113763 GH10213.5
13	245	14.3	648	9	AI403098 GH22464.5
14	243.4	14.2	646	9	AI109901 GH09292.5
15	243.4	14.2	646	9	AI293416 LH06524.5
16	241	14.1	526	9	AI108080 GH06811.5
17	239.8	14.0	516	9	AI108156 GH06911.5
18	239.2	14.0	658	13	BI564586 RH61888.5
19	238.4	13.9	656	13	BI619037 RH49995.5
20	236.8	13.8	656	13	BI614821 RH44296.5
21	236.6	13.8	669	13	BI588370 RH29561.5
22	236.2	13.8	656	13	BI621302 RH52624.5
23	233.2	13.6	628	9	AI109573 GH08808.5
24	232.2	13.6	630	9	AI403830 GH23353.5
25	231.4	13.5	619	9	AI516869 GH27454.5
26	231	13.5	638	13	BI564361 RH37254.5
27	230.8	13.5	628	9	AI513346 GH26524.5
28	230	13.4	614	12	BG641228 SD12519.5
29	230	13.4	647	13	BI575862 RH32195.5
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31	229.6	13.4	614	9	AI134360 GH11805.5
32	229.2	13.4	622	9	AI134524 GH12012.5
33	228	13.3	633	13	BI370683 RE57396.5
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35	219.8	12.8	614	13	BI617897 RH48369.5
36	219.2	12.8	615	13	BI588504 RH29849.5
37	218.6	12.8	587	9	AI517539 GH28541.5
38	218.6	12.8	588	13	BI638519 SD20822.5
39	218.6	12.8	607	13	BI624437 RH63994.5
40	218.6	12.8	609	13	BI567399 RH37771.5
41	218.6	12.8	609	13	BI607309 RH74350.5
42	218.6	12.8	609	13	BI622392 RH54254.5
43	218.6	12.8	609	13	BI630054 RH59016.5
44	218.6	12.8	611	13	BI572606 RH08182.5
45	217.8	12.7	612	13	BI631806 RH61455.5

ALIGNMENTS

RESULT 1
LOCUS AI062034 778 bp mRNA
DEFINITION GH01076.5prime GH Drosophila melanogaster head POT2 Drosophila melanogaster cDNA clone GH01076 5prime similar to U51050:
Drosophila melanogaster alpha esterase (ae7) gene, partial cds,
mRNA sequence.

ACCESSION AI062034
VERSION AI062034.1 GI:3337873
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 778)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.

AUTHORS BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: 10 row: G column: 4
High quality sequence stop: 363.
Location/Qualifiers


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OY 908 GTACAAATAGGTCATGTTCTTTGGTCCACGTGTGACCATATACAGCCGTCATT 967
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DB 484 GCATGAACAGATATGTTTGGCTTTGGCCCATCCCTGGAACATTTCTCCAGCCGAAT 543
OY 968 GTGCTTACCCCAACATCCTCGGAAATGGTTAAACCTGGTGGGTAATTCGATACCA 1027
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 544 GTGTGATATCCAGGCTCCCAAGAGATGATGAAGACCGGCTGAGTAATCATATCCCA 603
OY 1028 CTATGATGGTAACTTCAATATGAGGCTCTATT 1063
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DB 604 TGTATATAGGAACCTGCTGACGAGGCTGCTGT 639

RESULT 3
A1403569 688 bp mRNA linear EST 19-APR-2001
LOCUS GH23036.5prtime GH Drosophila melanogaster head POT2 Drosophila
DEFINITION melanogaster cDNA clone GH23036 5prtime similar to U51050:
Drosophila melanogaster alpha esterase (ae7) gene, partial cds,
mRNA sequence.
ACCESSION A1403569
VERSION A1403569.1 GI:4246656
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
REFERENCE Drosophila melanogaster
AUTHORS Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G. M.
BDGP/HMML Drosophila EST project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 230 row: C column: 12
High quality sequence stop: 648.
Location/Qualifiers
1. 688
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH23036"
/clone_lib="GH Drosophila melanogaster head POT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: POT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
POT2. Plasmid cDNA library."

BASE COUNT 161 a 174 c 197 g 156 t
ORIGIN
Query Match 15.5%; Score 265.2; DB 9; Length 688;
Best Local Similarity 65.2%; Pred. No. 1.7e-61;
Matches 390; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

OY 1 ATGAATTTCAAGTTAGTTGATGAGAAATTAATGCAAGTTAATGCATTGAAAT 60
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DB 91 ATGAATTAAGAACCTCGCTTGTGAGCGCTTCCGGGCGGCTCAAAACCATCGACAT 150
OY 61 AACTTTTAACTATCGTTTAACCTAACCAATGAACGCTGCTAGCTGAATGAATGCG 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 151 AAGTCCAGAGATATCGCCAGTGCAGCAATGAACAGTTGTGCCGACAGGATGCGC 210
OY 121 AAGTGAAGCGCTTAACGTTTAAGCTGTGACGATGATTCCTACTACAGTTTGAAGGT 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 211 CAAGTGAAGGGTATCAAGGCTCTATCTCTACGATGCTGCTACTTACCTTCAGCTTCGAGGGT 270
OY 181 ATACCGTAGCCCAACGCCAGTGGGAGCTGAGATTTAAACACCCCAAGCACA 240

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DB 271 ATCCCGTAGCCCAACGCTCCGGGTGGGAGACTGCGGTTTAAAGCCCTCGAGGCCATT 330
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OY 241 CCCTGGAGTGTGTGCGTGAATTTGCAATCATTAAGATTAAGTCAAGATTGATTTT 300
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 331 CCTGGAGGAGCATGTCGCCACTCGACGACCCAGATGAAGGCCGCTGAGTGCAGTTC 390
OY 301 ATACGGGCAAGTGTGTGCTCAGAGATTGTCTATACCTAAGTGTCTATAGGAATAT 360
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DB 391 GTCTTCATTAAGGTATAGAGGCTCCGAGACTGCTCTATCTCATGTGTACACCAAT 450
OY 361 CTAATATCCGAACATAACGCTCCGTTTGTATATACATCATGTGTGTTTATATC 420
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DB 451 GTGAAGCCGACAAAGCTGCCCGGTTATGTTGATTCACGAGAGAGCTTCATTATC 510
OY 421 GTGAAGAAATCATGCTGATATGATGTCCTGATTTATTTCAAAAAGATGTGGTTG 480
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DB 511 GCGAGGCCAATCGGAGATGTATGGCCGATTTACTTATGAAGAAGATGTTGTTCTC 570
OY 481 ATTAACATTAATATGCTTTGGAGCTCTAGTTTCTAAGTTTAATTCAGAAAGACTT 540
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DB 571 GTACAGATACAGTACGACACTTGGGCTTTGGATTATGAGTCTTAAGTCCCGGACTA 630
OY 541 AATGCGCCGTAATGCGCGCTTAAAGATCAATGATGCTTGCCTTGCGATTAA 598
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DB 631 AATGTACAGGAATATGTGGCTTCAGAGATCAGTGTGCGCTCAAGTGCATCAGA 688

RESULT 4
A1517692 671 bp mRNA linear EST 19-APR-2001
LOCUS GH28740.5prtime GH Drosophila melanogaster head POT2 Drosophila
DEFINITION melanogaster cDNA clone GH28740 5prtime similar to U51050:
Drosophila melanogaster alpha esterase (ae7) gene, partial cds,
mRNA sequence.
ACCESSION A1517692
VERSION A1517692.1 GI:4420792
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
REFERENCE Drosophila melanogaster
AUTHORS Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G. M.
BDGP/HMML Drosophila EST project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 287 row: D column: 4
High quality sequence stop: 538.
Location/Qualifiers
1. 671
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH28740"
/clone_lib="GH Drosophila melanogaster head POT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: POT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
POT2.. Plasmid cDNA library."

BASE COUNT 155 a 170 c 193 g 153 t
ORIGIN
Query Match 15.0%; Score 256.6; DB 9; Length 671;
Best Local Similarity 65.4%; Pred. No. 3.9e-59;

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[illegible]

Plate: RH 143 row: D column: 1
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 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="RH14337"
 /clone_lib="RH Drosophila melanogaster normalized Head
 pPic-1"
 /sex="male and female"
 /dev_stage="Adult"
 /lab_host="DH5-alpha Tona"
 /note="Organ: head; vector: pPic1, Site_1: XhoI, Site_2:
 BamHI; Library was kindly generated by Piero Carninci at
 the RIKEN. The library was normalized and excised using
 Cre recombinase. Plasmid cDNA library."
 BASE COUNT 126 a 147 c 167 g 129 t
 ORIGIN
 Query Match 14.9%; Score 254.4; DB 13; Length 569;
 Best Local Similarity 65.5%; Pred. No. 1.5e-58;
 Matches 372; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
 Oy 17 GTTTATGAGCAAAATTAATAATGGAAGATTAAATGCAATTAAGTAATAGTTTAACTATC 76
 1 GCTTTGTGAGCGCTTGGCGGTGGCGCCCTCAAAACCATTGACATAAAGTCACAGATAC 60
 Oy 77 GTTTAACTACCAATGAACGGGTGAGTGAAGTGAATATGCAAAAGTGAAGGCTTA 136
 61 GCCAGTCGACCAATGAACAGTTGTCCGCCGACAGGAGTACGGCAAGTGAGGGATCA 120
 Oy 137 AACGTTTAACTGTGACATGATCTCCCTACGTTTGAAGGATACCGTACCCGAC 196
 121 AACGCTATCTCTACAGATGCGCTTACTTCAGCTTGAGAGGTATCCCGTACCCGAC 180
 Oy 197 CGCCAGTGGGTGAGCTGAGATTTTAAAGCACCCGACACCAACCCCTGGGATGCTGC 256
 181 CTCGGGTGGGGAGTGGCGGTTAAGGCCCTCAGAGGCCCATTCCTCGGAGCGAGTTC 240
 Oy 257 GTGATTTGTCATCTATAAGATTAAGTACGTCGCAAGTTGATTTTAAAGGCAAGTGT 316
 241 GCGACTGCGACGCCGACCGAAGATTAAGGCGCGTCAAGTGCAGTTCCTTCGATTAAGTAG 300
 Oy 317 GGGGCTCAGAGGATTTGCTATCTATACCTAAGTGTCTATACGATTAATCTAAATCCGAACTA 376
 301 AGGAGCTCCGAGACCTCCCTCTATCTCAATGTGTACCCAAATGTGAAGTGAAGCCGACAAAG 360
 Oy 377 AACGTCCTTTTATGATACATACATACATGCTGTGCTTTTATTCGGTGAATAATCATCTG 436
 361 CTCGCCCGGTTATGTTGGATTACAGGAGGAGGCTCTATTATCGCGGAGGCCAATCCGG 420
 Oy 437 ATATGATGCTGCTGATTTATTCATTAAGAAAGATGTGCTGTGATTAACATACATATC 496
 421 AATGATATGACCCCGGATACCTTATGAAAGAAATGTTCTTCGACAGATACAGTACC 480
 Oy 497 GTTTGGAGAGCTAGAGTTTCTAAGTTTAATTCAGAAACCTTAATGCGCCGGTAATG 556
 481 GACTTGGGCGCTTTGGGATTTATGAGCTTAAAGTCCCGCAGCTAATGTAAGGAATG 540
 Oy 557 CCGGCTTAAGAAATCAAGTCAAGTCAAGCTT 584
 541 CTGGCTCAAGATCAAGTCTGCTGCGCTT 568
 RESULT 6
 B1628316 674 bp mRNA linear EST 10-SEP-2001
 LOCUS
 DEFINITION
 Drosophila melanogaster cDNA clone RH56862.5 similar to alpha-Est7
 P1an000112 Go: [carboxylesterase (Go:0004091)]; carboxylesterase
 (Go:0004091)] located on: 3R 84D5-84D5;: 08/22/2001, mRNA sequence
 B1628316
 ACCESSION
 B1628316.1 GI:15530524

KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster

REFERENCE
AUTHORS
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S., Mungall, C.J., Nuno, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.

TITLE BDGP/HMI RH Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST/estfruitfly.berkeley.edu>
Plate: RH.566 row: G column: 10
High quality sequence stop: 558.
Location/Qualifiers
1. 674
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH56682"
/clone_lib="RH Drosophila melanogaster normalized Head
pPic-1"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tona"
/note="Organ: Head; Vector: pPic1; Site:1: XhoI; Site:2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
BASE COUNT 153 a 170 c 195 g 155 t 1 others
ORIGIN

Query Match 14.6%; Score 250; DB 13; Length 674;
Best Local Similarity 65.2%; Pred. No. 2.5e-57;
Matches 367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 1 ATGAATTCACAGCTTACGTTGATGAGAAATTTAAATGAGATTTAAATGATTTGAAAT 60
DB 111 ATGAAATGAACCTCGGCTTTGTGAGCGCTTGGCGGCTCAAAACCATGAGCAT 170
QY 61 AAGTTTAACTATCGTTTAACATGCAATGAACGGTGGAGCTGAACGATATAGGC 120
DB 171 AAAGTCCAGACATGTCGCCAGTGCACCAATGAACAGTTGTCCGCGACGAGATACGC 230
QY 121 AAAGTGAAGCGCTTAACGTTTAACGTGTAGAGATTTCTACAGTTTGAAGGT 180
DB 231 CAAGTAGAGGGTATCAAGCGCTATCTCTACAGATGTGCCCTACTTACAGTTGAGGT 290
QY 181 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCACGACACACA 240
DB 291 ATCCCGTACGCCCAACCGCTCGGTGGGGAGTGGGCTTTAAGGCCCTCCAGAGGCCCAT 350
QY 241 CCCGTGAGTGTGGCTGATGTTGTCATCATTAAGATTAAGTACGCAAGTTGATTT 300
DB 351 CCCGTGAGGAGGATTCGCCAGCTGCAGCCAGCCGAGATTAAGGCCGCGCCAGGTGCAATTC 410
QY 301 ATACGGGCAAGTGTGGCTCAGAGATTTCTATACCTAAGTCTATACGAATAT 360
DB 411 GCTTGATAGTAGTAGGGCTCCGAGAGCTGCCTATCTCATGTGTAACCAACAT 470
QY 361 CTAAATCCCAAACTAAAGCTCCGTTTGTATATACATACATGTTGGTTTATTATC 420
DB 471 GTAAAGCCCAACAAGCTCCCGGTGTATGTTGATTCACGAGGAGGCTTCATTATC 530
QY 421 GTGAAATATGCTGATATGATGTCGATATTATTTAAAGGATGTGGTTG 480

DB 531 GCGAGCCCAATCGCGAGATGATGGCCCGGATTTATGAAGAAGATGTTGCTC 590
QY 481 ATTAACATTAACATATCGTTTGGAGCTCTAGCTTTCTAAGTTAAATTCAGAACCTT 540
DB 591 GTACAGATTAACATATCGCTTGGAGCTTGTGATTTAGTCTTAAGTCCCGGAGCTA 650
QY 541 AATGTCGGGATATGCGGCT 563
DB 651 AATGTACAGAAATGCTGGCT 673

RESULT 7
BI635372
LOCUS
DEFINITION SD16705.5,prime SD Drosophila melanogaster Schneider L2 cell culture
POT2 Drosophila melanogaster cDNA clone SD16705 5 similar to
alpha-Est7: FBan0001112 GO: [carboxyesterase (GO:0004091);
carboxyesterase (GO:0004091)] located on: 3R 84D5:: 05/18/2001
, mRNA sequence.
BI635372
BI635372.1 GI:15537582
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Drosophila melanogaster
fruit fly.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 676)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP
BDGP/HMI Drosophila EST Project
Unpublished (2001)
COMMENT Contact: Stapleton, M.
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST/estfruitfly.berkeley.edu>
Plate: SD.167 row: A column: 5
High quality sequence stop: 641.
Location/Qualifiers
1. 676
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="SD16705"
/clone_lib="SD Drosophila melanogaster Schneider L2 cell
culture POT2"
/lab_host="DH5-alpha"
/note="Vector: POT2; Site:1: EcoRI; Site:2: XhoI; Sized
fractionated cDNAs were directly ligated into POT2.
Plasmid cDNA library."
BASE COUNT 155 a 173 c 194 g 154 t
ORIGIN

Query Match 14.6%; Score 249.4; DB 13; Length 676;
Best Local Similarity 65.2%; Pred. No. 3.7e-57;
Matches 367; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 1 ATGAATTCACAGCTTACGTTGATGAGAAATTTAAATGAGATTTAAATGATTTGAAAT 60
DB 114 ATGAATGAACCTCGGCTTTGTGAGCGCTTGGCGGCTCAAAACCATGAGCAT 173
QY 61 AAGTTTAACTATCGTTTAACATGCAATGAACGGTGGAGCTGAACGATATAGGC 120
DB 174 AAAGTCCAGACATGTCGCCAGTGCACCAATGAACAGTTGTCCGCGACGAGATACGC 233
QY 121 AAAGTGAAGCGCTTAACGTTTAACGTGTAGAGATTTCTACAGTTTGAAGGT 180
DB 234 CAAGTAGAGGGTATCAAGCGCTATCTCTACAGATGTGCCCTACTTACAGTTGAGGT 293
QY 181 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCACGACACACA 240

Db 294 ATCCGTCAGCCGACGCTCCGGTGGGAGTTCGGTTAAGCCCTCAGAGCCCAT 353
 QY 241 CCTGGGATGTGTGCTGATTTGTCATCATTAAGTACAGTCAAGTTGATTT 300
 Db 354 CCCTGGGAGGATGTCGATCGATCGACGACGAGATTAAGCCGCTCAGGTGAC 413
 QY 301 ATAAAGGCGCAAGTGTGTGCTCAGAGATTTCTATACCTAGTGTCTATAGCAAT 360
 Db 414 GCTTCGATTAAGTAGAGGCTCCGAGATGCTCTATCATGTGTACACCAACAT 473
 QY 361 CTAATCCCGAATAAAGCTCCGTTTACTATACATACATGAGTGGGTTTATATC 420
 Db 474 GGAAGCCCGCAGAGCTGCGCGGTATGTTGATTCACGAGAGGCTTATATC 533
 QY 421 GGTGAATCATCGTATGATGCTGCTGATTTTCAATTAAGAGATGTGTG 480
 Db 534 GCGGAGCCCAATCGGGAATGATATGCGCGGATCTTATGAAGAAGATGTGTCTC 593
 QY 481 ATTAACATCAATATGCTTTGGAGCTAGTTTTCAAGTTTAATTCAGAGACCTT 540
 Db 594 GTACAGATACAGTACGACTTGGGCTTTGGATTATGAGTCTTAAGTCCCGAGCTA 653
 QY 541 AATGTCGCGGTAATGCGGCT 563
 Db 654 AATGTACAGAAATGCTGCT 676

RESULT 8
 LOCUS B1639486 660 bp mRNA linear EST 10-SEP-2001
 DEFINITION SD22067.5prtime SD Drosophila melanogaster cDNA clone SD22067 5 similar to
 POT2 Drosophila melanogaster cDNA clone SD22067 5 similar to
 alpha-Est7: Fban0001112 GO: [carboxyesterase (GO:0004091);
 carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5; : 05/19/2001
 , mRNA sequence.

ACCESSION B1639486
 VERSION B1639486.1 GI:15541696
 KEYWORDS EST
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 660)
 REFERENCE Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S. and Rubin, G. M.
 BDGP/HMI Drosophila EST Project
 Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
 Plate: SD.220 row: F column: 7
 High quality sequence stop: 546.

FEATURES
 SOURCE
 1..660
 Location/Qualifiers
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="SD22067"
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 culture pot2"
 /lab_host="DH5-alpha"
 /note="Vector: pot2; Site.1: EcoRI; Site.2: XhoI; Sited
 fractionated cDNAs were directly ligated into pot2.
 Plasmid cDNA library."

BASE COUNT 169 a 170 c 176 g 145 t
 ORIGIN

Query Match 14.5%; Score 248.6; DB 13; Length 660;
 Best Local Similarity 64.3%; Pred. No. 6e-57;
 Matches 390; Conservative 0; Mismatches 214; Indels 3; Gaps 1;

QY 535 GACCTAATGTGCGCGGATGATGCCCTTAAGTCAATGCGCTTGCTGATT 594
 Db 9 GAGCTAATGATGACGAGAAATGCTTGCCCTAAGAGATCAGGTGCGCCCTCAAGTGATC 68
 QY 595 AAAAATATGTGCGCACTTTGGTGCATCCGATTAATATTACAGCTTTGGAAGT 654
 Db 69 AAGAACATTTGGCGTAGTTTCGCGGAGATCCCACTGCATCAGTCTTTTGGAGAGAT 128
 QY 655 GCGGTCGCGCTCACTACCATGATGTTAAGCGAACAATCGCGCTTTCCAT 714
 Db 129 GCTGGAGCGGCTTCACCTACATGATGATACCGATACAGCCAGGCTTTTCAT 188
 QY 715 CGTGTACTAATATGTGGGTAATGCTATTGTCATTGGC---TAATACCAATGTCAA 771
 Db 189 GCGGCAATCTTCGACGTGCGGAGTGCATTTGCTTGGCCTACAGGCGCATTTAC 248
 QY 772 CATCGTCCTTCACCTTACGCAATTTGCGCGCTAATAGGTGAGATTAATAGAT 831
 Db 249 CATATCCCTACAGATAGCAAGCTGTTGGCTACAAAGGCGGAGACACAGAGAT 308
 QY 832 GTTTGGATTTCTTATGAAGCCAGCCAGAGATTTAATAACTTGAGGAAAAAGTT 891
 Db 309 GTGCTGAGTTCTTGCAAGCTAAGGCCAAGATCTTATCGCGTGAGGAAATGTC 368
 QY 892 TTAAGCTAAGAGCGTACAAATTAAGGTCATGTTCTTGGTCCCATGTTAGCCA 951
 Db 369 CTGACACTGGAGGAACGATGACAGATATATGTTGCTTGCCCATTCCTGGAACA 428
 QY 952 TATACAGCCGCTGATTTGTCTTACCCAAACATCTCGGGAATGTTAAACTGCTTGG 1011
 Db 429 TTTCCACGCGCCGAAATGATGATATCCAAAGCTCCAAAGAGATGATGAAGACGCGCTGG 488
 QY 1012 GGTAAATGATACCCACTATGATGATGATGATGATGATGATGATGATGATGATGAT 1071
 Db 489 AGTAATCCATCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 548
 QY 1072 ATTTTAAAGCAATGCTTATGAGATTTGAAGATTTGAATTTGTCATTTTGGCCA 1131
 Db 549 GAGGTAATGCTTATGCGGAGAGCTGAGAGCTGATGCTGACACCTTTCAATTC 608
 QY 1132 ACTGAAT 1138
 Db 609 AAGGATT 615

RESULT 9
 LOCUS B1614181 673 bp mRNA linear EST 07-SEP-2001
 DEFINITION RH43493.5prtime RH Drosophila melanogaster normalized Head pF1c-1
 Drosophila melanogaster cDNA clone RH43493 5 similar to alpha-Est7:
 Fban0001112 GO: [carboxyesterase (GO:0004091); carboxyesterase
 (GO:0004091)] located on: 3R 84D5-84D5; : 08/18/2001, mRNA sequence.
 B1614181
 VERSION B1614181.1 GI:15509706
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 673)
 REFERENCE Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
 J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
 R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,
 Mungall, C. J., Nunoo, J., Pacle, J., Parag, V., Park, S.,
 Phoumenavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin
 G. M.
 BDGP/HMI RH Drosophila EST Project
 Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu

Plate: RH.434 row: H column: 9

High quality sequence stop: 553.

FEATURES

source

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1. 673
/organism="Drosophila melanogaster"
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pfic-1"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tona"
/note="Organ: head; Vector: pfic1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
```

BASE COUNT 153 a 169 c 195 g 155 t 1 others

ORIGIN

Query Match 14.5%; Score 248.4; DB 13; Length 673;
Best Local Similarity 65.0%; Pred. No. 6.9e-57;
Matches 366; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

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OY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGCAAGTTAATGATGAAAT 60
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DB 111 ATGAATTAAGAACCTCGGCTTTGTGAGCGCTTGGGCGCCCAAAACCATGACAT 170
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OY 61 AAGTTTTAACTATCTTAACTACCAATGAAACGGTGTAGCTGAATGATGCG 120
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DB 171 AAGTCCAGAGATATCCGACGATGCAATGAACATTTGCGCCGACGAGATACGC 230
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OY 121 AAGTGAAGCGCTTAAAGCTTAACTGTAGAGATCTTAACTACAGTTTGAAGGT 180
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DB 231 CAAGTGGGGTATCAAGCTCTATCTCTAGAGTGTCCCTACTCAGCTTGCAGGCT 290
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 ATACCGTAGCCCAACGCCAGTGGGATGAGATTAAAGCCCGCCAGCCACACA 240
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
DB 291 ATCCCGTAGCCCAACGCCAGTGGGATGAGATTAAAGCCCGCCAGCCACAT 350
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OY 241 CCTGGAGTGTGCTGATGTTGTCATCAATTAAGATAGTCAAGTGTGATTTT 300
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 351 CCTGGAGAGAGTGTGCTGATGTCAGACGACCAAGATTAAGCCGTCAGAGTCTC 410
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 301 ATAAAGGCAAGTGTGCTGACAGAGATGTCTAATACCTAAGTGTCTATACCAAT 360
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 411 GTCTTCGATTAAGTAGAGGCTCGAGACTGCTCTATCTCAATGTCTACCAACAT 470
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 361 CTAAATCCGAACCTAAAGCCGTTTGTATACATACATGAGTGTGTTATATC 420
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 471 GTGAAGCCCAACAGCTGCGCCGTTATGATGATTAACGAGAGAGCTTATTATC 530
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 421 GGTGAATATCATGCTGATATGATGCTGATATTATTAATAAAGATGTGCTTG 480
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 531 GCGAGGCAATCGGAGATGATGAGCCGAGTACTTTAAGAAAGATGTGCTC 590
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 481 ATTAACATTAATATGCTTGGAGCTCTAGAGTTTCTAAGTTTAAATTCAGAGCCTT 540
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 591 GTACGATTAAGTAGACACTTGGGCTTTGGGATTTAGTCTTAAGTCCCGGACCTA 650
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 541 AATGTCCCGGTATGCGGCT 563
    ||||| ||| ||| ||||| |||||
DB 651 AATGTACAGGAATGCTGGCT 673
    ||||| ||| ||| ||||| |||||
```

RESULT 10
BI614443 672 bp mRNA linear EST 07-SEP-2001
LOCUS
DEFINITION RH43812: Sprime RH Drosophila melanogaster normalized Head, pfic-1
Drosophila melanogaster cDNA clone RH43812 5 similar to alpha-Est7:
Fban0001112 GO: [carboxyesterase (GO:0004091); carboxyesterase

ACCESSION BI614443
VERSION BI614443.1 GI:15509968
KEYWORDS EST.
SOURCE Drosophila melanogaster
ORGANISM fruit fly.

REFERENCE 1 (bases 1 to 672)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
J., Champey, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,
Mungall, C.J., Nunoo, J., Pacleb, J., Pargass, V., Park, S.,
Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
G.M.

TITLE BDGP/HHMI RH Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: RH.438 row: A column: 12
High quality sequence stop: 554.

FEATURES

source

```
1. 672
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1lb="RH Drosophila melanogaster normalized Head
pfic-1"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tona"
/note="Organ: head; Vector: pfic1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
```

BASE COUNT 154 a 169 c 194 g 155 t

ORIGIN

Query Match 14.4%; Score 246.8; DB 13; Length 672;
Best Local Similarity 64.9%; Pred. No. 1.9e-56;
Matches 365; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

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OY 1 ATGAATTTCAACGTTAGTTGATGAGAAATTAATGCAAGTTAATGATGAAAT 60
    ||||| ||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| |||
DB 111 ATGAATTAAGAACCTCGGCTTTGTGAGCGCTTGGGCGCCCAAAACCATGACAT 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 AAGTTTTAACTATCTTAACTACCAATGAAACGGTGTAGCTGAATGATGCG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 171 AAGTCCAGAGATATCCGACGATGCAATGAACATTTGCGCCGACGAGATACGC 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 121 AAGTGAAGCGCTTAAAGCTTAACTGTAGAGATCTTAACTACAGTTTGAAGGT 180
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 231 CAAGTGGGGTATCAAGCTCTATCTCTAGAGTGTCCCTACTCAGCTTGCAGGCT 290
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 ATACCGTAGCCCAACGCCAGTGGGATGAGATTAAAGCAACCCAGCAGACACA 240
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
DB 291 ATCCCGTAGCCCAACGCCAGTGGGATGAGATTAAAGCCCGCCAGAGGCCAT 350
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 241 CCTGGAGTGTGCTGATGTTGTCATCAATTAAGATAGTCAAGTGTGATTTT 300
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 351 CCTGGAGAGAGTGTGCTGATGTCAGACGTCAGAGAGTGTGCGCCGACGAGTCTC 410
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 301 ATAAAGGCAAGTGTGCTGACAGAGATGTCTAATACCTAAGTGTCTATACCAAT 360
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 411 GTCTTCGATTAAGTAGAGGCTCGAGAGACTGCTCTATCTCAATGTCTACCAACAT 470
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 361 CTAAATCCGAACCTAAAGCCGTTTGTATATACATACATGAGTGTGTTTATTATC 420
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


RESULT 12	LOCUS	DEFINITION	ACCESSION	VERSION	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
170	AAAGTCCAGCAGTATGCGCAGTCCAGC	AAAGTCCAGCAGTATGCGCAGTCCAGC	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
121	AAAGTGAAGAGCGCTTAAACGTTTAACTGTGTACGATGATTCCTTACTACATGTTTGAGGGT	AAAGTGAAGAGCGCTTAAACGTTTAACTGTGTACGATGATTCCTTACTACATGTTTGAGGGT	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
230	CAAGTGAAGAGCGCTTAAACGTTTAACTGTGTACGATGATTCCTTACTACATGTTTGAGGGT	CAAGTGAAGAGCGCTTAAACGTTTAACTGTGTACGATGATTCCTTACTACATGTTTGAGGGT	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
181	ATACCGTACGCCAACCGCCAGTGGGTGAGCGATTTTAAAGCACCCACGACCAACA	ATACCGTACGCCAACCGCCAGTGGGTGAGCGATTTTAAAGCACCCACGACCAACA	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
290	ATCCCGTACGCCAACCGCCAGTGGGTGAGCGATTTTAAAGCACCCACGACCAACA	ATCCCGTACGCCAACCGCCAGTGGGTGAGCGATTTTAAAGCACCCACGACCAACA	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
241	CCCTGGATGATGTTGGCTGATGTTGTTGCAATTCATTAAGATAGTCAAGTCAATGATTTT	CCCTGGATGATGTTGGCTGATGTTGTTGCAATTCATTAAGATAGTCAAGTCAATGATTTT	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
350	CCCTGGATGATGTTGGCTGATGTTGTTGCAATTCATTAAGATAGTCAAGTCAATGATTTT	CCCTGGATGATGTTGGCTGATGTTGTTGCAATTCATTAAGATAGTCAAGTCAATGATTTT	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
301	ATTAACGGCAAGTGTGTGCTCAGAGGATTTGCTATACCTAAGTCTATACGATTAAT	ATTAACGGCAAGTGTGTGCTCAGAGGATTTGCTATACCTAAGTCTATACGATTAAT	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
410	GTCTTCGATTAAGTAGAGGCTCCGAGACTGCTCTATCTCAATGTGTACCAACAAAT	GTCTTCGATTAAGTAGAGGCTCCGAGACTGCTCTATCTCAATGTGTACCAACAAAT	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
361	CTAAATCCCGAACCTTAACGCTCCGCTTTAGTATACATACATGTTGTGTGTTTATATC	CTAAATCCCGAACCTTAACGCTCCGCTTTAGTATACATACATGTTGTGTGTTTATATC	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
470	GTGAAGCCCGAACGAGGCTCCGCTTTAGTATACATACATGTTGTGTGTTTATATC	GTGAAGCCCGAACGAGGCTCCGCTTTAGTATACATACATGTTGTGTGTTTATATC	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
421	GGTGAATATCATCTGTGATATGTATGTCGATTAATTCATTAAGATAGTCAATGATTTT	GGTGAATATCATCTGTGATATGTATGTCGATTAATTCATTAAGATAGTCAATGATTTT	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
530	GCGCGAGGCAATCGGGAATGTATGAGCCCGGATTTACTTTATGNNAAACATGTGTCTC	GCGCGAGGCAATCGGGAATGTATGAGCCCGGATTTACTTTATGNNAAACATGTGTCTC	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
481	ATTACATATACATATCTGTTGGAGCTCTAGGTTTCTAAGTTTAATTACAGAACCTT	ATTACATATACATATCTGTTGGAGCTCTAGGTTTCTAAGTTTAAATTACAGAACCTT	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
590	GTACACGATATACAGTACAGCTTGGGCTTTGGATTTATGATCTTAAGTCCCGGAGCTTA	GTACACGATATACAGTACAGCTTGGGCTTTGGATTTATGATCTTAAGTCCCGGAGCTTA	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S., and Rubin, G. M.	BDGP/HMII <i>Drosophila</i> EST Project	Unpublished (2001), Contact: Stapleton, M. BDGP
541	AATGTGCCCGGTATATGCCGC	AATGTGCCCGGTATATGCCGC	AA113763	1	GI:3514566	fruit fly, <i>Drosophila melanogaster</i>	1 (bases 1 to 648)	Harvey, D., Brokstein		